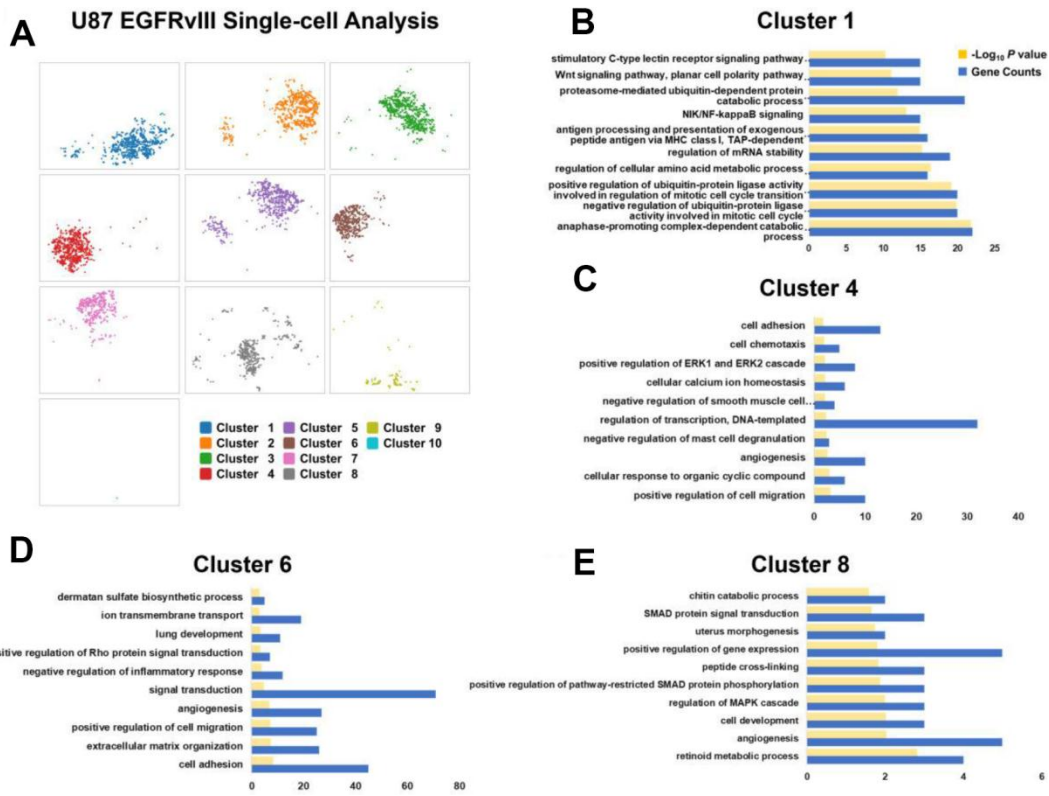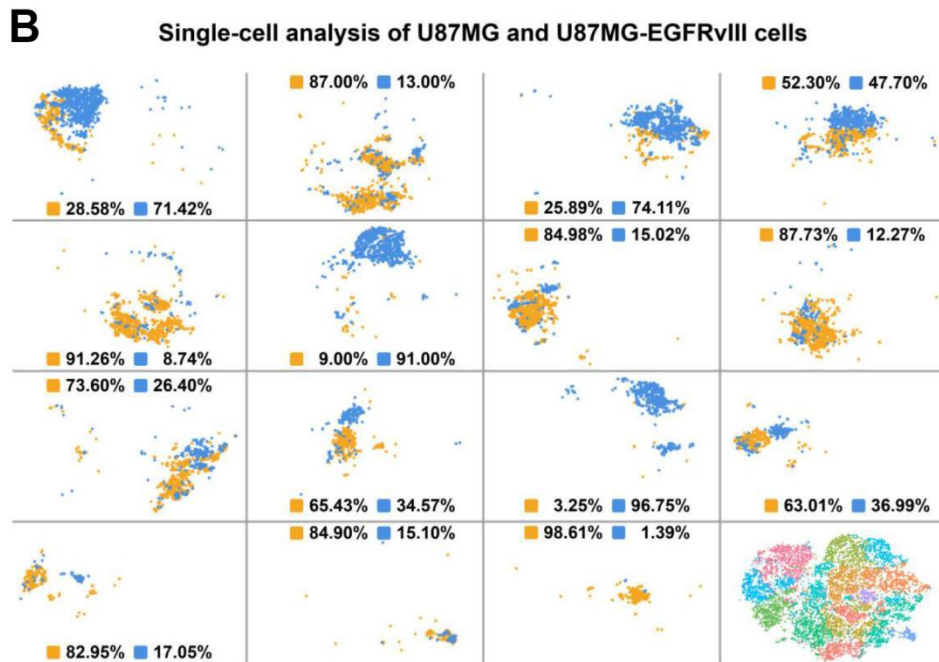