

Figure S1. Kaplan-Meier analysis of survival of miR-301a low-expressing and high-expressing glioma cases from The Cancer Genome Atlas database. The criterion to distinguish miRNA expression was the median of the samples. miR, microRNA.

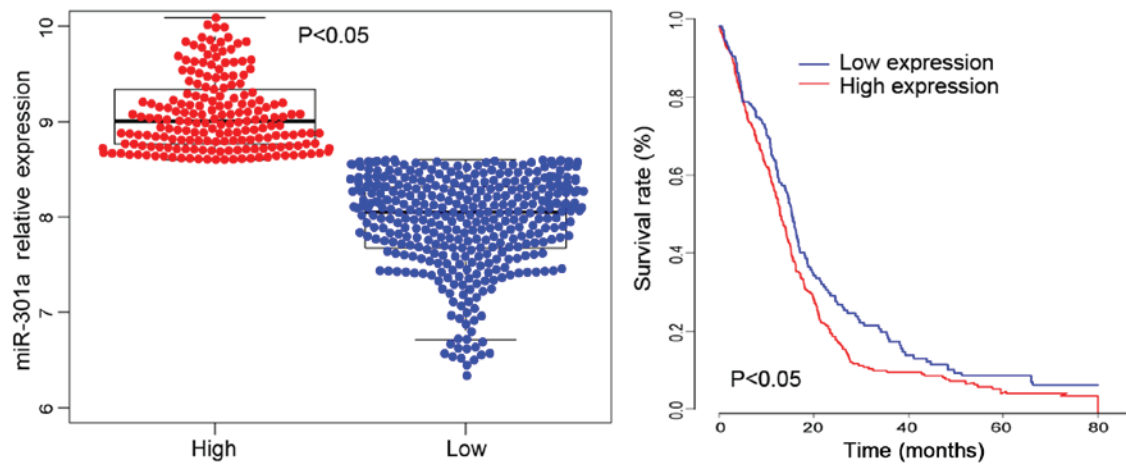


Figure S2. Reverse transcription-quantitative PCR was performed to detect the ZNRF3 expression in LN229 and U87 cells singly transfected with NC or siZNRF3. **P<0.01, ***P<0.001. NC, negative control; siRNA, small interfering RNA; ZNRF3, Zinc and ring finger 3.

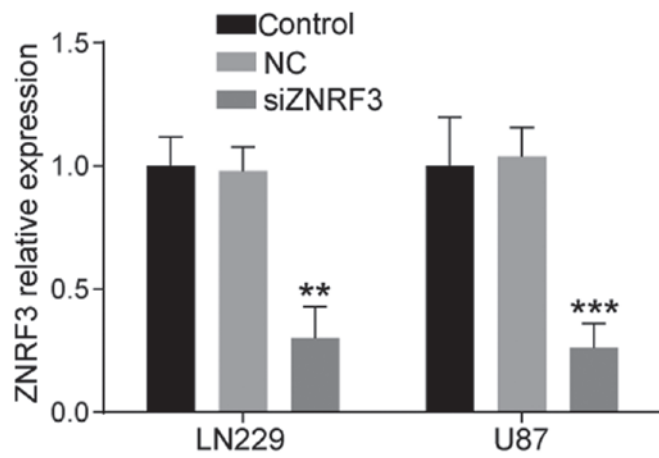


Figure S3. Clinical parameters of ZNRF3 expression from the Chinese Glioma Genome Atlas dataset (Mseq-325) were analyzed based on (A) sex, (B) age and (C) progression status. ZNRF3, Zinc and ring finger 3.

