

Research Article

Ying Yang, Jin Wang*, Shihai Xu*, Fei Shi, Aijun Shan

Calumenin contributes to epithelial-mesenchymal transition and predicts poor survival in glioma

<https://doi.org/10.1515/tnsci-2021-0004>

received July 20, 2020; accepted December 14, 2020

Abstract

Background – Calumenin (CALU) has been reported to be associated with invasiveness and metastasis in some malignancies. However, in glioma, the role of CALU remains unclear.

Methods – Clinical and transcriptome data of 998 glioma patients, including 301 from CGGA and 697 from TCGA dataset, were included. R language was used to perform statistical analyses.

Results – CALU expression was significantly upregulated in more malignant gliomas, including higher grade, IDH wildtype, mesenchymal, and classical subtype. Gene Ontology analysis revealed that CALU-correlated genes were mainly enriched in cell/biological adhesion, response to wounding, and extracellular matrix/structure organization, all of which were strongly correlated with the epithelial-mesenchymal transition (EMT) phenotype. GSEA further validated the profound involvement of CALU in EMT. Subsequent GSVA suggested that CALU was particularly correlated with three EMT signaling pathways, including TGF β , PI3K/AKT, and hypoxia pathway. Furthermore, CALU played synergistically with EMT

key markers, including *N*-cadherin, vimentin, snail, slug, and TWIST1. Survival and Cox regression analysis showed that higher CALU predicted worse survival, and the prognostic value was independent of WHO grade and age.

Conclusions – CALU was correlated with more malignant phenotypes in glioma. Moreover, CALU seemed to serve as a pro-EMT molecular target and could contribute to predict prognosis independently in glioma.

Keywords: calumenin, glioma, epithelial-mesenchymal transition

1 Introduction

In central nervous system, glioma is the most prevalent and fatal primary cancer in adults [1]. Despite a substantial body of improvements in therapy, the prognosis for most glioma patients is still dismal. Particularly for patients who suffered from higher grade glioma (WHO grade IV, glioblastoma, GBM), which is the most malignant and lethal type, the median survival remains less than 15 months [2,3]. There is a growing recognition that epithelial-mesenchymal transition (EMT) plays a key role in mediating tumorigenesis, stemness, invasiveness, resistance to radiochemotherapy, and early recurrence in glioma [4–7]. It is therefore imperative to identify novel EMT-related molecules for potential glioma diagnosis and intervention.

Calumenin (CALU) has been widely reported in a range of malignancies including head and neck cancer [8], endometrial cancer [9], colon [10] and colorectal cancer [11], lung cancer [10,12], melanoma [13], hepatocellular and pancreatic carcinoma [14], and breast cancer [15]. CALU, a calcium-binding protein localized in the endoplasmic reticulum (ER), is mainly involved in such ER functions as protein folding and sorting. Besides, CALU has recently been shown to influence cell mobility, migration, invasion, and metastasis during particular

* **Corresponding author: Jin Wang**, Department of Emergency, Shenzhen People's Hospital (The Second Clinical Medical College, Jinan University; The First Affiliated Hospital, Southern University of Science and Technology), Shenzhen 518020, China, e-mail: szph3022@szhospital.com, tel: +86-159-1414-1979

* **Corresponding author: Shihai Xu**, Department of Emergency, Shenzhen People's Hospital (The Second Clinical Medical College, Jinan University; The First Affiliated Hospital, Southern University of Science and Technology), Shenzhen 518020, China, e-mail: heykojnu@163.com

Ying Yang: Department of Pediatrics, Futian Women and Children Health Institute, Shenzhen 518045, China

Fei Shi, Aijun Shan: Department of Emergency, Shenzhen People's Hospital (The Second Clinical Medical College, Jinan University; The First Affiliated Hospital, Southern University of Science and Technology), Shenzhen 518020, China

events, such as tumorigenesis, wound healing, immune response, and coagulation [16–21]. Several studies have explored the relationship between CALU expression and survival and yielded relatively consistent results. In most types of cancer, a higher level of CALU in lesions indicated a more malignant phenotype and a shorter survival for patients.

However, the expression patterns and biological functions of CALU in gliomas have rarely been described. Only one study presented by Sreeranthreddy *et al.* [22] investigated the prognostic potential of serum CALU in GBM, which accounted for about 40% of pan-glioma. Here, we analyzed clinical and transcriptome data of 998 patients, aiming at exploring the role of CALU in gliomas.

2 Materials and methods

2.1 Sample and data collection

From Chinese Glioma Genome Atlas website (CGGA, <http://www.cgga.org.cn/>), we selected 301 glioma samples with mRNA microarray data. From The Cancer Genome Atlas website (TCGA, <http://cancergenome.nih.gov/>), we obtained 697 glioma patients with RNA-sequencing data. Clinical data, including WHO grade, IDH mutation status, molecular subtype, and prognosis, were also available. Thus, a total of 998 samples were included in the present study. Baseline characteristics of glioma samples in both datasets were summarized in Table S1. In CGGA_301 dataset, microarray data, which had already been normalized and centered (using GeneSpring GX 11.0 platform) by data provider, were directly utilized. However, in TCGA_697 dataset, RNAseq data (RSEM normalized, level 3) were log₂ transformed before data analysis. Because this study used online databases, it did not require approval of the Ethics Committee.

Ethical approval: The conducted research is not related to either human or animals use.

