

SUPPLEMENTARY MATERIAL

A Novel Tumor-Suppressor, CDH18, Inhibits Glioma Cell Invasiveness Via UQCRC2 and Correlates with the Prognosis of Glioma Patients

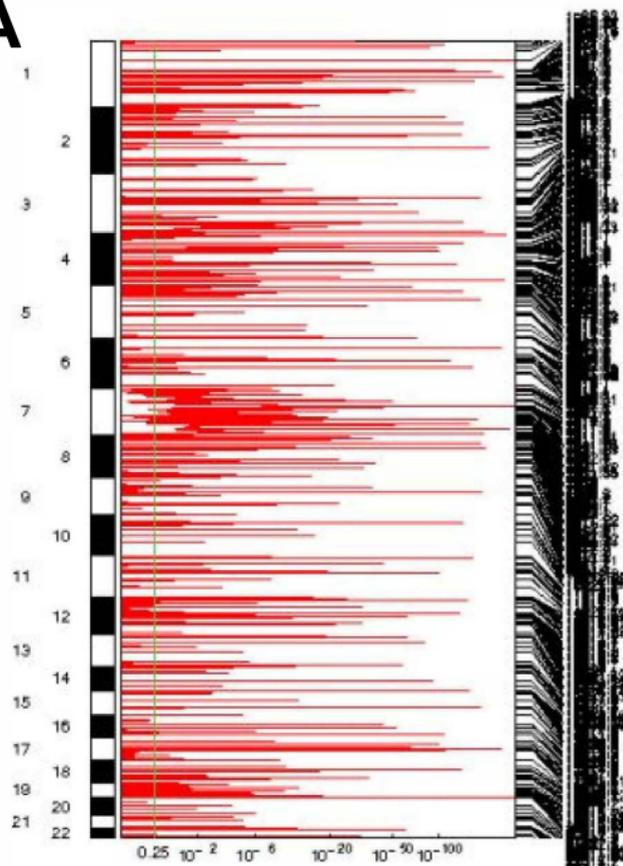
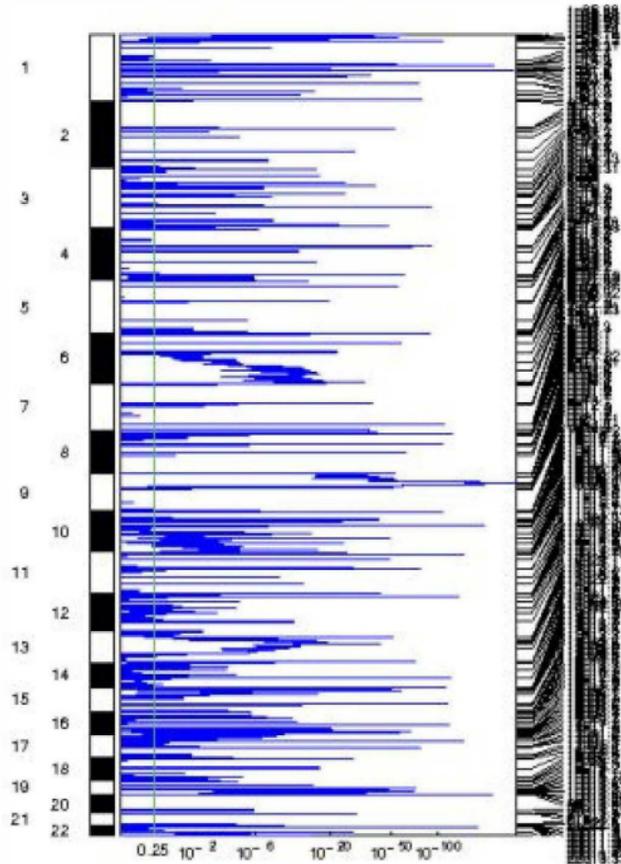
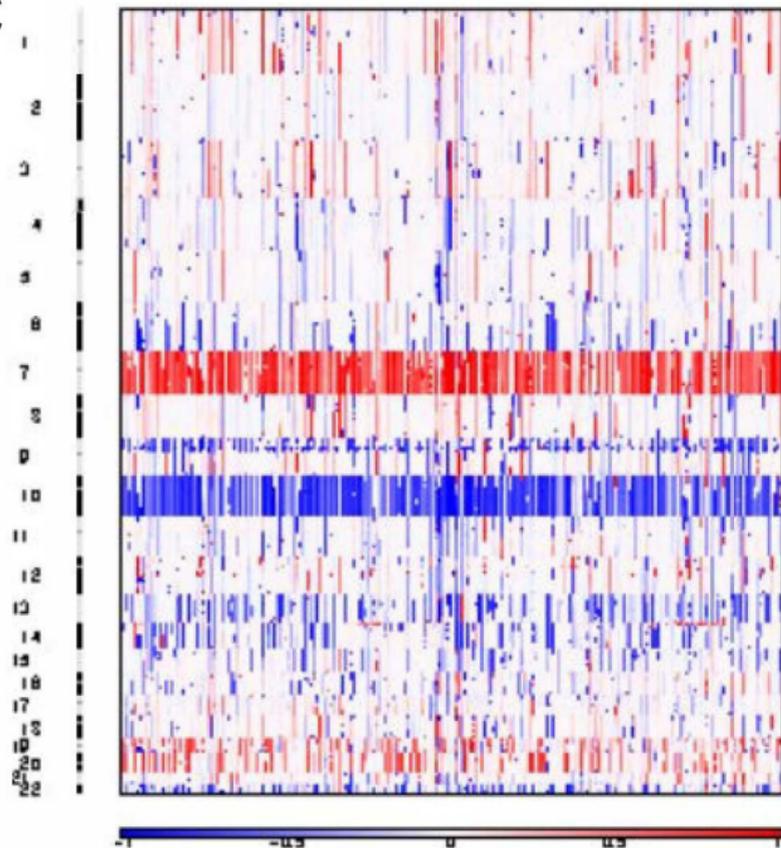
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Supplementary Figure 1 Analysis of DNA copy number variations(CNVs) in TCGA GBM cohort

