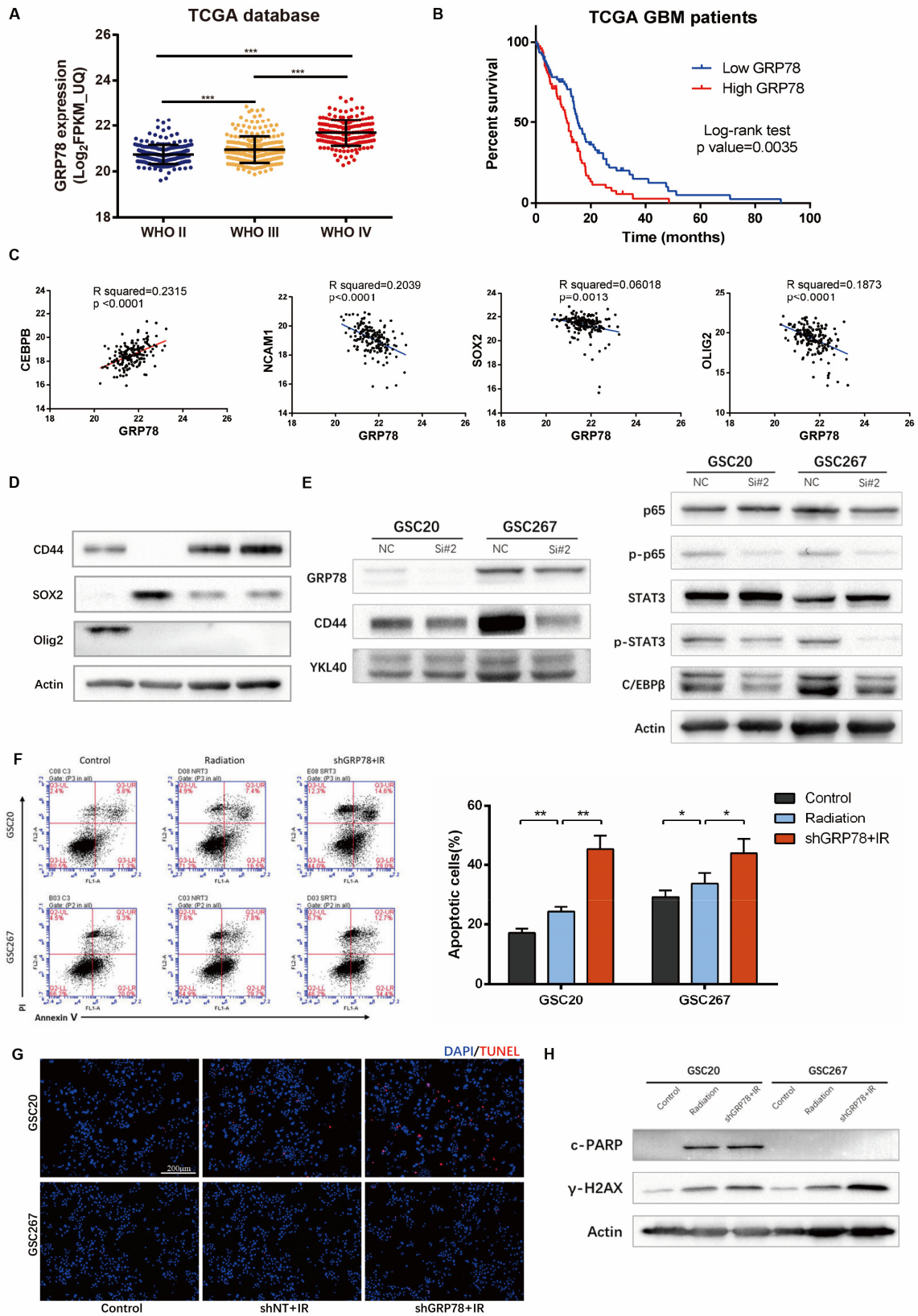


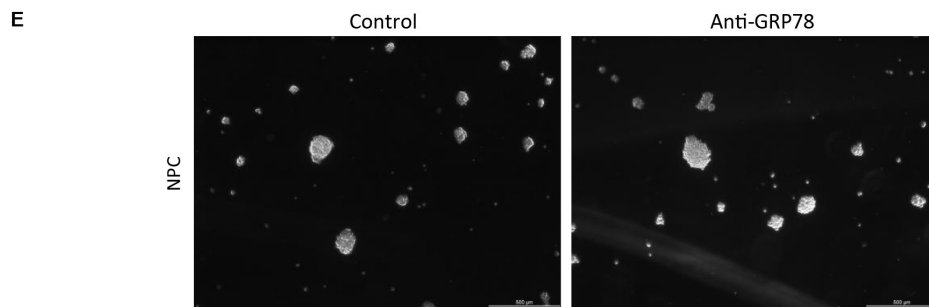
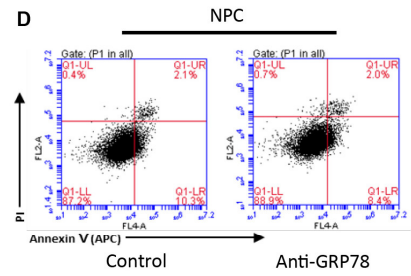
