A five-miRNA signature with prognostic and predictive value for *MGMT* promoter-methylated glioblastoma patients

Supplementary Material

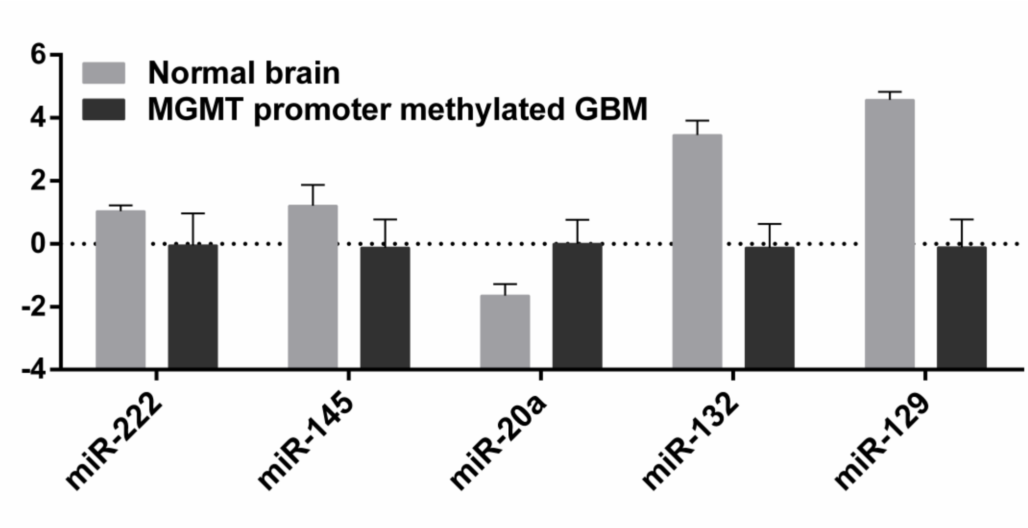


Figure S1. Comparison of the expression levels of five miRNAs comprising the miRNA signature between normal brain tissue and GBM specimens with MGMT promoter methylation. Bars indicate standard deviation.

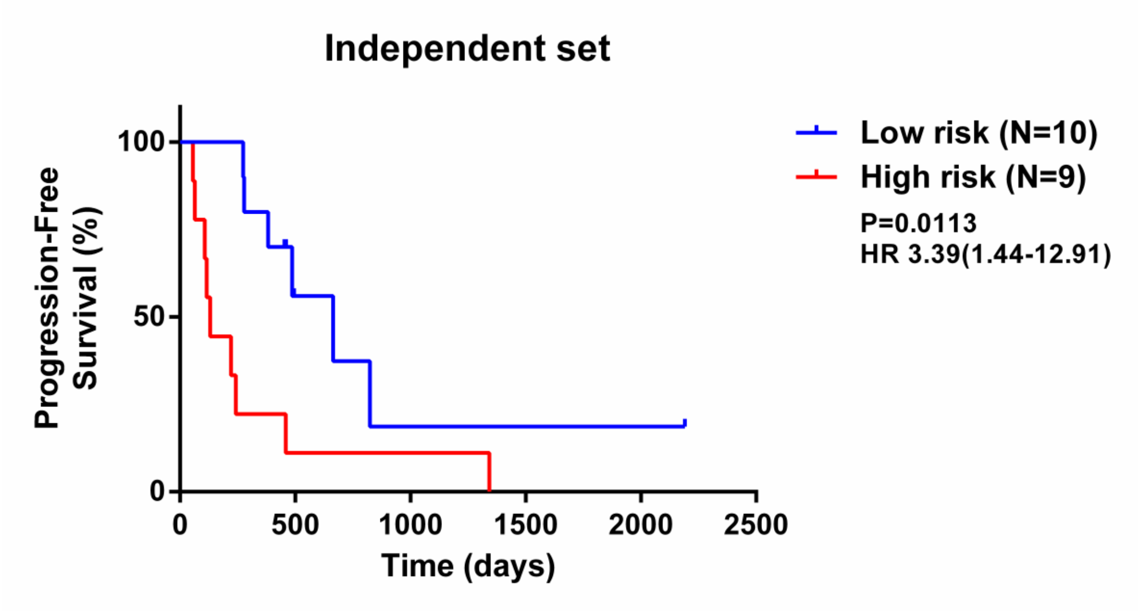


Figure S2. Prognostic value of the five-miRNA signature for PFS using independent set.

