

Supplementary materials

Table S1 Characteristics of patients in this study

	<i>IDH</i> -mutant (<i>n</i> = 187)		<i>IDH</i> -wildtype (<i>n</i> = 173)	
Age (years)	41 (24–66)		52 (18–79)	
Gender				
Male	114	61.0%	111	64.2%
Female	73	39.0%	62	35.8%
Type				
Primary	59	31.6%	127	73.4%
Recurrent/secondary	128	68.4%	46	26.6%
Resection				
Gross total	119	63.6%	116	67.1%
Subtotal	60	32.1%	48	27.7%
Unknown	8	4.3%	9	5.2%
Radiotherapy				
Yes	84	44.9%	123	71.1%
No	85	45.5%	39	22.5%
Unknown	18	9.6%	11	6.4%
Chemotherapy (TMZ)				
Yes	130	69.5%	99	57.3%
No	37	19.8%	10	5.8%
Unknown	20	10.7%	64	36.9%
MGMT promoter methylation				
Methylated ($\geq 30\%$)	36	19.3%	28	16.2%
Weakly methylated ($\geq 10\%$, $< 30\%$)	40	21.4%	33	19.1%
Unmethylated ($< 10\%$)	22	11.8%	112	64.7%
Unknown	89	47.6%	0	0.0%
MGMT RNA expression				
Available	143	76.5%	129	74.6%
Unavailable	44	23.5%	44	25.4%

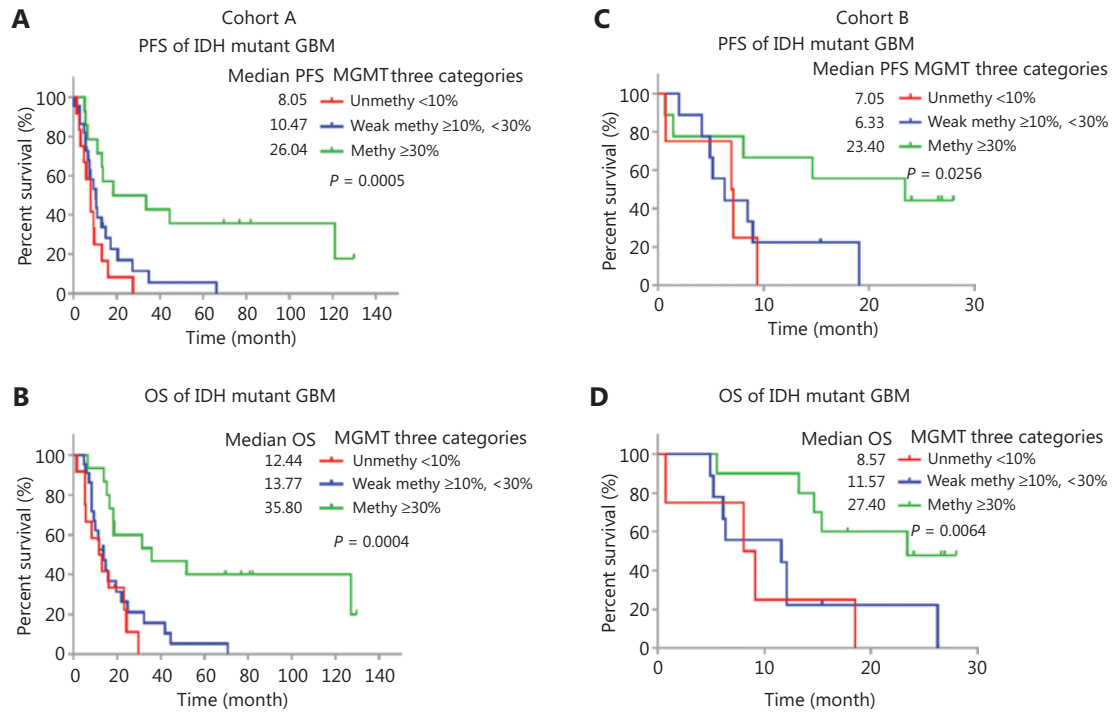


Figure S1 Survival analysis of TMZ-treated IDH-mutant GBM with different MGMT promoter methylation levels. (A, B) Kaplan-Meier curves for PFS and OS of IDH-mutant patients with GBM in different methylation groups in cohort A. MGMT promoter methylation levels were calculated by the average levels of CpG sites 75–78. (C, D) Kaplan-Meier curves for PFS and OS of IDH-mutant patients with GBM in different methylation groups in cohort B. MGMT promoter methylation levels were calculated by the average levels of CpG sites 76–79. Unmethy: unmethylated, methy: methylated. P -value calculated by the log-rank test.