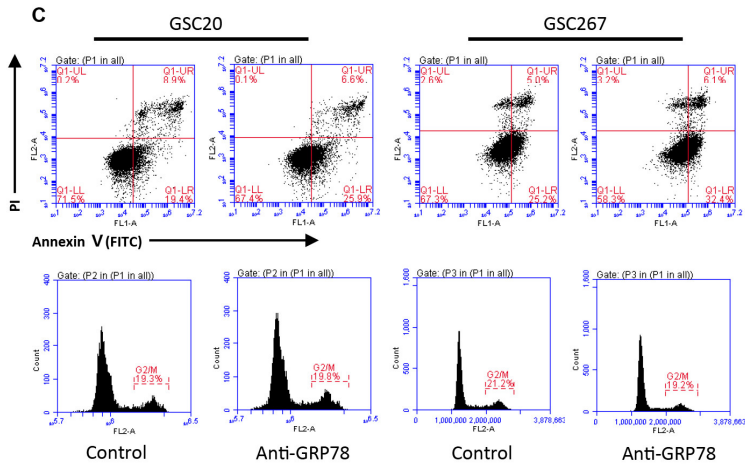
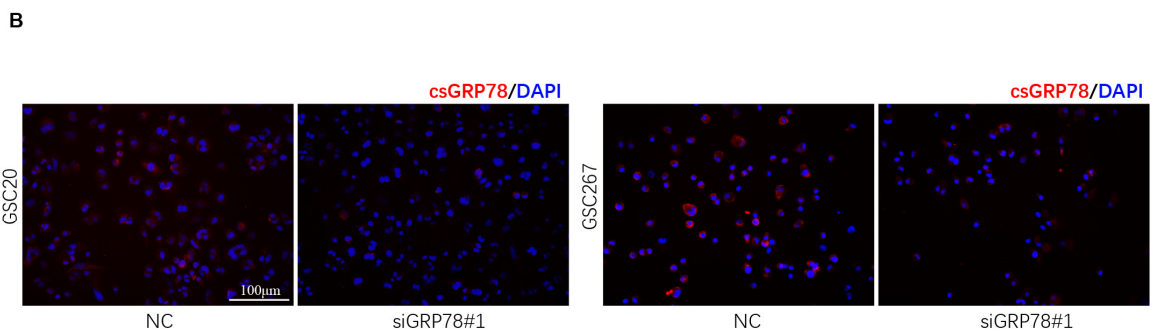
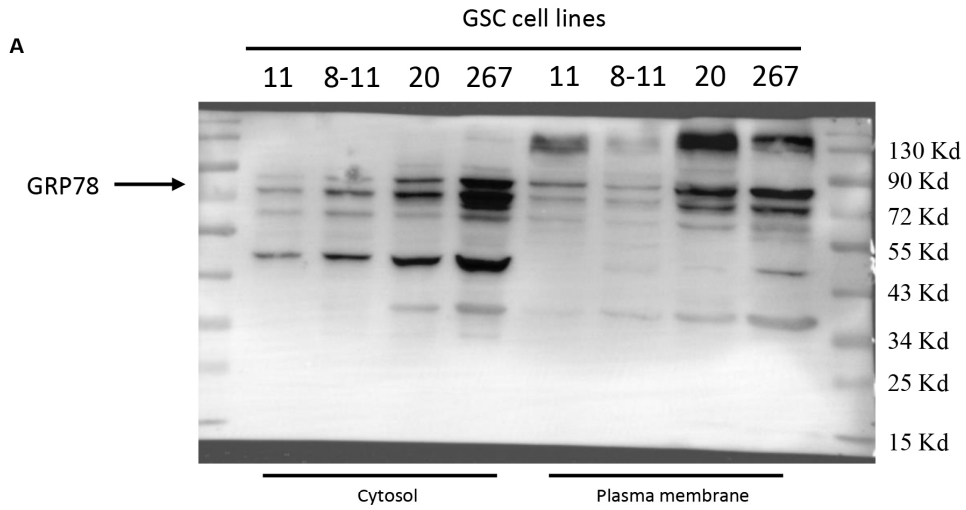
Supplementary figures