2.2 Statistical analysis

Statistical analyses were primarily performed with R language (version 3.6.2). A set of R packages, such as ggplot2, pROC [23], pheatmap, corrgram, circlize [24], and gsva, were used to handle corresponding calculations and to produce figures. Cox proportional hazard regression analyses were performed with coxph function

of survival package. Gaussian test was performed before data analysis that required Gaussian distribution. We performed Pearson correlation to calculate the correlation coefficient between CALU and every gene. Genes that strongly correlated with CALU were screened out with Pearson $|r| > 0.6$ in each dataset. Gene Ontology analysis (GO) of CALU-correlated genes was implemented based on DAVID [25] website (version 6.8, <https://david.ncifcrf.gov/>). For Gene Set Enrichment Analysis (GSEA) [26] and Gene Set Variation Analysis (GSVA) [27], a series of gene sets were obtained from the GSEA network (<http://software.broadinstitute.org/>). A *p*-value less than 0.05 was considered to be statistically significant. Two-sided significance tests were adopted throughout.

3 Results

3.1 CALU was significantly upregulated in GBM, IDH wildtype, mesenchymal, and classical subtype

According to the WHO grade system, CALU expression was analyzed in both CGGA and TCGA datasets, and the results congruently showed a significantly positive correlation between WHO grade and CALU expression (Figure 1a and d). Moreover, when IDH mutation status was defined as a subclassifier, we observed that IDH wild-type GBM exhibited the highest expression pattern of CALU in both CGGA and TCGA datasets. Besides, CALU expression in IDH mutant glioma seemed to be universally lower than that in IDH wildtype, across different WHO grade, except for lower grade glioma (LGG) in CGGA, which exhibited apparent trends although not significant (Figure 1b and e). Subsequently, the distribution of CALU expression among different molecular subtypes (defined by TCGA network) was investigated. As shown in Figure 1c and f, CALU was significantly upregulated in classical and mesenchymal subtype compared to neural and proneural subtype. These findings indicated that higher CALU expression was usually accompanied by higher malignancy potential of glioma.

3.2 CALU-related biological process

In total, 621 genes in CGGA cohort and 965 in TCGA cohort were identified as CALU-related genes. To ensure the

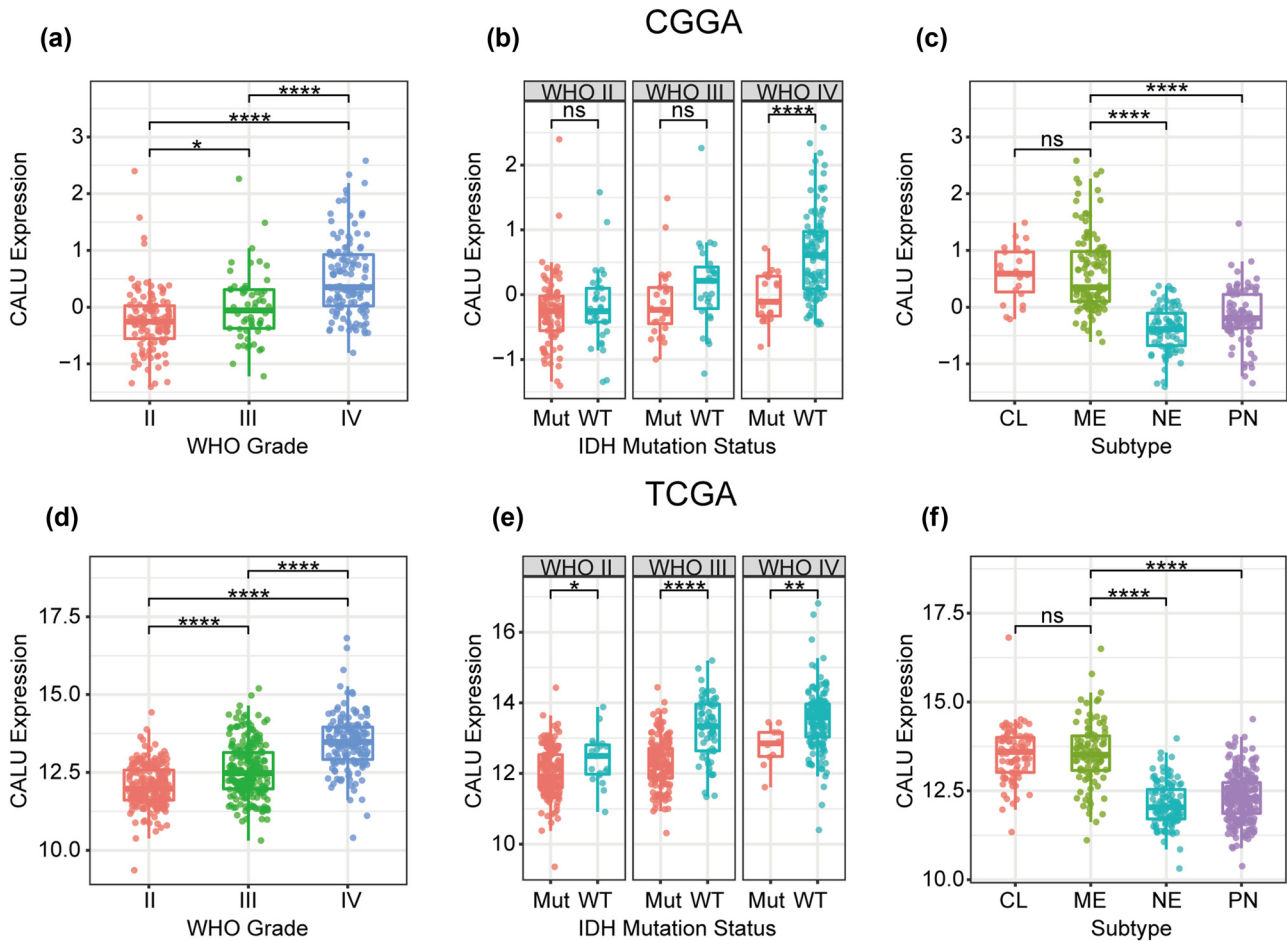


Figure 1: CALU expression in CGGA and TCGA dataset according to WHO grade (a and d), IDH mutation status (b and e), TCGA molecular subtype (c and f). * indicates p value < 0.05, ** indicates p value < 0.01, *** indicates p value < 0.001, **** indicates p value < 0.0001.