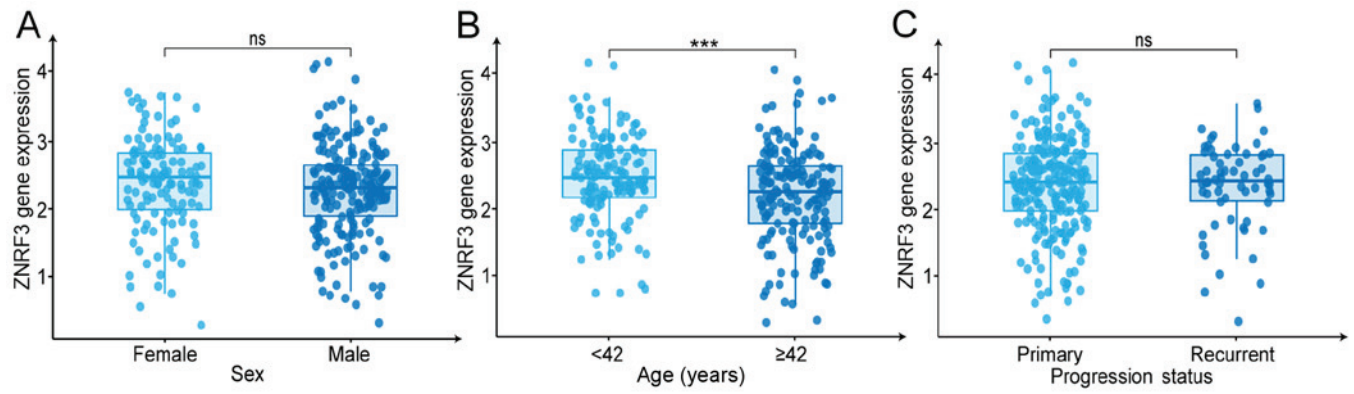


Figure S4. Determination of transfection efficiencies. LN229 and U87 cells singly transfected with (A) miR-301a mimics, (B) TCF4 overexpression plasmid or (C) TCF4 siRNA were analyzed via reverse transcription-quantitative PCR to analyze the expression levels of miR-301a and TCF4. ** $P < 0.01$, *** $P < 0.001$. NC, negative control; siRNA, small interfering RNA; ZNRF3, Zinc and ring finger 3; miR, microRNA.

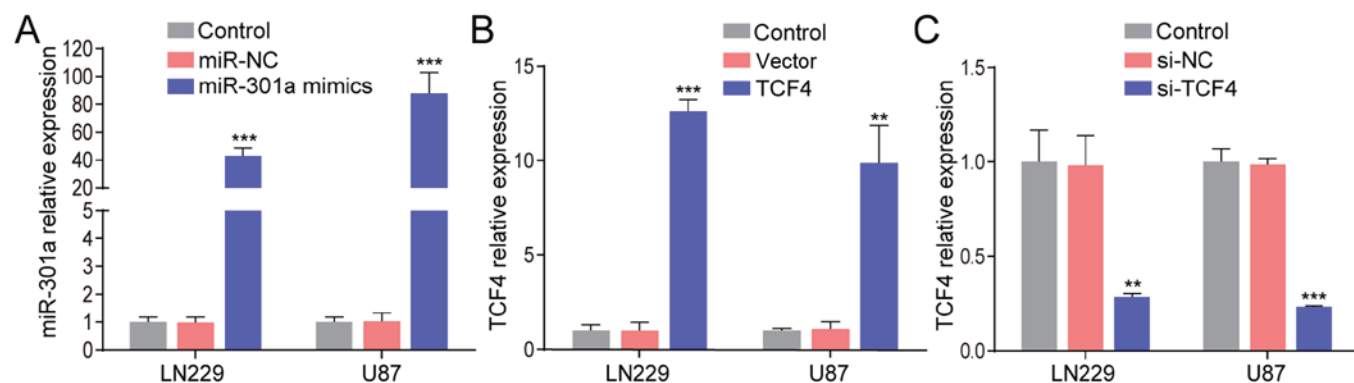


Table SI. Reverse transcription-quantitative PCR primer sequences.

Primer	Forward (5' →3')	Reverse (5' →3')
miR-301a	ACACTCCAGCTGGGCAGTGCAATAGTATTGTC	CTCAACTGGTGTCGTGGA
U6	CTCGCTTCGGCAGCACA	AACGCTTCACGAATTTGCGT
ZNRF3	GCGGGTCATCCCCTGTAC	GCTTGGGTTTCCCTTTTGT
Cyclin D1	AACTACCTGGACCGCTTCCT	CCACTTGAGCTTGTTACCA
TCF4	CAAATAGAGGAAGCGGGGC	TGCTGAGAGAGATGGAGGAGA
c-myc	TTCGGGTAGTGGAACACCAG	CAGCAGCTCGAATTTCTTCC
GAPDH	CATGAGAAGTATGACAACAGCCT	AGTCCTTCCACGATACCAAAGT
miR, microRNA; TCF, transcription factor 4; ZNRF3, zinc and ring finger 3.		