Supplementary figure 1

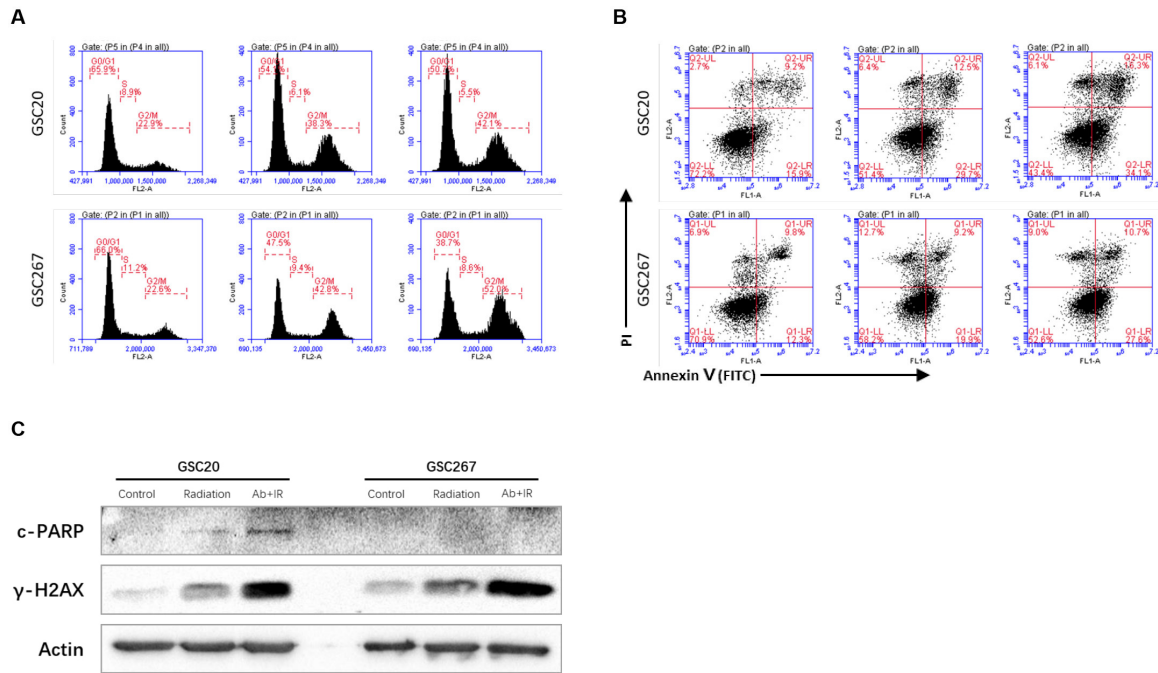
- A.** GRP78 mRNA expression in glioma grouped by WHO grade from TCGA database.
- B.** Survival curve and log-rank test for TCGA GBM patients with low or high expressed GRP78.
- C.** Same as Figure 1C, correlation of GRP78 expression with CEBPB, NCAM1, SOX2 and OLIG2 in TCGA database for glioma.
- D.** Protein expression of CD44, SOX2 and Olig2 in four GSC cell lines.
- E.** Same blot as Figure 1F using another siGRP78 sequence targeted total GRP78.
- F.** AnnexinV-PI dual staining detected apoptosis in GSC20 and 267 with treatment of control, radiation combined with or without shGRP78. (IR = ionizing radiation)
- G.** TUNEL staining for GSCs grouped by same treatments mentioned above. Scale bar, 200 μm .
- H.** Western blotting for cleaved-PARP and γ -H2AX.