accuracy of the analysis, we subsequently identified 203 genes that overlapped between two independent cohorts, all of which were positively correlated with CALU (Table S2). Based on these genes, GO analysis revealed that genes that significantly correlated with CALU were highly enriched in a set of biological processes that correlated with EMT, including cell/biological adhesion, response to wounding, extracellular matrix/structure organization, collagen fibril organization, and collagen biosynthetic process (Figure 2a and b). Moreover, the association between CALU expression and EMT was revealed by GSEA analysis. CALU expression was found to be positively associated with the gene set of HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION in both CGGA dataset (NES = 1.897, FDR = 0.035) and TCGA dataset (NES = 1.818, FDR = 0.075) (Figure 2c and d). These findings suggested that CALU might be particularly involved in EMT process during glioma progression.

3.3 CALU-related EMT signaling pathways

To get further understanding of the association between CALU and EMT, seven gene sets, representing distinct EMT signaling pathways [28], were obtained from GSEA network (Table S3). Through cluster analyses, we identified 3 EMT signaling pathways (TGF- β , PI3K/AKT, and hypoxia), which might be strongly correlated with CALU (Figure 3a and b). Moreover, seven gene sets were transformed into seven metagenes with GSVA analysis, which were subsequently put into Pearson correlation together with CALU. According to Pearson r among seven metagenes and CALU, Corrgrams were plotted to assess their interrelationships. CALU was found to be positively correlated with TGF- β , PI3K/AKT, and hypoxia, in line with what we observed in clusters. However, only a very weak correlation was revealed between CALU expression and four other pathways (WNT, MAPK, NOTCH, and HEDGEHOG), which might be ascribed to signal noise (Figure 3c and d).

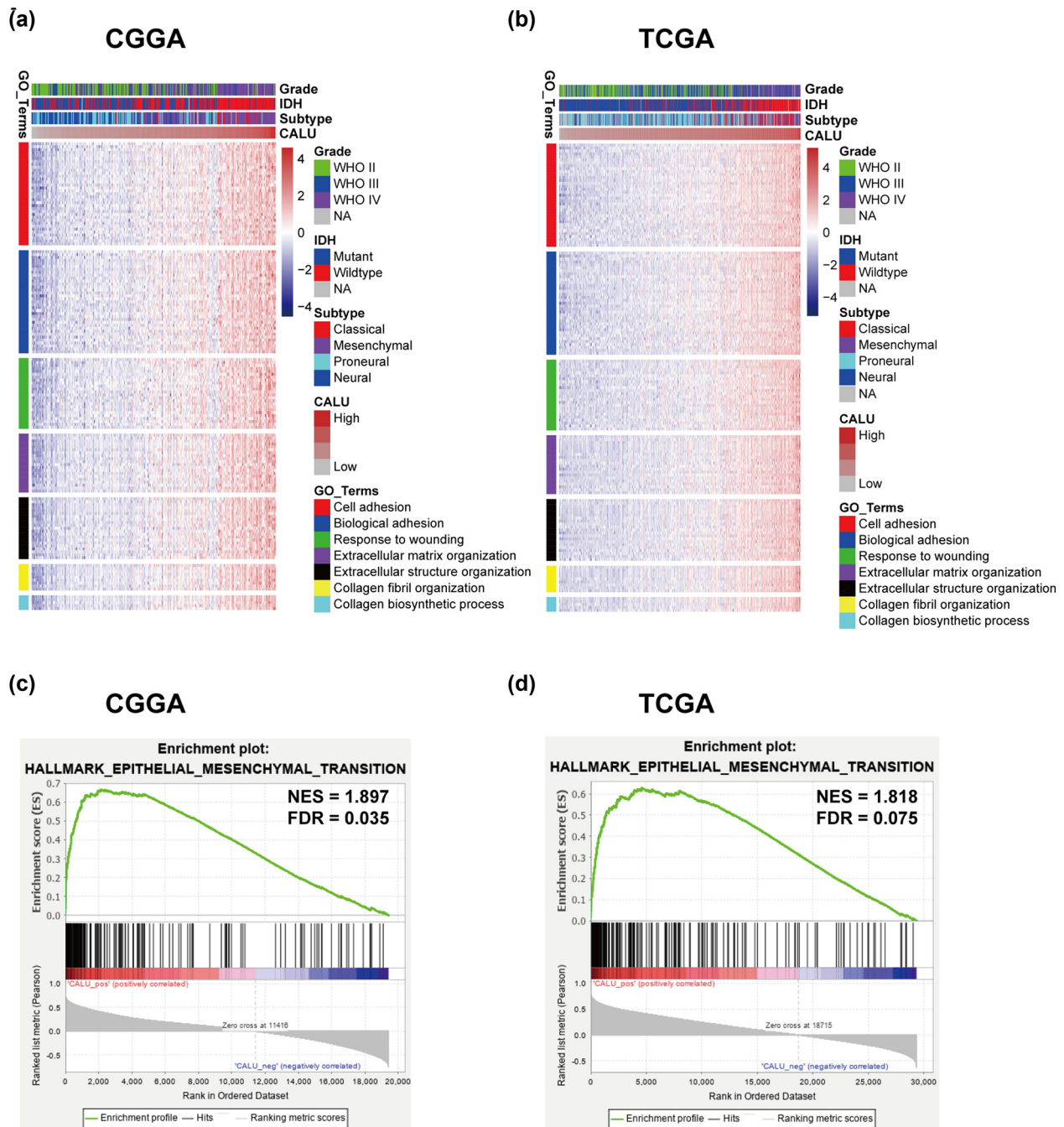


Figure 2: Functional enrichment of CALU in glioma. Gene Ontology analysis (a and b) and Gene set enrichment analysis (c and d).