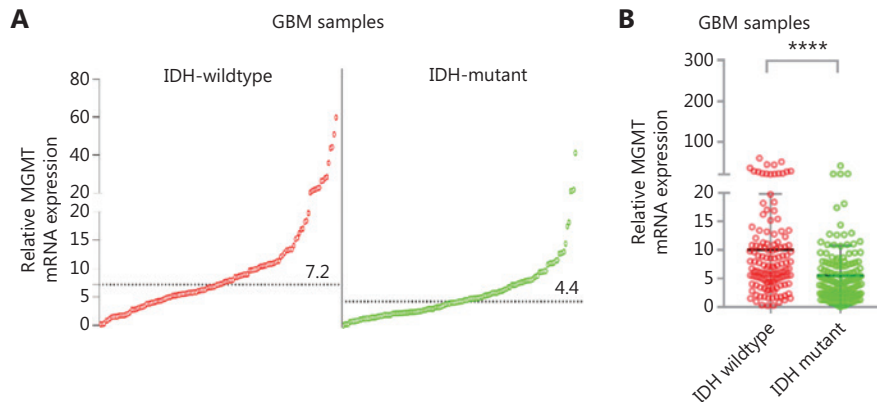


Figure S2 MGMT expression in GBM with or without IDH mutation. (A, B) MGMT mRNA expression levels were compared between GBM with ($n = 143$) or without ($n = 129$) IDH mutation. **** $P < 0.0001$ calculated by the t test.

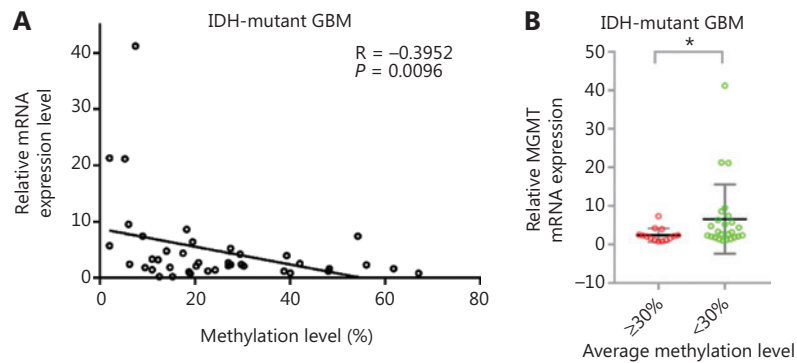


Figure S3 *MGMT* promoter methylation is negatively correlated with *MGMT* mRNA expression in *IDH*-mutant GBM. (A) Correlation of *MGMT* promoter methylation with *MGMT* mRNA expression in *IDH*-mutant GBM. R and P-value obtained by the Spearman R test. (B) *MGMT* mRNA expression levels were compared between *IDH*-mutant GBM with and without *MGMT* promoter methylation. **P* < 0.05 calculated by t test.

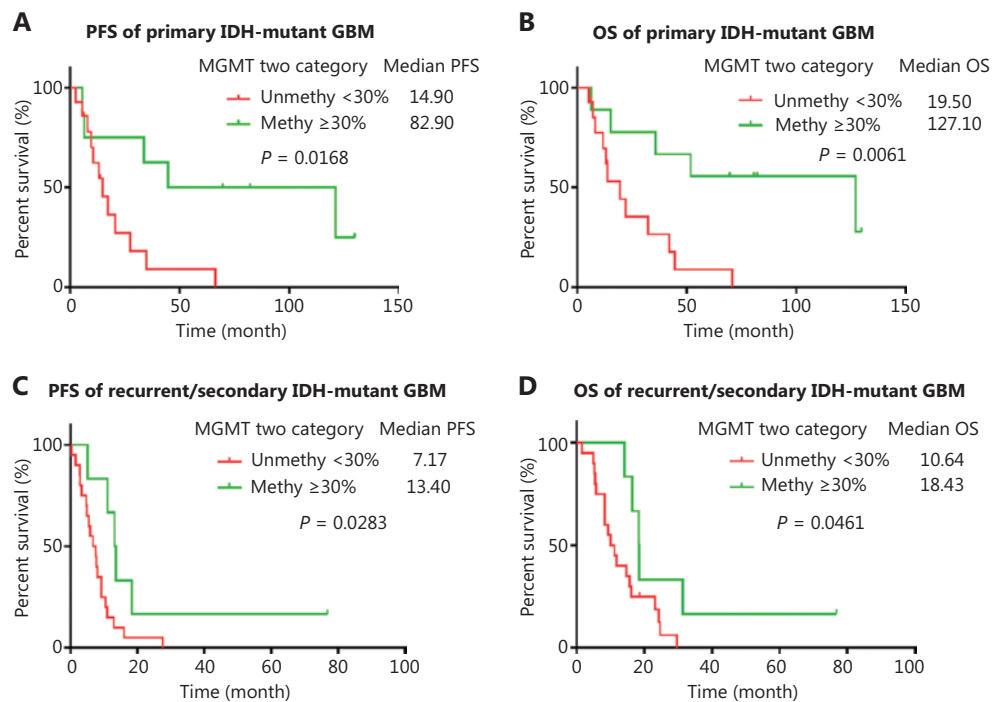


Figure S4 The predictive value of *MGMT* promoter methylation in primary and recurrent/secondary *IDH*-mutant GBM. (A, B) Kaplan-Meier curves for PFS and OS of primary *IDH*-mutant patients with GBM in different methylation groups. (C, D) Kaplan-Meier curves for PFS and OS of recurrent/secondary *IDH*-mutant patients with GBM in different methylation groups. Unmethy: unmethylated, methy: methylated. *P*-value calculated by log-rank test. *MGMT* promoter methylation levels were calculated by the average methylation levels of CpG sites 75–78.