Error bar indicates at least three independent experiments. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.



Supplementary figure 2

- A.** Isolation and purification of plasma membrane fraction showed GRP78 is highly expressed in plasma membrane of MES GSCs, using sodium-potassium ATPase as the marker of plasma membrane.
- B.** The nonpermeabilized immunofluorescence for scGRP78 in MES GSCs with siGRP78#1 targeting total GRP78. Scale bar, 100 μm .
- C.** C6 flow cytometer plots of Figure 2D.
- D.** C6 flow cytometer plots of Figure 2H.
- E.** Images of neurosphere formation assay for NPCs with or without anti-GRP78 treatment. Scale bar, 500 μm .

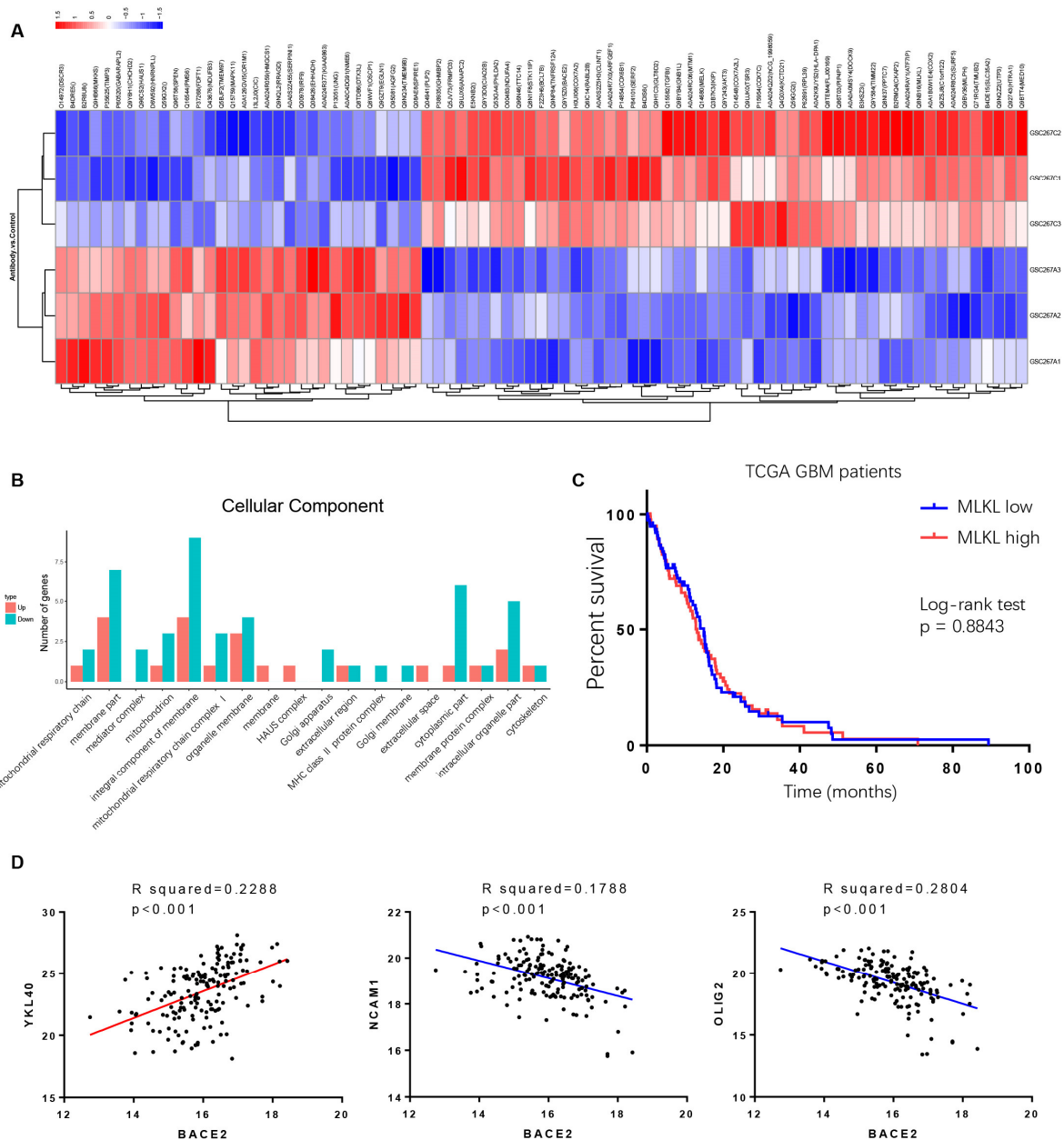


Supplementary figure 3

A. C6 flow cytometer plots of Figure 3B.

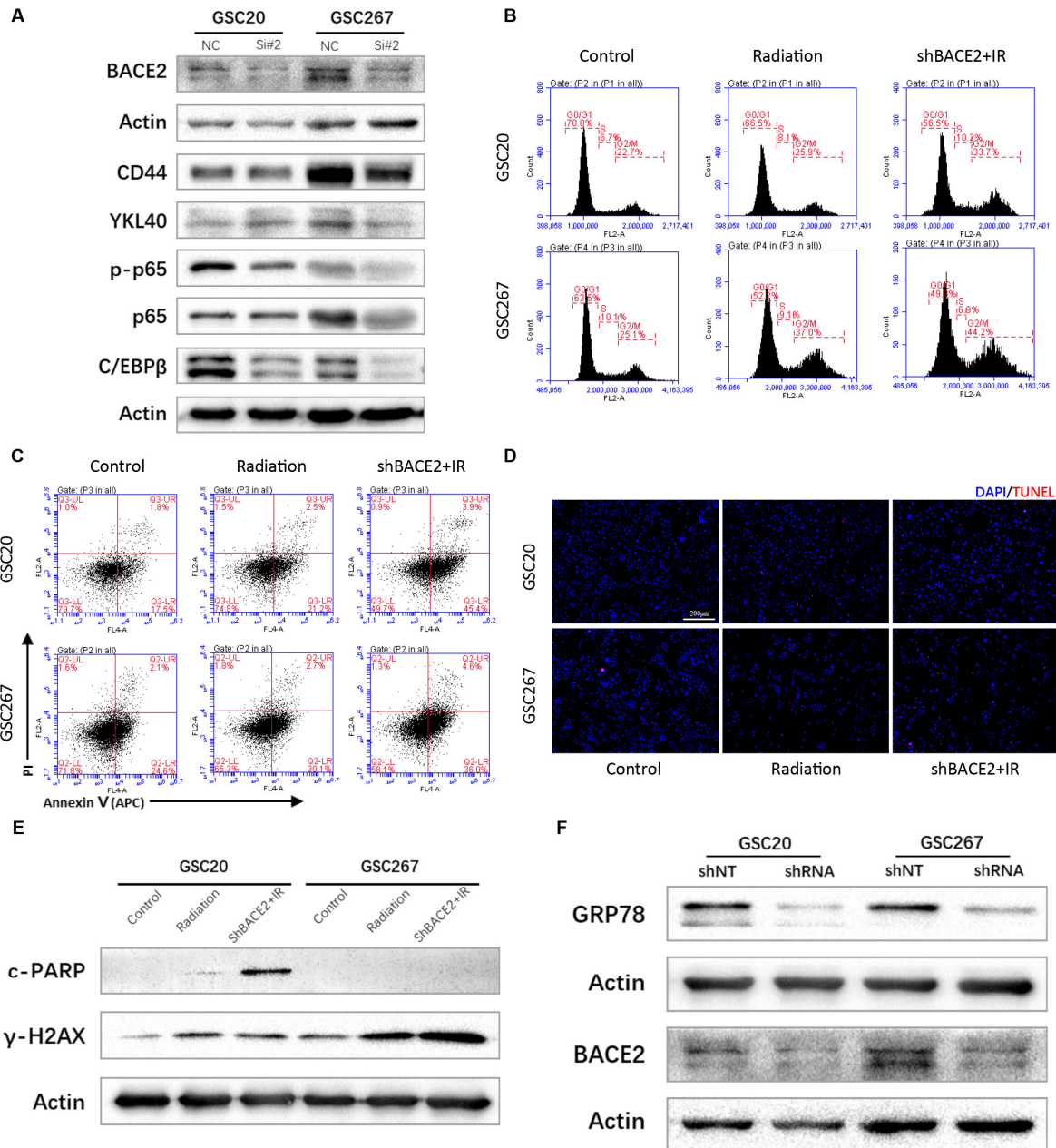
B. C6 flow cytometer plots of Figure 3C.

