



Research article

Transcriptome analysis revealed CENPF associated with glioma prognosis

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Supplementary

Table S1. GO analysis of the DEGs.

Category	Term	Count	P-Value	FDR
GOTERM_BP_DIRECT	GO: 0060333~interferon-gamma-mediated signaling pathway	10	2.99E-05	0.051034599
GOTERM_BP_DIRECT	GO: 0043547~positive regulation of GTPase activity	29	8.90E-05	0.151570947
GOTERM_BP_DIRECT	GO: 0007165~signal transduction	43	1.69E-03	2.843490887
GOTERM_BP_DIRECT	GO: 0000226~microtubule cytoskeleton organization	7	5.30E-03	8.660935755
GOTERM_BP_DIRECT	GO: 0042493~response to drug	15	9.32E-03	14.75498688
GOTERM_BP_DIRECT	GO: 0051301~cell division	16	1.35E-02	20.61670118
GOTERM_BP_DIRECT	GO: 0007155~cell adhesion	18	3.19E-02	42.43547169

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Category	Term	Count	P-Value	FDR
GOTERM_CC_DIRECT	GO: 0005737~cytoplasm	163	9.67E-07	0.001338778
GOTERM_CC_DIRECT	GO: 0048471~perinuclear region of cytoplasm	35	1.71E-06	0.002371533
GOTERM_CC_DIRECT	GO: 0030054~cell junction	29	1.84E-06	0.002552474
GOTERM_CC_DIRECT	GO: 0005886~plasma membrane	126	1.05E-04	0.145413077
GOTERM_CC_DIRECT	GO: 0005829~cytosol	101	8.28E-04	1.140086138
GOTERM_MF_DIRECT	GO: 0005515~protein binding	236	2.50E-04	0.370787171
GOTERM_MF_DIRECT	GO: 0004672~protein kinase activity	20	6.44E-04	0.953706048
GOTERM_MF_DIRECT	GO: 0005102~receptor binding	19	1.34E-03	1.976784684
GOTERM_MF_DIRECT	GO: 0005524~ATP binding	49	1.03E-02	14.2606997
GOTERM_MF_DIRECT	GO: 0005096~GTPase activator activity	13	2.74E-02	33.78236987
GOTERM_MF_DIRECT	GO: 0008144~drug binding	6	3.00E-02	36.42209753

Table S2. KEGG analysis of the DEGs.

Category	Term	Count	P-Value
KEGG_PATHWAY	hsa04012: ErbB signaling pathway	8	4.14E-04
KEGG_PATHWAY	hsa04727: GABAergic synapse	8	9.83E-04
KEGG_PATHWAY	hsa04914: Progesterone-mediated oocyte maturation	7	5.95E-03
KEGG_PATHWAY	hsa04024: cAMP signaling pathway	11	3.85E-03
KEGG_PATHWAY	hsa05206: MicroRNAs in cancer	9	8.00E-03
KEGG_PATHWAY	hsa04261: Adrenergic signaling in cardiomyocytes	8	1.44E-02
KEGG_PATHWAY	hsa04912: GnRH signaling pathway	6	1.43E-02
KEGG_PATHWAY	hsa04722: Neurotrophin signaling pathway	7	1.42E-02
KEGG_PATHWAY	hsa05230: Central carbon metabolism in cancer	5	1.38E-02
KEGG_PATHWAY	hsa04725: Cholinergic synapse	7	1.26E-02

Table S3. KEGG analysis of the related genes.

Category	Term	Count	P-Value
KEGG_PATHWAY	hsa04110: Cell cycle	4	3.36E-06
KEGG_PATHWAY	hsa05203: Viral carcinogenesis	4	5.57E-05
KEGG_PATHWAY	hsa04914: Progesterone-mediated oocyte maturation	3	9.76E-05
KEGG_PATHWAY	hsa04114: Oocyte meiosis	3	1.88E-04
KEGG_PATHWAY	hsa04115: p53 signaling pathway	2	1.96E-03
KEGG_PATHWAY	hsa04218: Cellular senescence	3	2.75E-03
KEGG_PATHWAY	hsa05169: Epstein-Barr virus infection	2	3.18E-02
KEGG_PATHWAY	hsa05166: HTLV-I infection	2	4.79E-02

Table S4. Correlation between TOP2A expression and clinicopathological in gliomas.