3.4 CALU was synergistic with EMT key markers

Assuming that CALU played a vital role in regulating glioma EMT, we investigated the association between CALU and EMT markers, including *N*-cadherin, *E*-cadherin, snail, slug, and vimentin. Pearson correlation tests were performed with CALU and the above five EMT markers in both CGGA and TCGA. Circos plots were derived from Pearson *r*-values between CALU and five markers.

As shown in Figure 4a and b, CALU expression showed high agreement with *N*-cadherin, snail, slug, and vimentin. In contrast, a weak relationship between CALU and *E*-cadherin was found in Circos plots, which could be defined as a noise. Heretofore, some other members, including TWIST1/2, β -catenin, and ZEB1/2, have been reported as key markers in EMT [29]. Thus, we additionally put them into analysis together with CALU. CALU expression was tightly associated with TWIST1 in both CGGA and TCGA datasets (Figure 4c and d).

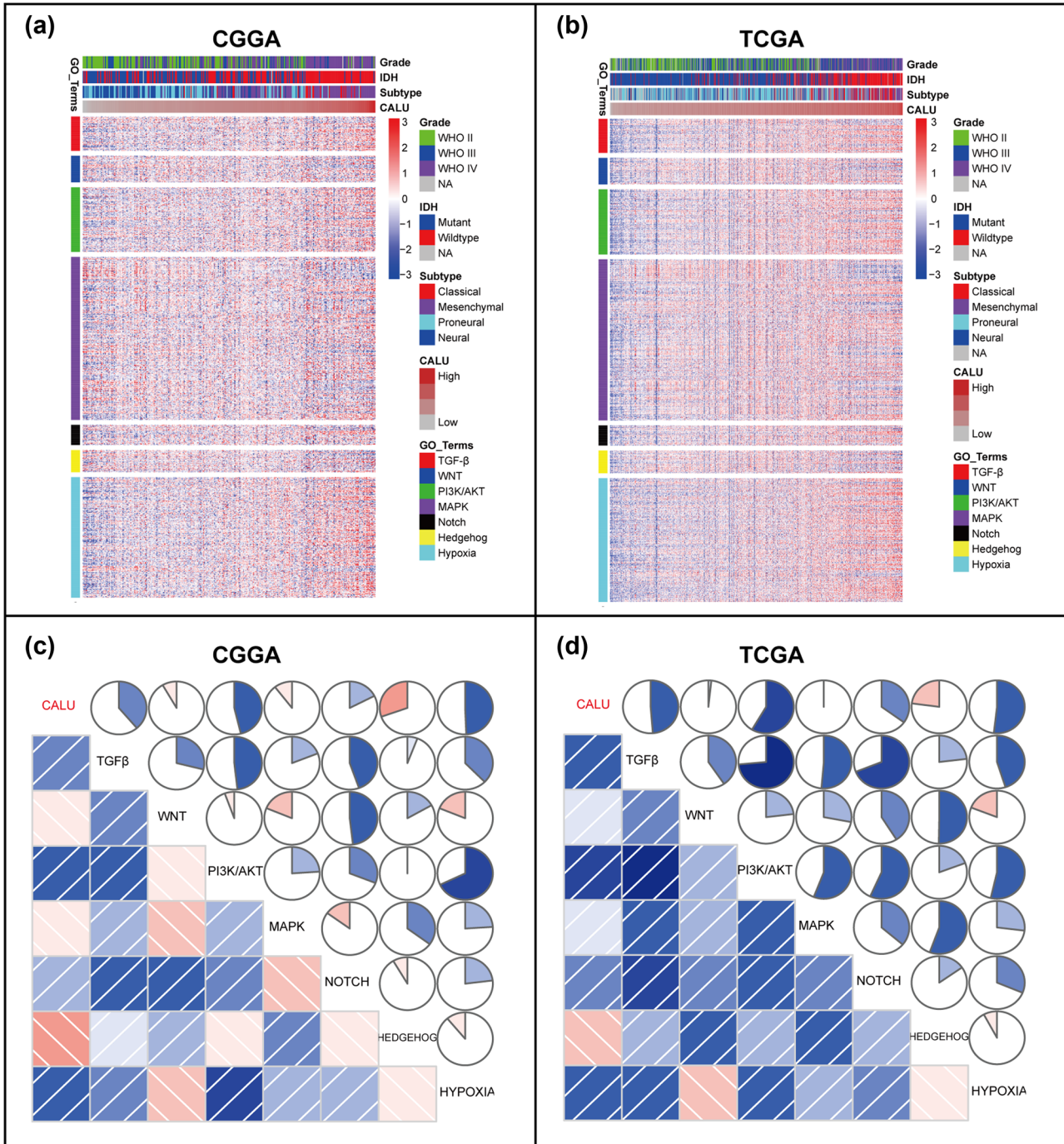


Figure 3: Cluster (a and b) and GSVA (c and d) of CALU-related EMT signaling pathways in glioma.