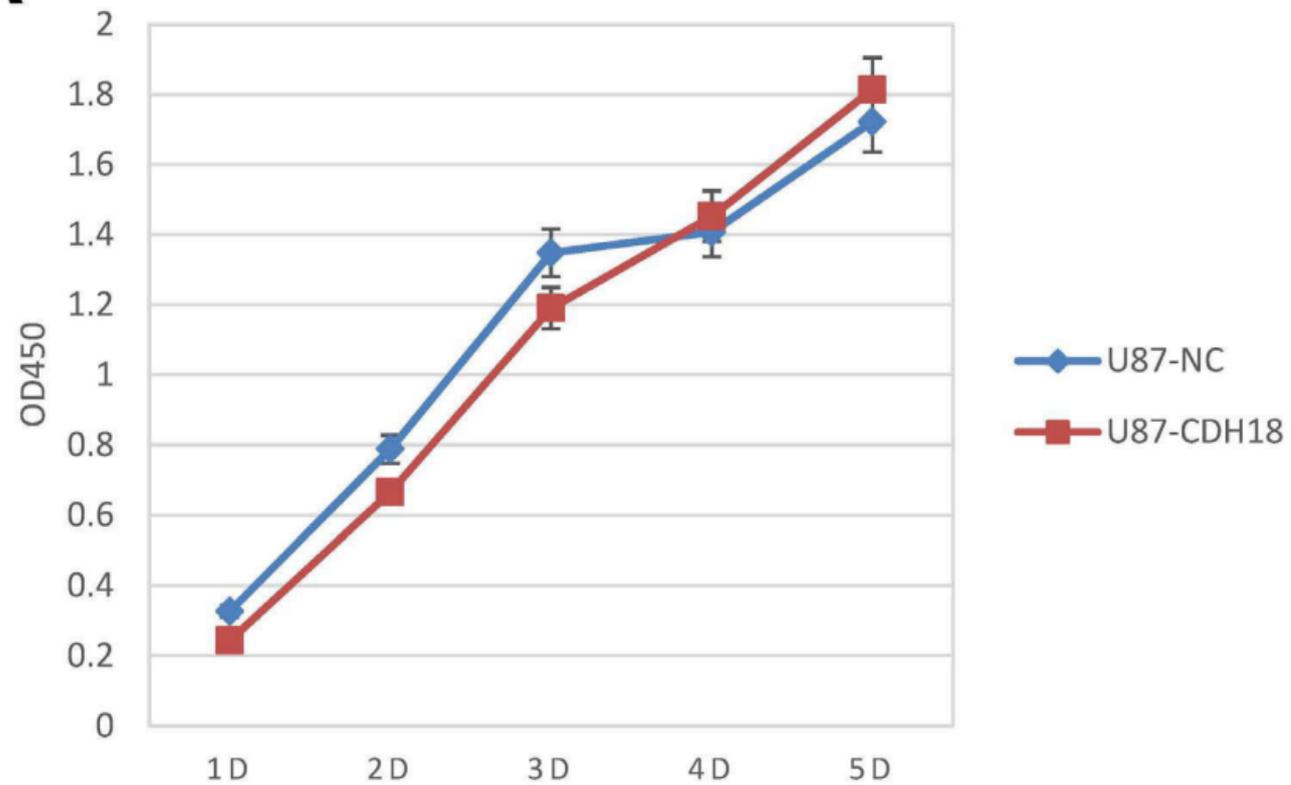
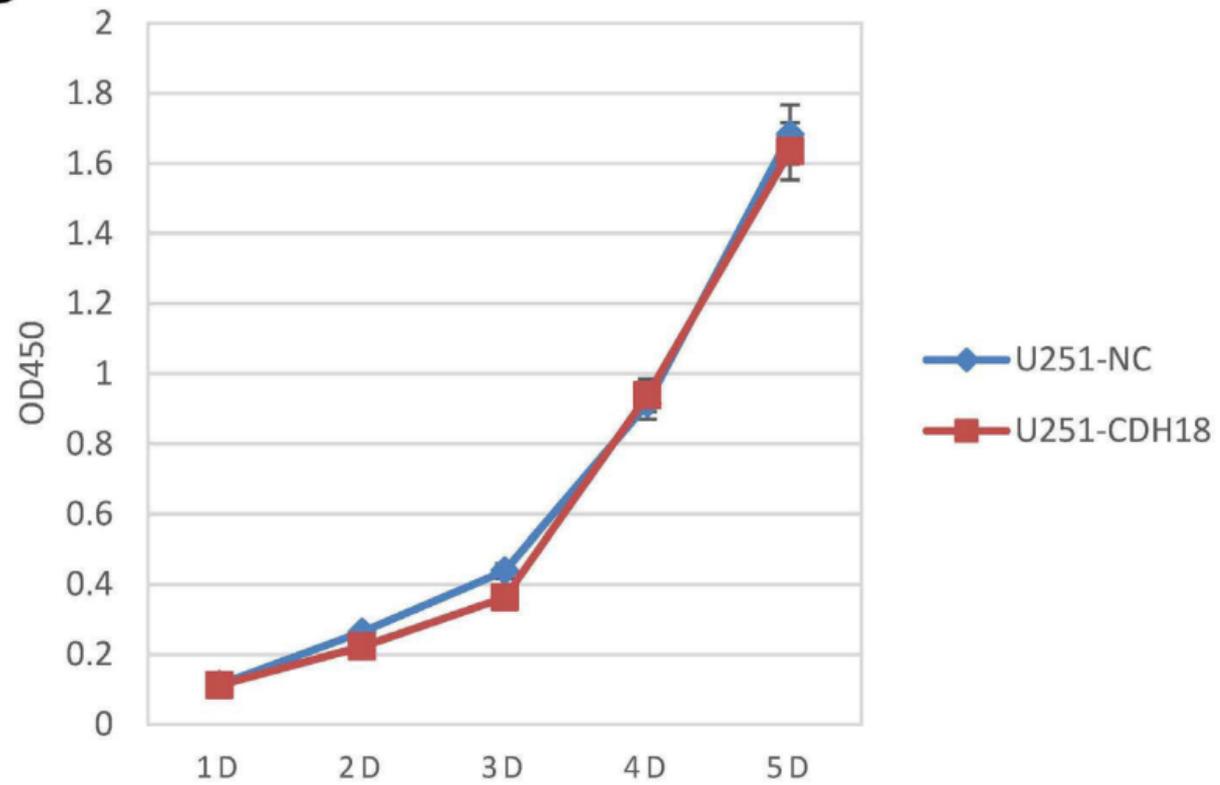
(A) Distribution of DNA copy number amplification on the genome. (B) Distribution of DNA copy number deletion on the genome. X-axis represented the significance by Q value. The green line represents the significance cutoff at Q value=0.25. (C) Diagram depicting the DNA CNVs of GBM. Blue represented deletion of DNA copy number and red represented amplification of DNA copy number. The color scale shown at the bottom indicated the fold changes.

