Suppl. Figure S1:
Primer specifications relevant for this study.
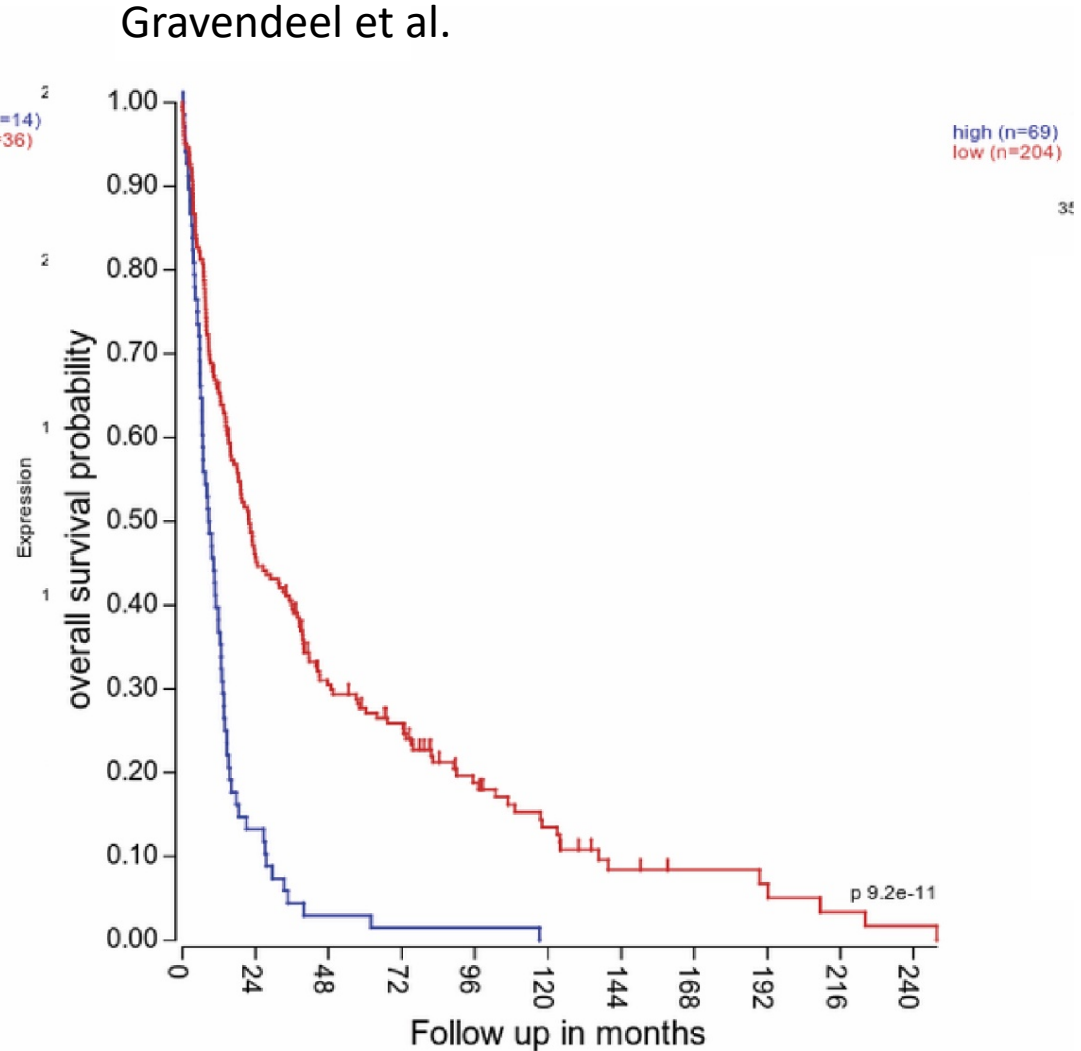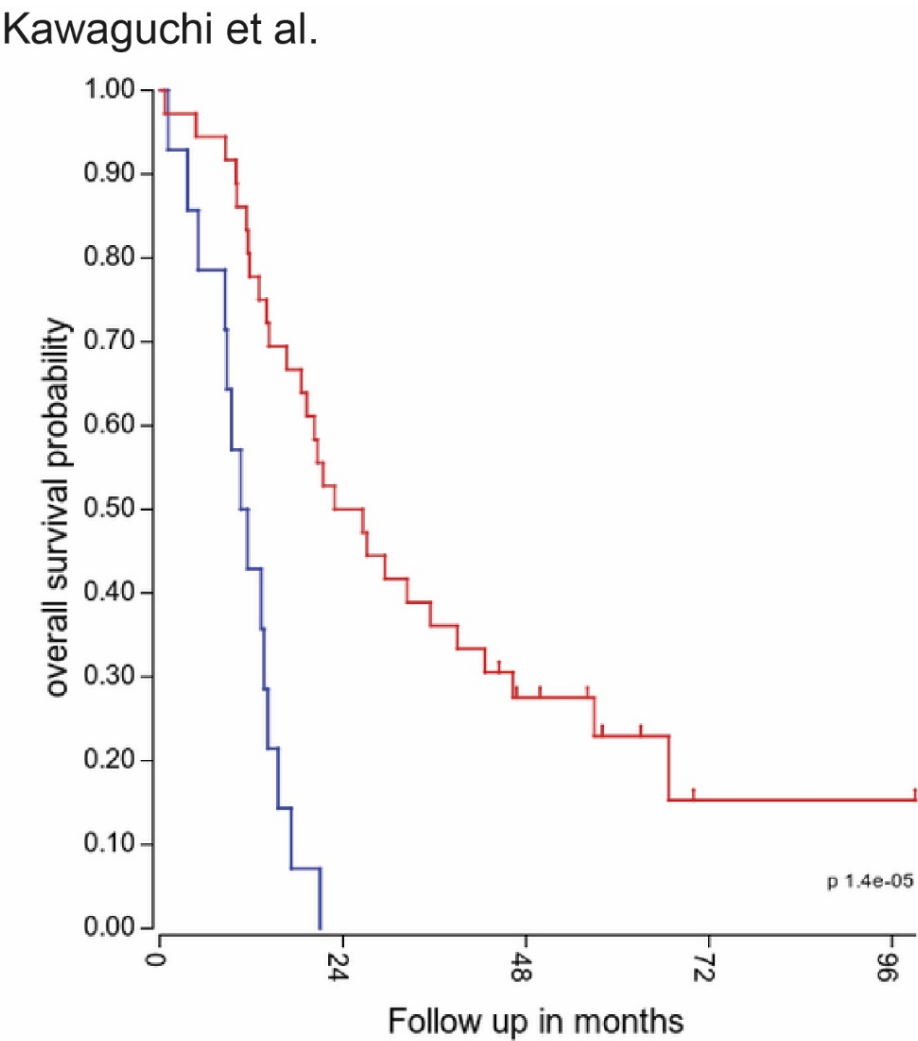
Name	Primer Seq(5->3)
Beta actin fwd	CCCAGCACAATGAAGATCAA
Beta actin rev	CGATCCACACGGAGTACTTG
Nestin F	GGCGCACCTCAAGATGTCC
Nestin R	CTTGGGGTCCTGAAAGCTG
SOX2_f	TGGACAGTTACGCGCACAT
SOX2_r	CGAGTAGGACATGCTGTAGGT
cd44-s-f	ATAATAAAGGAGCAGCACTTCAGGA
cd44-s-r	ATAATTGTGTCTTGGTCTCTGGTAGC
CA XII -F	ACTGCGGCAGGACTGAGTCT
CA XII -R	CACAATACAGATGCCAAGAATGC
CD133-F	GTGTCCTGGGGCTGCTGTTTA
CD133-R	CCATTTTCCTTCTGTCGCTGG
ZEB1-f	AAGAATTCACAGTGGAGAGAAGCCA
ZEB1-r	CGTTTCTTGCAGTTTGGGCATT

