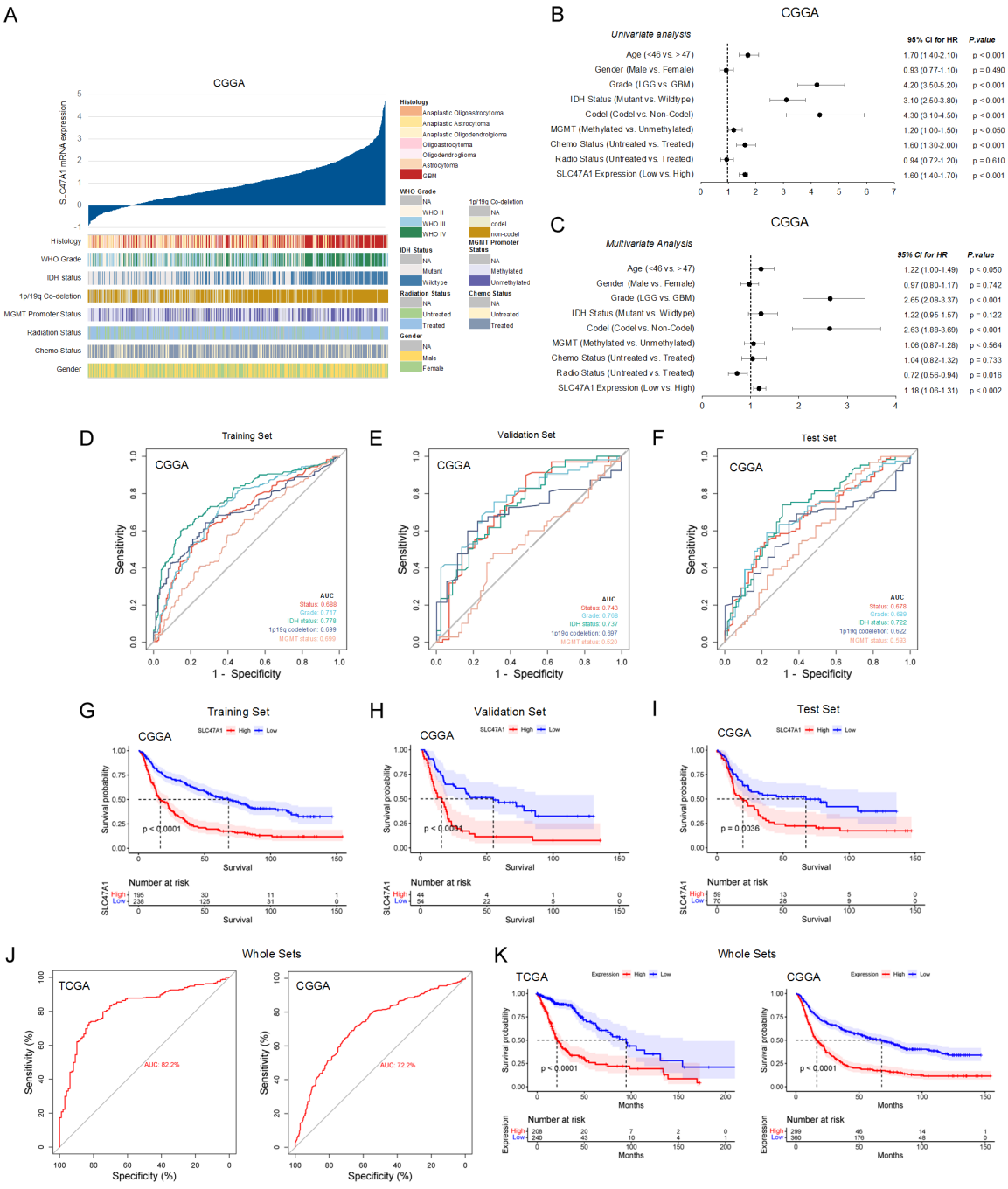

Figure S1. (A) Correlation between SLC47A1 mRNA expression and glioma histological features and prognostic biomarkers in CGGA dataset (n = 1013). (B, C) Univariate (B) and multivariate (C) Cox regression analyses to evaluate the correlation of expression with prognosis of glioma patients in the CGGA cohorts. (D-F) ROC curve and the risk score distribution stratified by SLC47A1 expression levels in patient survival status, grade, 1p/16q codeletion, and MGMT promoter methylation in the CGGA Training set (D), Validation set (E), and Test set (F). (G-I) Kaplan-Meier analysis for SLC47A1 high and low expressions in the CGGA Training set (G), Validation set (H), and Test set (I). (J) ROC curve and the risk score distribution stratified by SLC47A1 expression levels in patient survival status in TCGA and CGGA Whole set. (K) Kaplan-Meier analysis for SLC47A1 high and low expressions in the TCGA and CGGA Whole set.