C. Western blotting for cleaved-PARP and γ -H2AX in MES GSCs with treatment of Control, radiation combined with or without anti-GRP78 pretreatment.



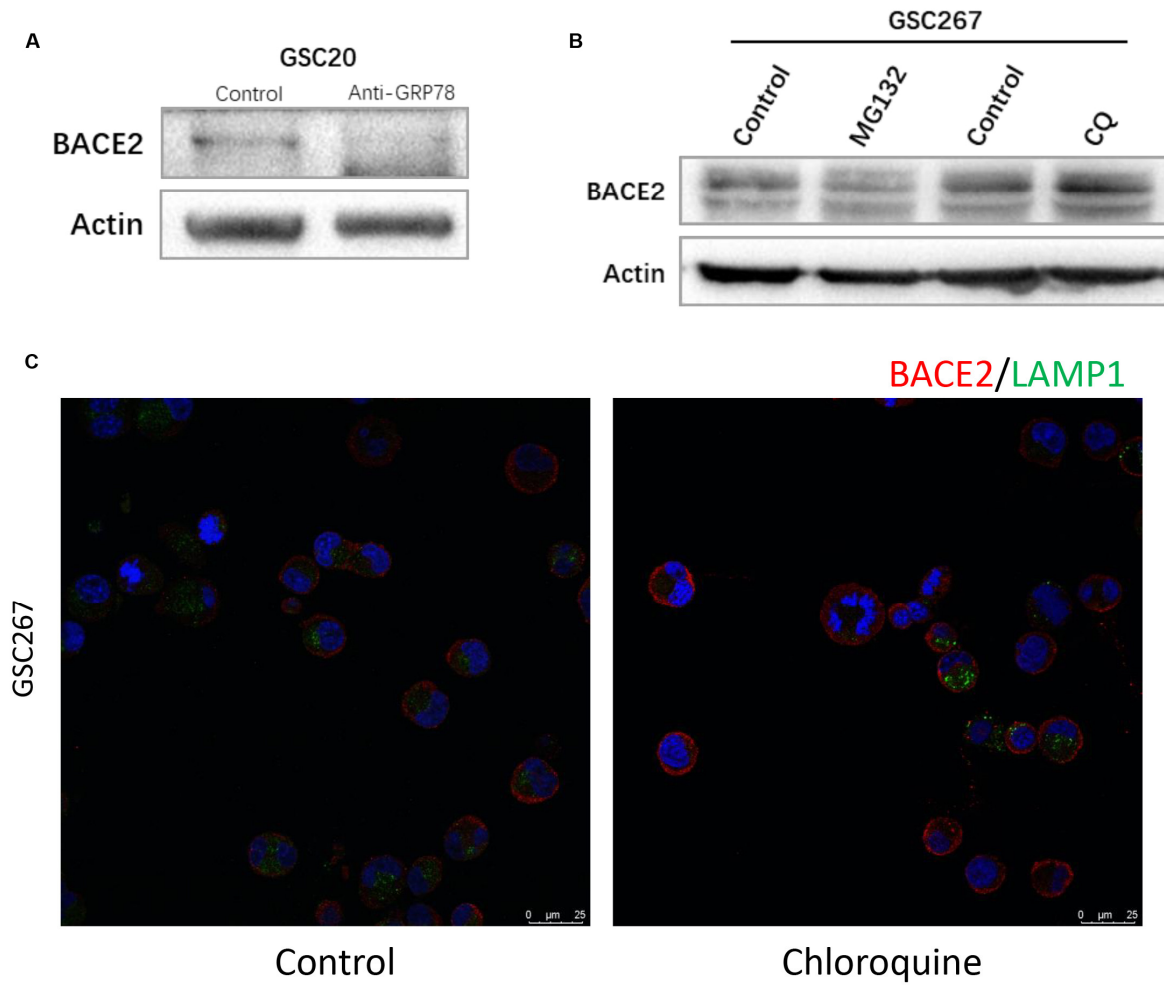
Supplementary figure 4

- Heat map with detailed gene name of differential proteins in GSC267 treated with anti-GRP78 for 72 h.
- Gene Ontology analysis for differential genes in MS revealed number of genes contributing to cellular components.
- Survival curve and statistical analysis for GBM patients from TCGA based on MLKL mRNA expression.
- Correlation of BACE2 expression with YKL40, NCAM1 or OLIG2 in TCGA database for glioma.