Suppl. Figure S2:
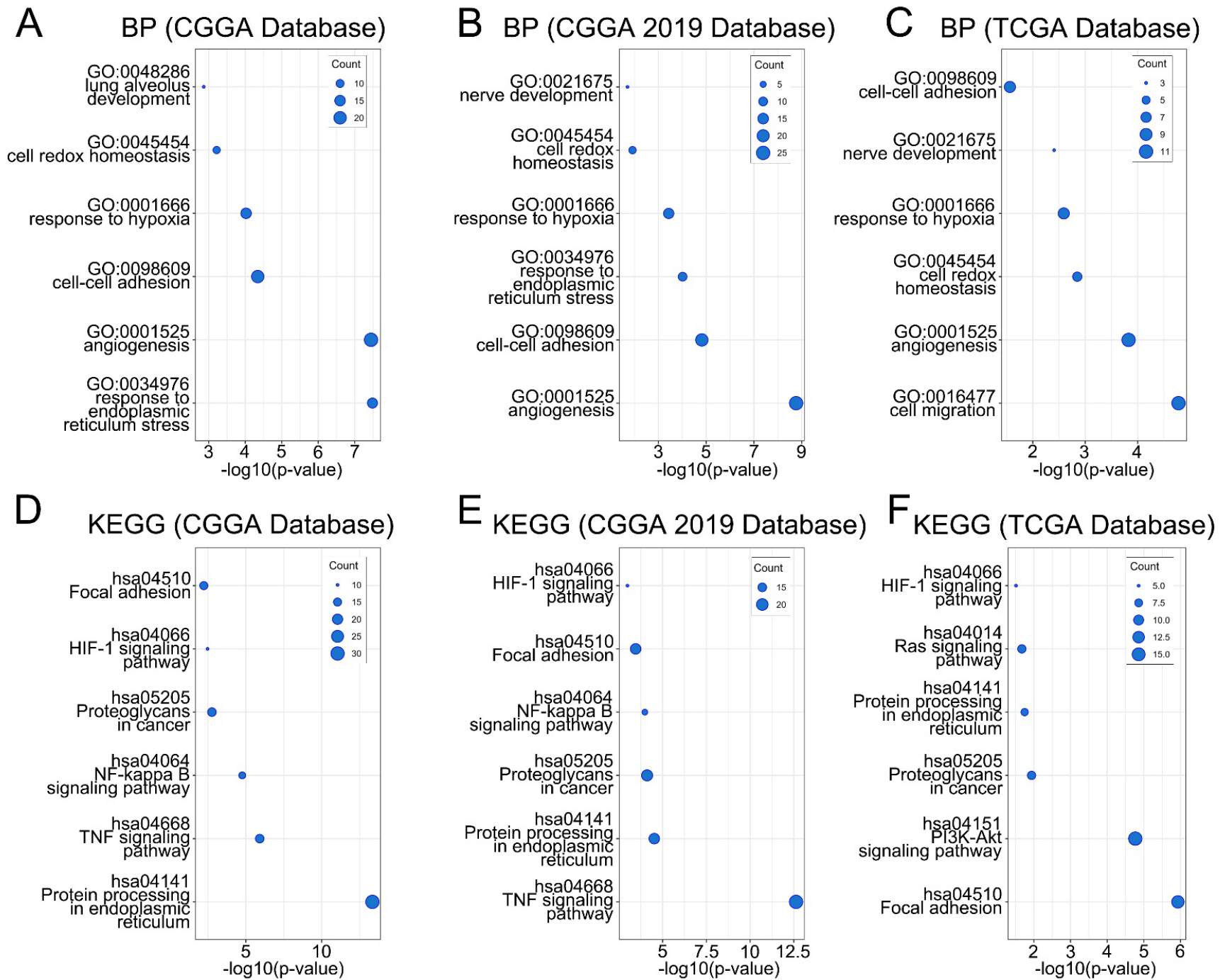## Antibody specifications relevant for this study.