3.5 Higher CALU was related to a worse prognosis

To evaluate the prognostic value of CALU in glioma, Kaplan-Meier (KM) survival curves were plotted. In pan-glioma samples, when comparing the two groups defined by median CALU expression, we observed that higher CALU expression predicted a significantly shorter survival,

as shown in Figure 5a and d. Moreover, glioma patients were further divided into LGG and GBM subgroup. In both subgroups, patients with higher CALU exhibited universally worse survival than those with relatively lower CALU (Figure 5b, c, e and f), except for TCGA GBM, which also showed an apparent trend. To identify the independent effect of CALU on glioma prognosis, Cox regression analyses were performed with covariates including CALU

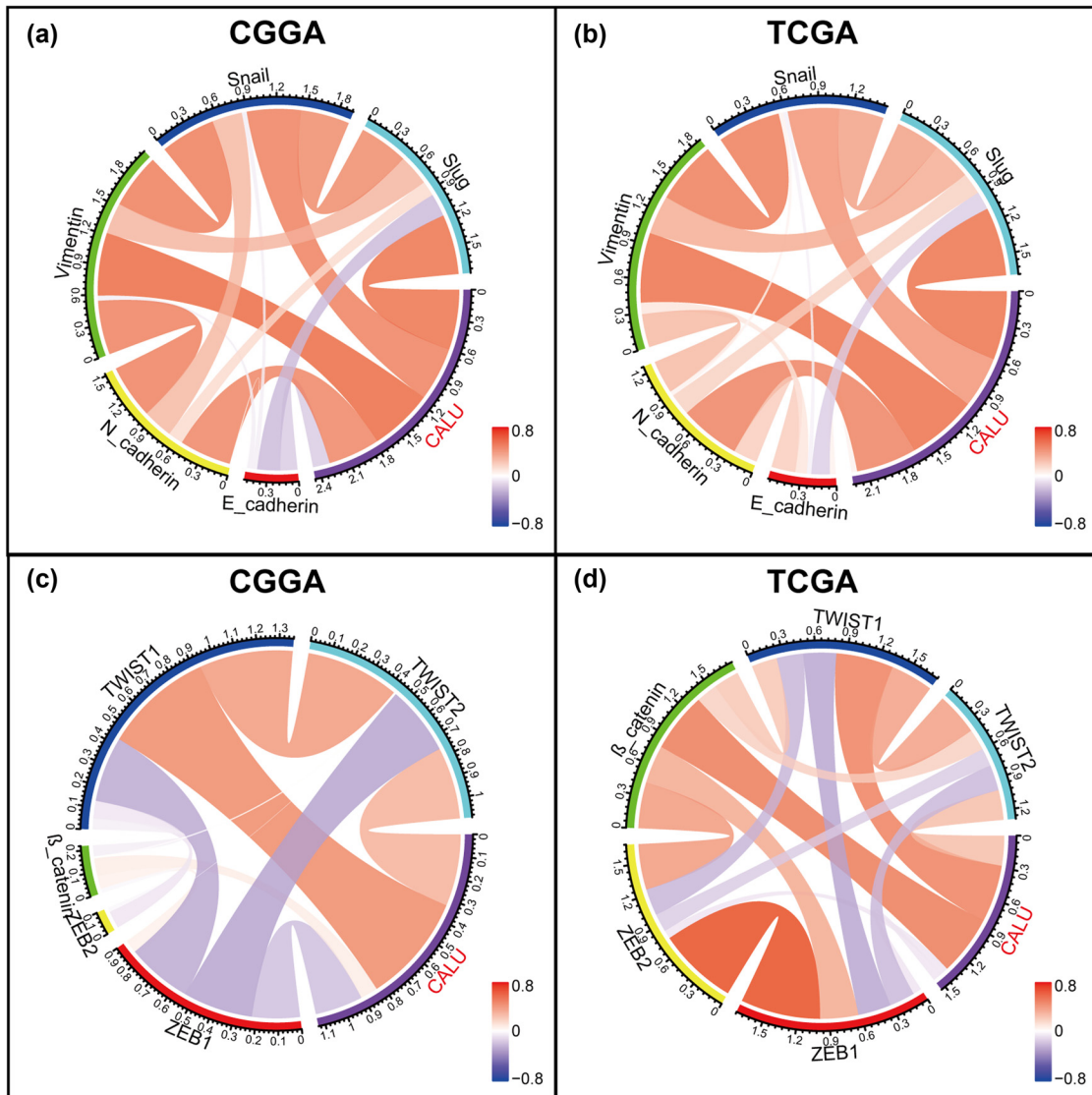


Figure 4: Correlation of CALU and EMT biomarkers in glioma (a and b, key biomarkers; c and d, other biomarkers).

expression, age, and WHO grade. Multivariate analyses revealed that CALU expression was a significant prognosticator independent of age and WHO grade in both CGGA and TCGA (Table 1).

4 Discussion

We explored CALU expression at transcriptional level via a cohort of 998 glioma samples and demonstrated that CALU expression was positively correlated with WHO grade. In addition, upregulation of CALU was usually paralleled with a more malignant and aggressive phenotype, such as IDH wildtype, classical subtype, and mesenchymal

subtype. Survival analyses revealed that higher CALU was related to a worse prognosis, independent of age and WHO grade. These results concordantly indicated that CALU might contribute to malignant progression of glioma, which were in line with the results from a previous GBM study [22]. Thus, unveiling the regulative mechanism of CALU may facilitate to develop a novel gene for potential glioma diagnosis and treatment.