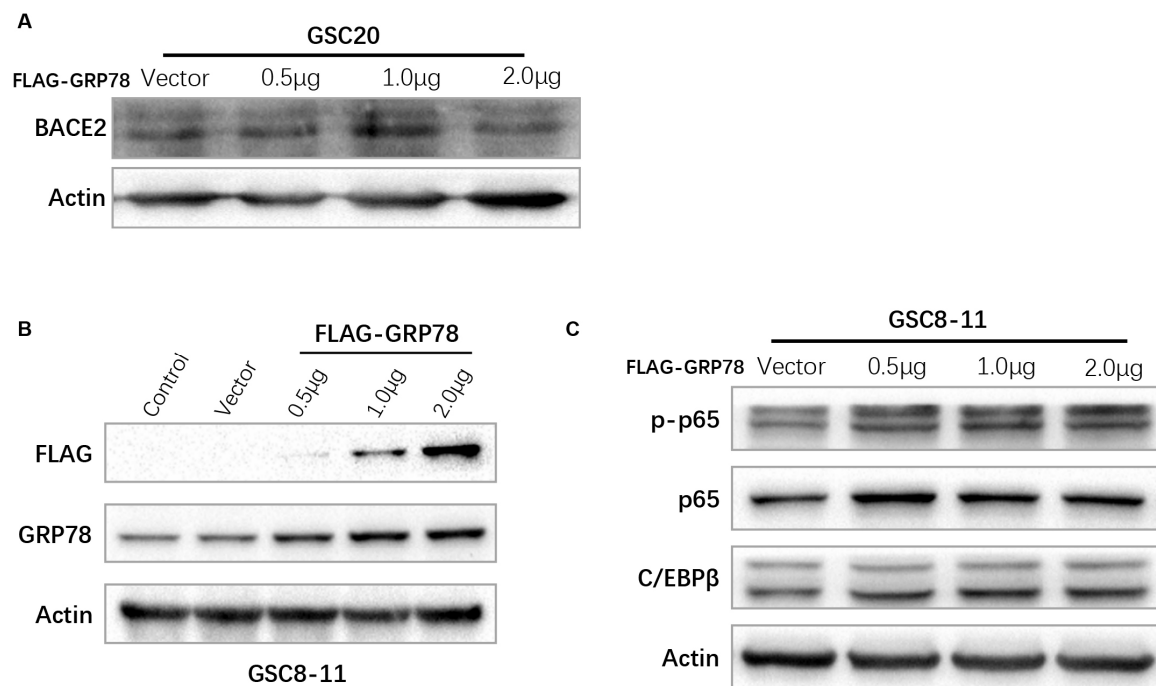
Supplementary figure 5

- Same blot as Figure 5A, another effective siBACE2 sequence targeted total BACE2 in GSC20 and 267.
- C6 flow cytometer plots of Figure 5D.
- C6 flow cytometer plots of Figure 5E.
- TUNEL staining of GSC20 and 267 with treatment of control, radiation only and radiation combined with shBACE2. Scale bar, 200 μ m.
- Western blotting for cleaved-PARP and γ -H2AX in GSCs grouped as designed.
- Western blotting for GRP78 and BACE2 in GSC20 and 267 that transfected with lentiviral shGRP78 or shBACE2.



Supplementary figure 6

- A.** Western blotting of BACE2 in GSC20 treated with anti-GRP78 for 72 h.
- B.** Western blotting for BACE2 in GSC267 treated with MG-132 or chloroquine (CQ) for indicated time.
- C.** Immunofluorescence for BACE2 (red) and LAMP1 (green) in GSC267 treated with chloroquine for indicated time. Scale bar, 25 μ m.



Supplementary figure 7

- A.** Western blotting of BACE2 in GSC20 transfected with WT FLAG-GRP78 or vector for 48 h.
- B.** Western blotting for FLAG tag and total GRP78 in GSC8-11 transfected with WT FLAG-GRP78 or vector for 48 h, comparing with control.
- C.** Western blotting for p-p65, p65 and C/EBP β in GSC8-11 transfected with WT FLAG-GRP78 or vector.