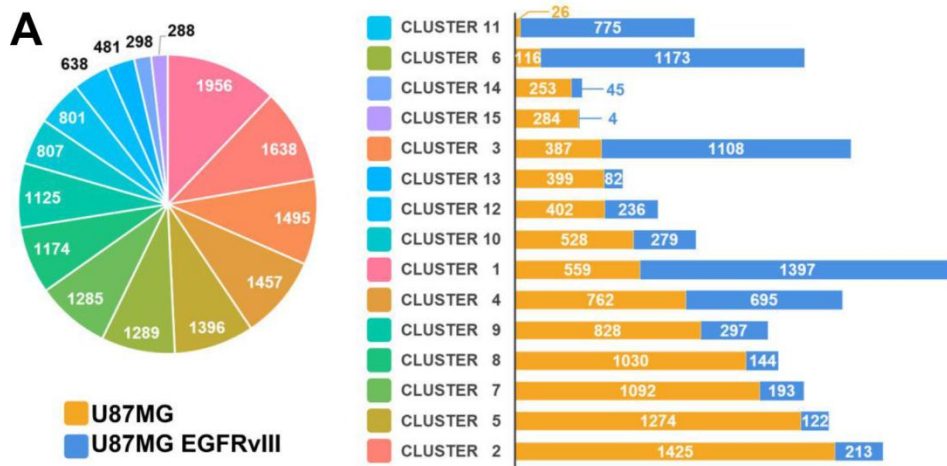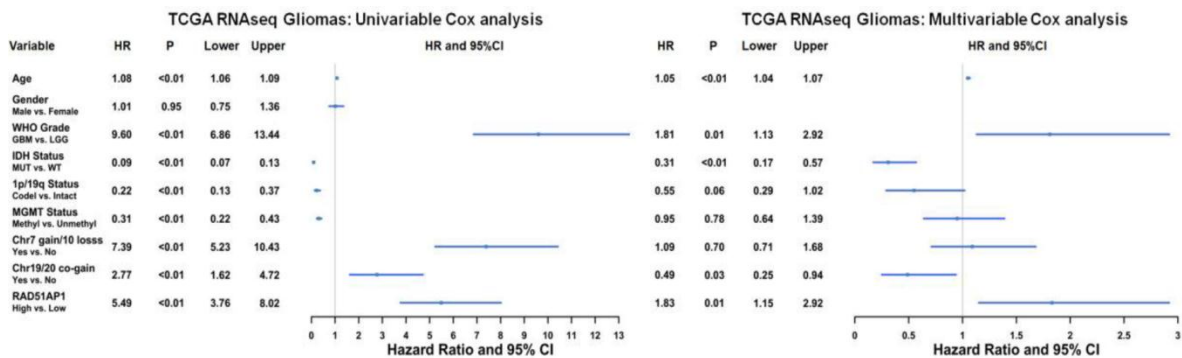# SUPPLEMENTARY FIGURES