CALU is one of the members of CREC protein family. This molecule family mainly consists of Cab45, Reticulocalbin 1, ERC-55, and CALU and is characterized by multiple EF-hand motifs with low affinity of Ca^{2+} -binding [30]. Under normal physiological conditions, CALU primarily participates in regulating Ca^{2+} -dependent protein folding, sorting and maturation in the ER [31], Ca^{2+} homeostasis [32,33],

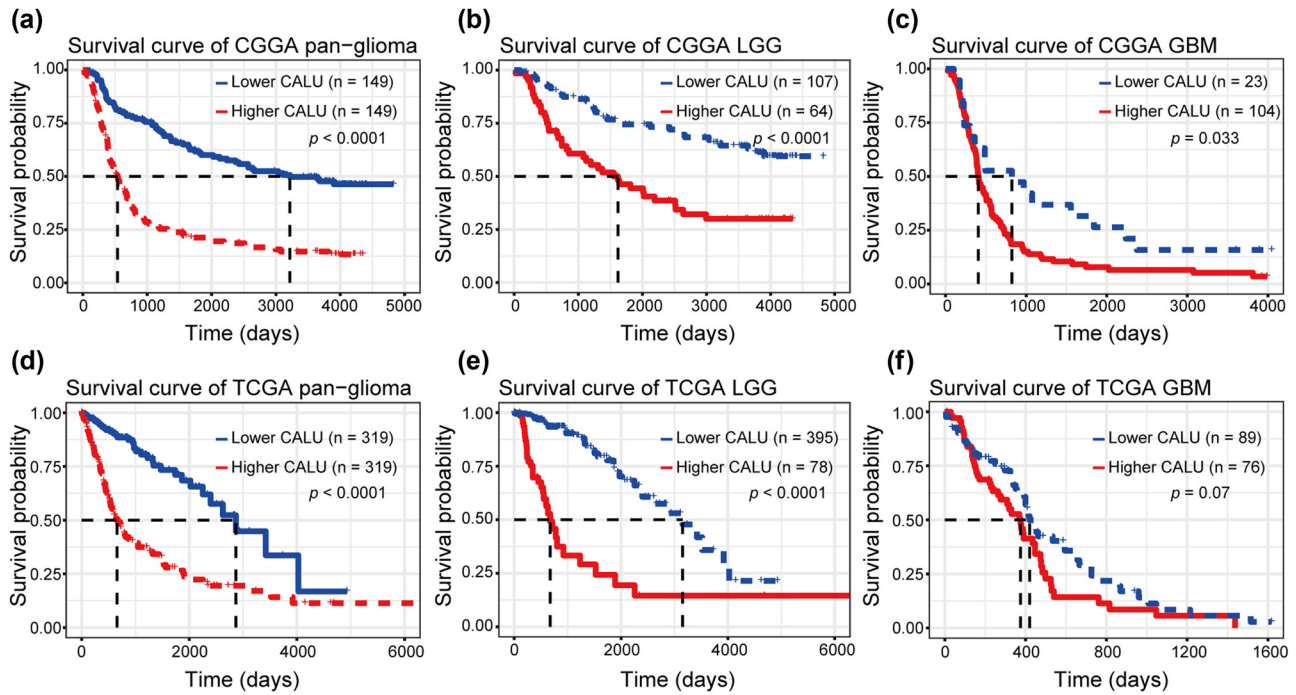


Figure 5: Survival analysis for CALU in pan-glioma (a and d), LGG (b and e), and GBM (c and f).

and muscle contraction/relaxation [34]. However, in tumor microenvironment, CALU was reported to play a critical role in promoting a series of malignant phenotypes including cancer cell survival [21], filopodia formation and cell migration [20], invasiveness [12], metastasis [15,35], cancer development [10], and resistance to chemotherapy [13]. So far, very little is known about the biological function of CALU in glioma. In the current study, GO analysis was performed to elucidate the biological function of CALU in glioma and it revealed that CALU showed high association with multiple EMT-related biological processes, including cell adhesion, biological adhesion, extracellular matrix/structure organization, collagen fibril organization, and collagen biosynthetic process. GSEA in both CGGA and TCGA further exhibited a remarkable relationship between CALU and EMT. EMT has been extensively reported to act as a critical mechanism not only in invasiveness, but also in early

recurrence and resistance to therapy in glioma [5,6,36]. These findings suggested that CALU might facilitate the malignant progression of glioma primarily via modulating EMT process, which has not yet been reported previously. Despite no report with regard to the pro-EMT effect of CALU, the other two members (Cab45 [37] and EFHD2 [38]) from the same protein family have been described in EMT regulation, which indirectly supported the potential role of CALU in glioma EMT.

We then chose a panel of EMT pathways and markers and examined their interrelationships with CALU. CALU was revealed to be highly associated with TGFβ, PI3K/AKT, as well as hypoxia pathway, indicating that CALU might regulate glioma EMT through these signaling pathways. Furthermore, most of the EMT biomarkers showed robust correlation with CALU, suggesting a synergistic effect among CALU and these members during EMT

Table 1: Cox regression analysis of overall survival in glioma

Covariates	CGGA_301				TCGA			
	Univariate		Multivariate		Univariate		Multivariate	
	HR (95% CI)	P	HR (95% CI)	P	HR (95% CI)	P	HR (95% CI)	P
Age	1.041 (1.027–1.055)	0.000	1.017 (1.004–1.031)	0.010	1.075 (1.062–1.087)	0.000	1.046 (1.032–1.060)	0.000
Grade	2.670 (2.221–3.210)	0.000	2.292 (1.867–2.814)	0.000	5.057 (3.915–6.532)	0.000	3.033 (2.273–4.047)	0.000
CALU	2.123 (1.746–2.581)	0.000	1.300 (1.033–1.636)	0.025	2.159 (1.892–2.463)	0.000	1.295 (1.094–1.534)	0.003

process. These findings further validated the potential role of CALU during EMT process in glioma.