Supplementary Fig 1

A**B****C**

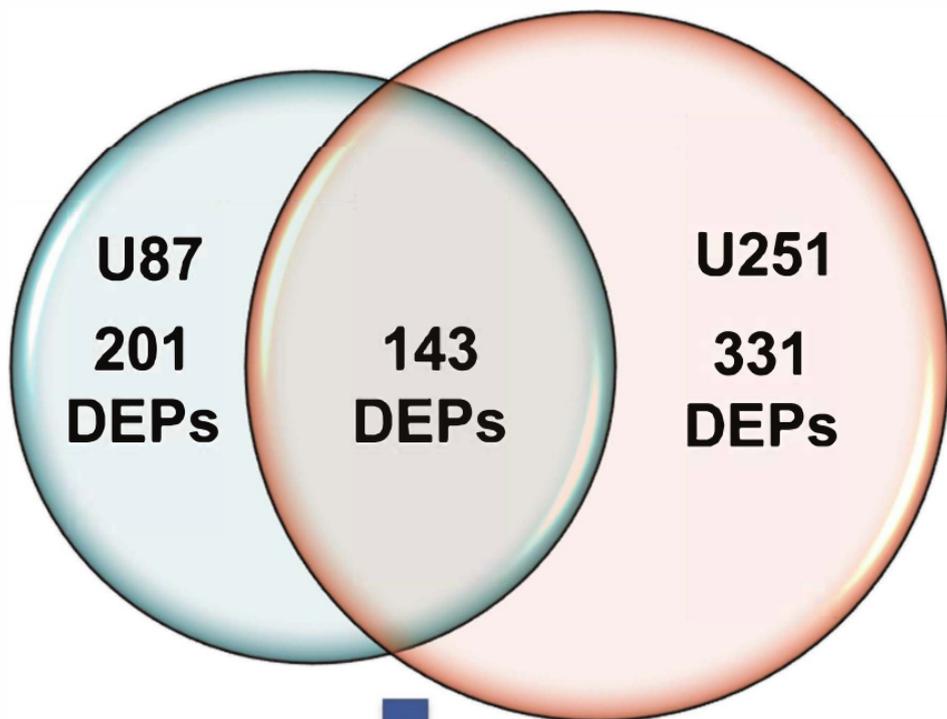
Supplementary Figure 2 CCK-8 assay was performed to investigate the effects of CDH18 on cell viability of U87 and U251 cells. Data are shown as Mean+SD (n = 3).