Supplementary Figure 1. Gene Ontology (GO) analysis of each subset using cluster-specific genes in U87MG cells.

Supplementary Figure 2. Gene Ontology (GO) analysis of each subset using cluster-specific genes in U87MG-EGFRvIII cells.

A

Cluster	U87MG	U87MG EGFRvIII
CLUSTER 11	26	775
CLUSTER 6	116	1173
CLUSTER 14	253	45
CLUSTER 15	284	4
CLUSTER 3	387	1108
CLUSTER 13	399	82
CLUSTER 12	402	236
CLUSTER 10	528	279
CLUSTER 1	559	1397
CLUSTER 4	762	695
CLUSTER 9	828	297
CLUSTER 8	1030	144
CLUSTER 7	1092	193
CLUSTER 5	1274	122
CLUSTER 2	1425	213

B

Single-cell analysis of U87MG and U87MG-EGFRvIII cells

Supplementary Figure 3. The distributions and percentages of U87MG and U87MG-EGFRvIII cells in each cluster.

Variable	HR	P	Lower	Upper		HR	P	Lower	Upper	
Age	1.08	<0.01	1.06	1.09		1.05	<0.01	1.04	1.07	
Gender Male vs. Female	1.01	0.95	0.75	1.36						
WHO Grade GBM vs. LGG	9.60	<0.01	6.86	13.44		1.81	0.01	1.13	2.92	
IDH Status MUT vs. WT	0.09	<0.01	0.07	0.13		0.31	<0.01	0.17	0.57	
1p/19q Status Codel vs. Intact	0.22	<0.01	0.13	0.37		0.55	0.06	0.29	1.02	
MGMT Status Methyl vs. Unmethyl	0.31	<0.01	0.22	0.43		0.95	0.78	0.64	1.39	
Chr7 gain/10 losss Yes vs. No	7.39	<0.01	5.23	10.43		1.09	0.70	0.71	1.68	
Chr19/20 co-gain Yes vs. No	2.77	<0.01	1.62	4.72		0.49	0.03	0.25	0.94	
RAD51AP1 High vs. Low	5.49	<0.01	3.76	8.02		1.83	0.01	1.15	2.92	

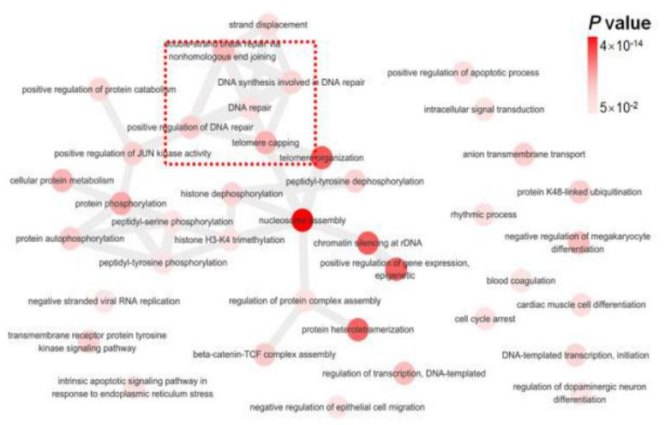TCGA RNAseq Gliomas: Univariable Cox analysis — TCGA RNAseq Gliomas: Multivariable Cox analysis

Supplementary Figure 4. Uni- and multivariable Cox analyses were performed to evaluate the role of RAD51AP1 in gliomas in the TCGA database.
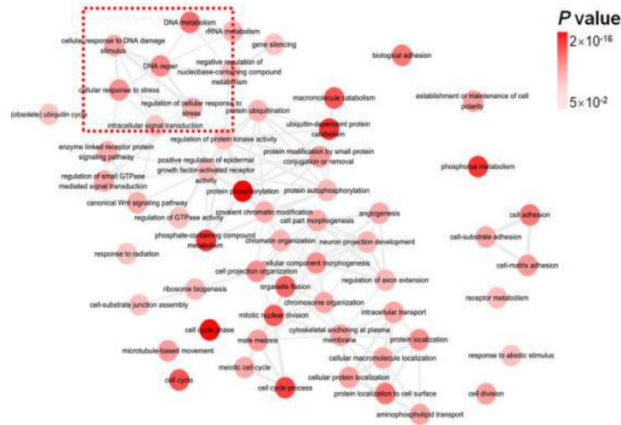
Supplementary Figure 5. GO and KEGG analyses were employed to profile the pathways of RAD51AP1-related genes in the CGGA database.