In conclusion, CALU was upregulated in more malignant gliomas and predicted much worse prognosis. Furthermore, CALU seemed to be mainly involved in EMT process of glioma, potentially through modulating TGF β , PI3K/AKT, and hypoxia pathway. However, limitations still exist in this study. First, no biological validation was performed, which might compromise the robustness of results. Further researches focusing on *in vivo/in vitro* experimental studies are warranted. Second, despite the large sample in our study, data from TCGA and CGGA were mainly retrospectively collected, the control of data quality was heterogeneous, and some data were unavailable, which might lead to potential bias.

Acknowledgments: We appreciate the generosity of CGGA project and TCGA project for sharing data.

Funding: This work was supported by Medical Scientific Research Foundation of Shenzhen Health Commission (szfz2018022), Shenzhen Science and Technology Innovation Foundation (JCYJ20190806150005453), and Futian Public Welfare Scientific Research Project (FTWS2020099).

Author contributions: Ying Yang performed the analysis and wrote the manuscript. Shihai Xu, Fei Shi, and Aijun Shan provided technical support and analyzed the data. Jin Wang designed the study and reviewed the manuscript. Ying Yang and Shihai Xu provided financial support. All of the authors read and approved the final manuscript.

Conflict of interest: Authors state no conflict of interest.

Data Availability Statement: The datasets analyzed during the current study are available in the Chinese Glioma Genome Atlas repository, <http://www.cgga.org.cn/>, and in the The Cancer Genome Atlas repository, <http://cancergenome.nih.gov/>. All data generated during this study are included in this published article and its supplementary information files.

References

- [1] Meng X, Zhao Y, Han B, Zha C, Zhang Y, Li Z, et al. Dual functionalized brain-targeting nanoinhibitors restrain temozolomide-resistant glioma via attenuating EGFR and MET signaling pathways. *Nat Commun.* 2020;11(1):594.
- [2] Yang W, Wu PF, Ma JX, Liao MJ, Wang XH, Xu LS, et al. Sortilin promotes glioblastoma invasion and mesenchymal transition through GSK-3 β / β -catenin/twist pathway. *Cell Death Dis.* 2019;10(3):208.
- [3] Wei J, Ouyang X, Tang Y, Li H, Wang B, Ye Y, et al. ER-stressed MSC displayed more effective immunomodulation in RA CD4(+)CXCR5(+)ICOS(+) follicular helper-like T cells through higher PGE2 binding with EP2/EP4. *Mod Rheumatol.* 2019;30(3):509–16.
- [4] Ma YS, Wu ZJ, Bai RZ, Dong H, Xie BX, Wu XH, et al. DRR1 promotes glioblastoma cell invasion and epithelial-mesenchymal transition via regulating AKT activation. *Cancer Lett.* 2018;423:86–94.
- [5] Li C, Zheng H, Hou W, Bao H, Xiong J, Che W, et al. Long non-coding RNA linc00645 promotes TGF- β -induced epithelial-mesenchymal transition by regulating miR-205-3p-ZEB1 axis in glioma. *Cell Death Dis.* 2019;10(10):717.
- [6] Li H, Li J, Zhang G, Da Q, Chen L, Yu S, et al. HMGB1-induced p62 overexpression promotes snail-mediated epithelial-mesenchymal transition in glioblastoma cells via the degradation of GSK-3 β . *Theranostics.* 2019;9(7):1909–22.
- [7] Sun H, Long S, Wu B, Liu J, Li G. NKCC1 involvement in the epithelial-to-mesenchymal transition is a prognostic biomarker in gliomas. *Peer J.* 2020;8:e8787.
- [8] Wu W, Tang X, Hu W, Lotan R, Hong WK, Mao L. Identification and validation of metastasis-associated proteins in head and neck cancer cell lines by two-dimensional electrophoresis and mass spectrometry. *Clin Exp Metastasis.* 2002;19(4):319–26.
- [9] Voisin SN, Krakovska O, Matta A, DeSouza LV, Romaschin AD, Colgan TJ, et al. Identification of novel molecular targets for endometrial cancer using a drill-down LC-MS/MS approach with iTRAQ. *PLoS One.* 2011;6(1):e16352.
- [10] Nasri Nasrabadi P, Nayeri Z, Gharib E, Salmanpour R, Masoomi F, Mahjoubi F, et al. Establishment of a CALU, AURKA, and MCM2 gene panel for discrimination of metastasis from primary colon and lung cancers. *PLoS One.* 2020;15(5):e0233717.
- [11] Torres S, Bartolome RA, Mendes M, Barderas R, Fernandez-Acenero MJ, Pelaez-Garcia A, et al. Proteome profiling of cancer-associated fibroblasts identifies novel proinflammatory signatures and prognostic markers for colorectal cancer. *Clin Cancer Res.* 2013;19(21):6006–19.
- [12] Nagano K, Imai S, Zhao X, Yamashita T, Yoshioka Y, Abe Y, et al. Identification and evaluation of metastasis-related proteins, oxysterol binding protein-like 5 and calumenin, in lung tumors. *Int J Oncol.* 2015;47(1):195–203.
- [13] Tang H, Ma M, Dai J, Cui C, Si L, Sheng X, et al. miR-let-7b and miR-let-7c suppress tumorigenesis of human mucosal melanoma and enhance the sensitivity to chemotherapy. *J Exp Clin Cancer Res.* 2019;38(1):212.
- [14] Wang Q, Shen B, Chen L, Zheng P, Feng H, Hao Q, et al. Extracellular calumenin suppresses ERK1/2 signaling and cell migration by protecting fibulin-1 from MMP-13-mediated proteolysis. *Oncogene.* 2015;34(8):1006–18.
- [15] Kurpinska A, Suraj J, Bonar E, Zakrzewska A, Stojak M, Sternak M, et al. Proteomic characterization of early lung response to breast cancer metastasis in mice. *Exp Mol Pathol.* 2019;107:129–40.
- [16] Voora D, Koboldt DC, King CR, Lenzini PA, Eby CS, Porche-Sorbet R, et al. A polymorphism in the VKORC1 regulator