Supplementary Fig 2

A**U87****B****U251**

Supplementary Figure 3 Venn diagram showed differential expressed proteins(DEPs) between U87-NC vs U87-CDH18 groups, and DEPs between U251-NC vs U251-CDH18 groups.

Supplementary Fig 3



GO, KEGG Analyses

Supplementary Table 1

Fisher's exact test on the relationship between the 33 differential genes and CNVs

Name	P Value
ADH1B	0
SLC18A1	0
CDH18	0.007
ADAMTS20	0.05
CCNB3	0.247
TMEM196	0.264
F5	0.27
ST8SIA2	0.356
ZNF208	0.442
ZNF98	0.442
ZNF676	0.442
OR4N2	0.452
ALPK2	0.51
PCDH11X	0.556
PABPC5	0.556
PCDH15	0.65
ZNF560	0.741
NTN4	0.748
SLC1A6	0.767
GBAS	0.82
PSPH	0.82
PCDHA9	0.839
CLIC6	0.852
SUSD5	0.894
KLRC2	0.896
CNTNAP5	0.899
SPHKAP	0.957
GRIP2	0.978
POU4F1	0.986
TACR1	0.986
SLITRK1	0.986
SCGN	0.989

Supplementary Table 2 Univariate analysis of prognostic factors for OS in glioma patients (n = 453).

Factors	No. of cases	5-year OS (%)	P-value
Sex			
Male	256	32.6	0.788
Female	197	34.8	
Age			
≤50	247	50.5	<0.001
>50	206	12.0	
KPS			
≤80	148	39.8	0.221
>80	305	29.7	
Extent of resection			
Gross total	343	34.4	0.007
Subtotal	110	30.9	
RT			
Yes	357	37.5	<0.001
No	96	21.6	
CHT			
Yes	333	37.6	<0.001
No	120	22.4	
CDH18			
High	225	49.6	<0.001
Low	228	9.80	
Grade			
II	160	77.0	<0.001
III	90	19.7	
IV	203	0.0	
UQCRC2			
High	177	55.7	<0.001
Low	276	18.3	

Supplementary Table 3 KEGG pathway analysis of the differential expressed genes(DEPs) between CDH18 overexpression and control groups of glioma cell lines

Term	Count	PValue	Genes
hsa05012:Parkinson's disease	9	2.45E-05	UQCRC2, NDUFA6, PPID, COX6B1, COX7C, ATP5O, UQCRQ, UQCRB, COX6C
hsa00190:Oxidative phosphorylation	9	2.75E-05	UQCRC2, COX11, NDUFA6, COX6B1, COX7C, ATP5O, UQCRQ, UQCRB, COX6C
hsa05016:Huntington's disease	10	4.32E-05	UQCRC2, CLTB, NDUFA6, PPID, COX6B1, COX7C, ATP5O, UQCRQ, UQCRB, COX6C
hsa04260:Cardiac muscle contraction	6	8.40E-04	UQCRC2, COX6B1, COX7C, UQCRQ, UQCRB, COX6C
hsa05010:Alzheimer's disease	8	8.44E-04	UQCRC2, NDUFA6, COX6B1, COX7C, ATP5O, UQCRQ, UQCRB, COX6C
hsa04142:Lysosome	6	0.005033	AGA, GNS, CLTB, HEXB, GALNS, GBA
hsa00511:Other glycan degradation	3	0.010016	AGA, HEXB, GBA
hsa00531:Glycosaminoglycan degradation	3	0.016999	GNS, HEXB, GALNS
hsa00280:Valine, leucine and isoleucine degradation	3	0.066611	BCKDHA, DBT, ALDH6A1