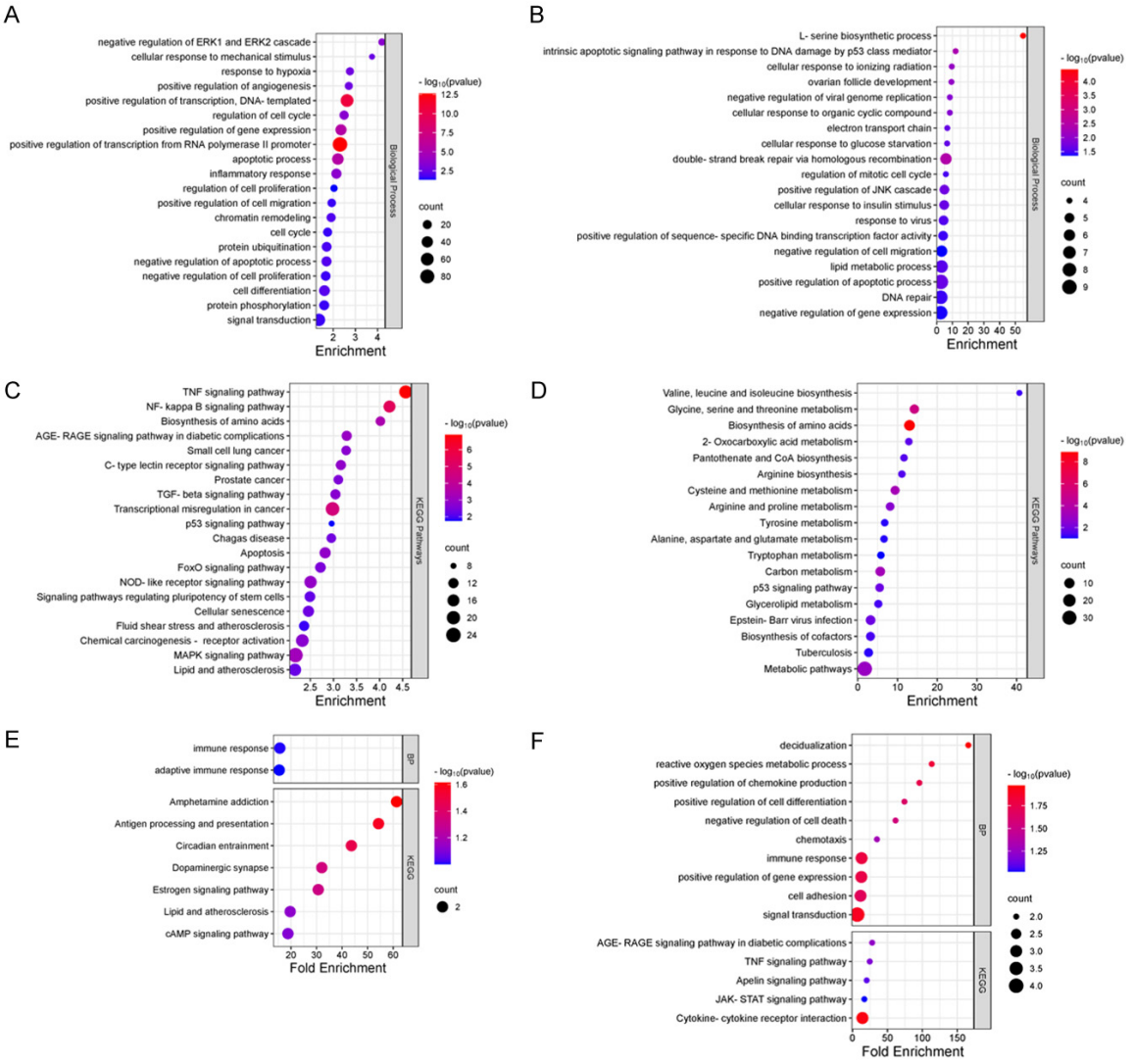

Figure S2. RNA sequencing analysis between SLC47A1 knockdown and non-target control GSC11 and GSC23 cells. (A, B) Gene Ontology analysis on the differentially upregulated genes between SLC47A1 knockdown and non-target control GSC11 (A) and GSC23 (B) cells. (C, D) KEGG pathway analysis on the differentially upregulated genes between SLC47A1 knockdown and non-target control GSC11 (C) and GSC23 (D) cells. (E, F) Gene Ontology and KEGG pathway analysis on the significantly downregulated genes between SLC47A1 knockdown and non-target control GSC11 (E) and GSC23 (F) cells.

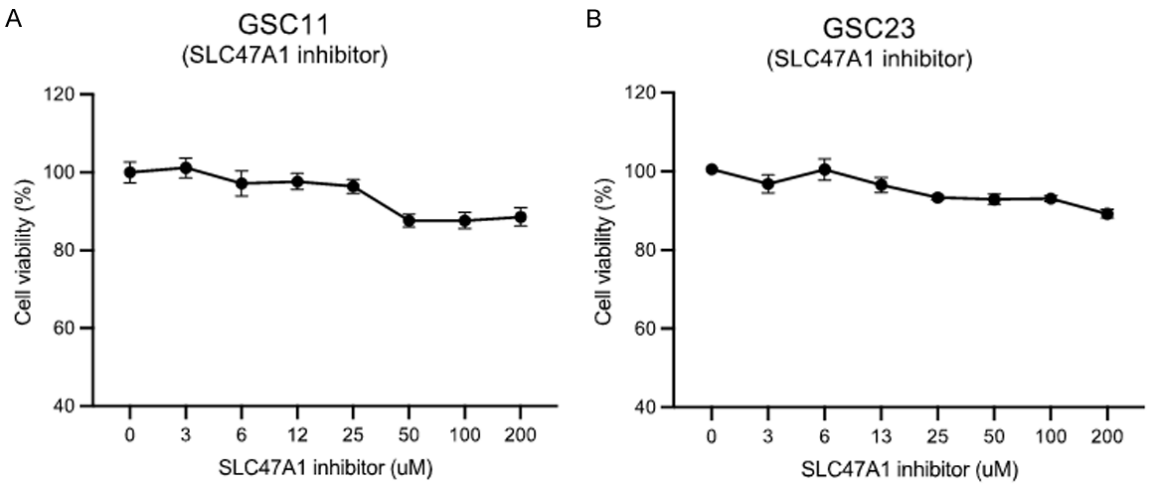

Figure S3. (A, B) Cell viability (%) of GSC11 (A) and GSC23 (B) after 72 h treatment with various concentrations of SLC47A1 inhibitor, Famotidine (3, 6, 12, 25, 50, 100, 200 μM).