Antibodies used in FACS

Primary Antibody	company	Host species	addition	Dilution factor
CD133/1-PE, human CD133/1 Antibody, anti-human, PE	Miltenyi Biotech	Mouse	Monoclonal Clone AC133	1:200 (5 µl/ml)
Anti-carbonic anhydrase XII Antibody (FITC)	Sino Biological	Mouse	Monoclonal Clone #07	1:200 (0.5 µl/ml)

Antibodies used in western blot

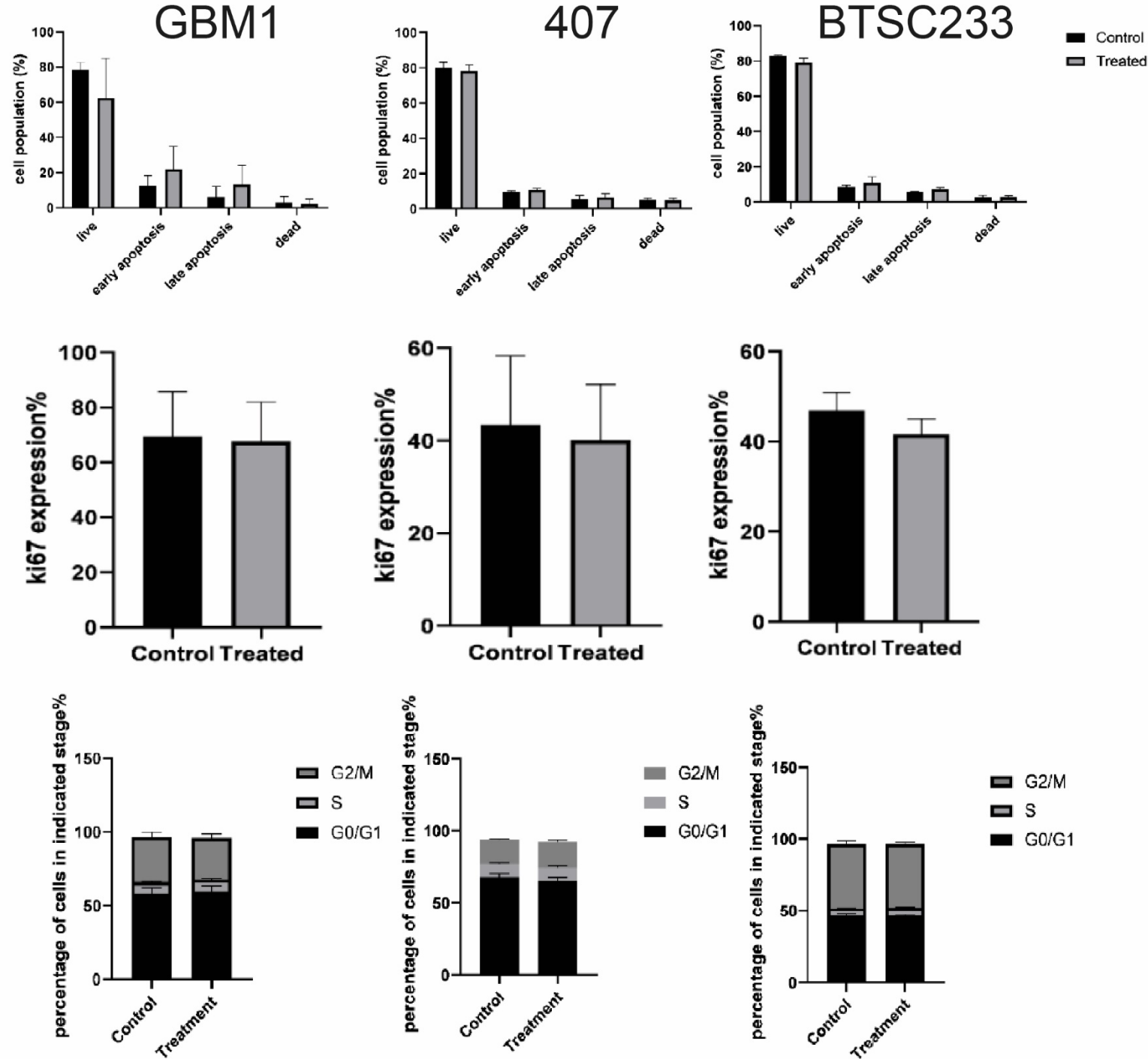| Primary Antibody	company	Host species	addition	Dilution factor
Anti-ZEB1 antibody	Sigma-Aldrich	Rabbit	Polyclonal	1:1000
beta-actin	Invitrogen	Mouse	Monoclonal	1:5000
GAPDH	Proteintech	Mouse	Monoclonal	1:8000
CA XII Antibody	Proteintech	Rabbit	Polyclonal	1:2000
CD133/1 (AC133) antibody, human	Miltenyi Biotech	Mouse	Monoclonal (clone W6B3C1)	1:1000
Secondary Antibody	**company**	**species**	**addition**	
IRDye 680RD Donkey anti-Mouse IgG	LiCor Biosciences	Donkey	Polyclonal	1:10000
IRDye 800CW Goat anti-Rabbit IgG	LiCor Biosciences	Goat	Polyclonal	1:10000

Suppl. Figure S3: Additional clinical datasets verified the significant clinical prognostic value of high CA12 mRNA to predict overall survival of glioma patients.

Suppl. Figure S4:
Biological function and pathway enrichment analysis of CA12 in CGGA, CGGA 2019 and TCGA databases reveals association to networks known to be relevant for the maintenance of cancer stem cells.

Suppl. Figure S5:
6A10 treatment with no effect on proliferation, trend of induction of apoptosis in GBM1, no effect on cell cycle progression.

Suppl. Figure S6: Low similarity between expression of CA family members in clinical samples

Unsupervised cluster analysis found that CA family members cannot be grouped stably in CGGA (A), CGGA 2019 (B) and TCGA (C) databases. Expression correlation matrix analysis found that CA family members have no stable expression correlation in CGGA (D), CGGA 2019 (E) and TCGA (F) databases.