- calumenin predicts higher warfarin dose requirements in African Americans. *Clin Pharmacol Ther.* 2010;87(4):445–51.
- [17] Wang Y, Cui X, Wang Y, Fu Y, Guo X, Long J, et al. Protective effect of miR378* on doxorubicin-induced cardiomyocyte injury via calumenin. *J Cell Physiol.* 2018;233(10):6344–51.
- [18] Wang Y, Sun Y, Fu Y, Guo X, Long J, Xuan LY, et al. Calumenin relieves cardiac injury by inhibiting ERS-initiated apoptosis during viral myocarditis. *Int J Clin Exp Pathol.* 2017;10(7):7277–84.
- [19] Zhao L, Wang Y, Shao L, Gu J, Long J, Zhao M, Calumenin DNA Methylation and gene expression in viral myocarditis. *Int J Clin Exp Pathol.* 2018;11(2):808–12.
- [20] Feng H, Chen L, Wang Q, Shen B, Liu L, Zheng P, et al. Calumenin-15 facilitates filopodia formation by promoting TGF-beta superfamily cytokine GDF-15 transcription. *Cell Death Dis.* 2013;4:e870.
- [21] Ren Y, Yeoh KW, Hao P, Kon OL, Sze SK. Irradiation of epithelial carcinoma cells upregulates calcium-binding proteins that promote survival under hypoxic conditions. *J Proteome Res.* 2016;15(12):4258–64.
- [22] Sreekanthreddy P, Srinivasan H, Kumar DM, Nijaguna MB, Sridevi S, Vrinda M, et al. Identification of potential serum biomarkers of glioblastoma: Serum osteopontin levels correlate with poor prognosis. *Cancer Epidemiol Biomarkers Prev.* 2010;19(6):1409–22.
- [23] Robin X, Turck N, Hainard A, Tiberti N, Lisacek F, Sanchez JC, et al. pROC: An open-source package for R and S+ to analyze and compare ROC curves. *BMC Bioinforma.* 2011;12:77.
- [24] Gu Z, Gu L, Eils R, Schlesner M, Brors B. Circlize Implements and enhances circular visualization in R. *Bioinformatics.* 2014;30(19):2811–2.
- [25] Huang da W, Sherman BT, Lempicki RA. Systematic and integrative analysis of large gene lists using DAVID bioinformatics resources. *Nat Protoc.* 2009;4(1):44–57.
- [26] Subramanian A, Tamayo P, Mootha VK, Mukherjee S, Ebert BL, Gillette MA, et al. Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles. *Proc Natl Acad Sci USA.* 2005;102(43):15545–50.
- [27] Hanzelmann S, Castelo R, Guinney J. GSEA: Gene set variation analysis for microarray and RNA-seq data. *BMC Bioinforma.* 2013;14:7.
- [28] Gonzalez DM, Medici D. Signaling mechanisms of the epithelial-mesenchymal transition. *Sci Signal.* 2014;7(344):re8.
- [29] Xu J, Zhang Z, Qian M, Wang S, Qiu W, Chen Z, et al. Cullin-7 (CUL7) is overexpressed in glioma cells and promotes tumorigenesis via NF- κ B activation. *J Exp Clin Cancer Res.* 2020;39(1):59.
- [30] Mazzorana M, Hussain R, Sorensen T. Ca-dependent folding of human calumenin. *PLoS One.* 2016;11(3):e0151547.
- [31] Suzuki N, Ban S, Itoh E, Chen S, Imai FL, Sawano Y, et al. Calcium-dependent structural changes in human reticulo-calbin-1. *J Biochem.* 2014;155(5):281–93.
- [32] Sahoo SK, Kim DH. Calumenin interacts with SERCA2 in rat cardiac sarcoplasmic reticulum. *Mol Cell.* 2008;26(3):265–9.
- [33] Jung DH, Mo SH, Kim DH. Calumenin, a multiple EF-hands Ca²⁺-binding protein, interacts with ryanodine receptor-1 in rabbit skeletal sarcoplasmic reticulum. *Biochem Biophys Res Commun.* 2006;343(1):34–42.
- [34] Sahoo SK, Kim DH. Characterization of calumenin in mouse heart. *BMB Rep.* 2010;43(3):158–63.
- [35] Zheng P, Wang Q, Teng J, Chen J. Calumenin and fibulin-1 on tumor metastasis: Implications for pharmacology. *Pharmacol Res.* 2015;99:11–5.
- [36] Li H, Li J, Chen L, Qi S, Yu S, Weng Z, et al. HERC3-mediated SMAD7 ubiquitination degradation promotes autophagy-induced EMT and chemoresistance in glioblastoma. *Clin Cancer Res.* 2019;25(12):3602–16.
- [37] Luo J, Li Z, Zhu H, Wang C, Zheng W, He Y, et al. A novel role of Cab45-G in mediating cell migration in cancer cells. *Int J Biol Sci.* 2016;12(6):677–87.
- [38] Fan CC, Cheng WC, Huang YC, Sher YP, Liou NJ, Chien YC, et al. EFHD2 promotes epithelial-to-mesenchymal transition and correlates with postsurgical recurrence of stage I lung adenocarcinoma. *Sci Rep.* 2017;7(1):14617.