Clinicopathological Parameter, value	TOP2A expression			χ^2	P value
	N	Low expression (%)	High expression (%)		
Gender					
Male	398 (57.4)	209 (52.5)	189 (47.5)		
Female	295 (42.6)	137 (46.4)	158 (53.6)	2.499	0.114
Age					
≥ 43	349 (50.4)	165 (47.3)	184 (52.7)		
< 43	343 (49.5)	181 (52.8)	162 (47.2)	2.087	0.149
Missing	1 (0.1)	0 (0.0)	1 (100.0)		
WHO grade					
II	188 (27.1)	141 (75.0)	47 (25.0)		
III	255 (36.8)	125 (49.0)	130 (51.0)		
IV	249 (36.0)	80 (32.1)	169 (67.9)	78.909	< 0.001*
Missing	1 (0.1)	0 (0.0)	1 (100.0)		
IDH mutation					
Wildtype	286 (41.3)	118 (41.3)	168 (58.7)		

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Clinicopathological Parameter, value	TOP2A expression				
	<i>N</i>	Low expression (%)	High expression (%)	χ^2	<i>P</i> value
Mutant	356 (51.4)	202 (56.7)	154 (43.3)	15.207	< 0.001*
Missing	51 (7.3)	26 (51.0)	25 (49.0)		
1p, 19q codeletion status					
Non-codel	478 (69.0)	200 (41.8)	278 (58.2)	7.991	0.005*
Codel	145 (20.9)	80 (55.2)	65 (44.8)		
Missing	70 (10.1)	66 (94.3)	4 (5.7)		
Recurrent				9.993	0.002*
Yes	271 (39.1)	115 (42.4)	156 (57.6)		
No	422 (60.9)	231 (54.7)	191 (45.3)		
Radiotherapy status				4.936	0.026*
Yes	509 (73.4)	243 (47.7)	266 (52.3)		
No	113 (16.3)	67 (59.3)	46 (40.7)		
Missing	71 (10.3)	36 (50.7)	35 (49.3)	8.461	0.004*
Chemotherapy status					
Yes	457 (65.9)	210 (46.0)	247 (54.0)		
No	151 (21.8)	90 (59.6)	61 (40.4)	8.461	0.004*
Missing	85 (12.3)	46 (54.1)	39 (45.9)		

Table S5. Correlation between CDC20 expression and clinicopathological in gliomas.

Clinicopathological Parameter, value	CDC20 expression				<i>P</i> -value
	<i>N</i>	Low expression	High expression	χ^2	
Gender				0.933	0.334
Male	398 (57.4)	205 (51.5)	193 (48.5)		
Female	295 (42.6)	141 (47.8)	154 (52.2)	2.087	0.149
Age					
≥ 43	349 (50.4)	165 (47.3)	184 (52.7)		
< 43	343 (49.5)	181 (52.8)	162 (47.2)	2.087	0.149
Missing	1 (0.1)	0 (0.0)	1 (100.0)		

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Clinicopathological Parameter, value	CDC20 expression				
	<i>N</i>	Low expression	High expression	χ^2	<i>P</i> -value
WHO grade					
II	188 (27.1)	144 (76.6)	44 (23.4)	106.962	< 0.001
III	255 (36.8)	134 (52.5)	121 (47.5)		
IV	249 (36.0)	67 (26.9)	182 (73.1)		
Missing	1 (0.1)	1 (100.0)	0 (0.0)		
IDH mutation					
Wildtype	286 (41.3)	99 (34.6)	187 (65.4)	53.912	< 0.001
Mutant	356 (51.4)	227 (63.8)	129 (36.2)		
Missing	51 (7.3)	20 (39.2)	31 (60.8)		
1p, 19q codeletion status					
Non-codel	478 (69.0)	176 (36.8)	302 (63.2)	54.775	< 0.001
Codel	145 (20.9)	104 (71.7)	41 (28.3)		
Missing	70 (10.1)	66 (94.3)	4 (5.7)		
Recurrent					
Yes	271 (39.1)	108 (39.9)	163 (60.1)	18.071	< 0.001
No	422 (60.9)	238 (56.4)	184 (43.6)		
Radiotherapy status					
Yes	509 (72.5)	248 (48.7)	261 (51.3)	1.828	0.176
No	113 (16.3)	63 (55.8)	50 (44.2)		
Missing	71 (10.2)	35 (49.3)	36 (50.7)		
Chemotherapy status					
Yes	457 (65.9)	210 (46.0)	247 (54.0)	8.461	0.004
No	151 (21.9)	90 (59.6)	61 (40.4)		
Missing	85 (12.2)	46 (54.1)	39 (45.9)		



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