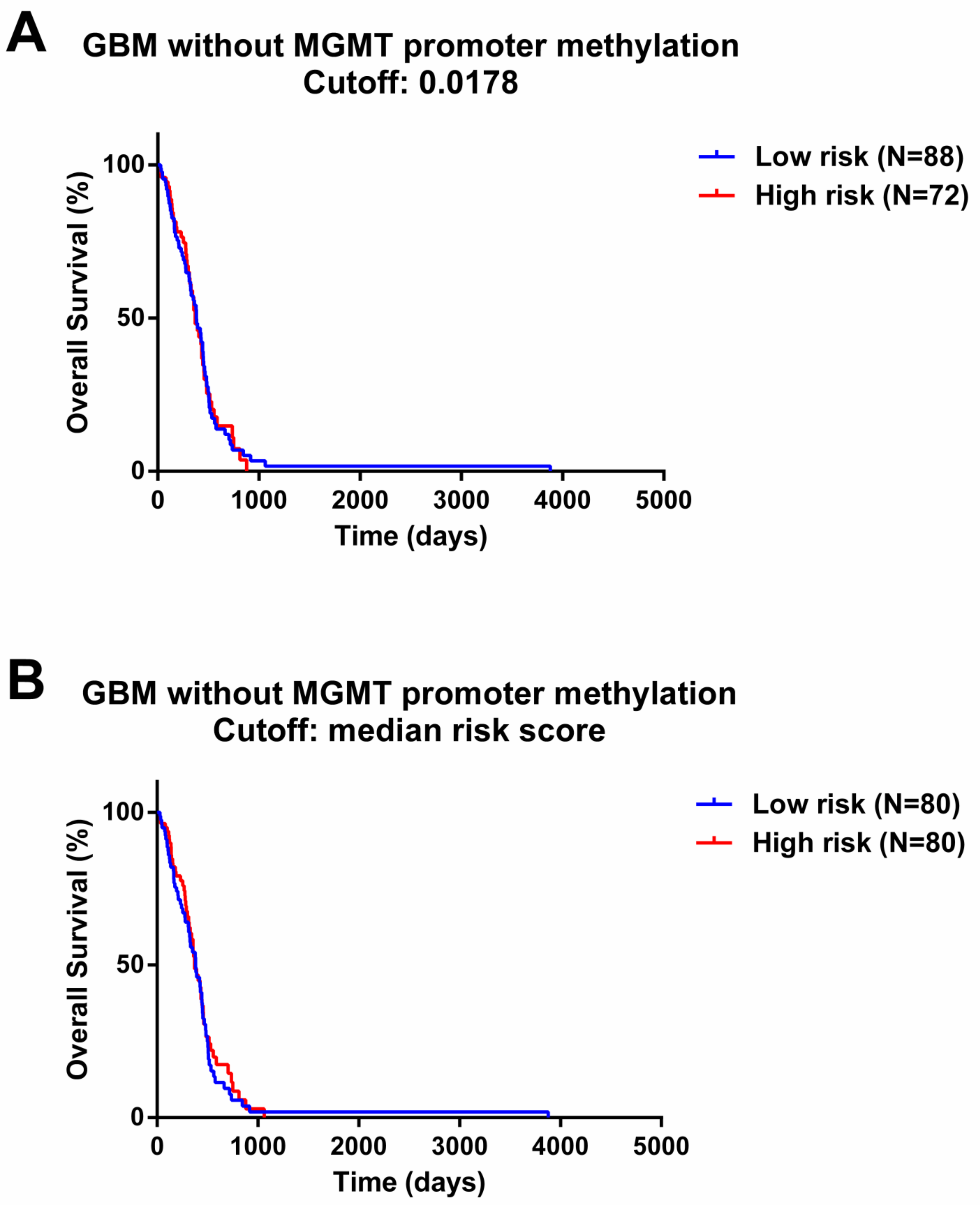


Figure S3. Lack of prognostic value for the five-miRNA signature in GBM patients without *MGMT* promoter methylation using the cutoff value of 0.0178 (A) or the median risk value (B).

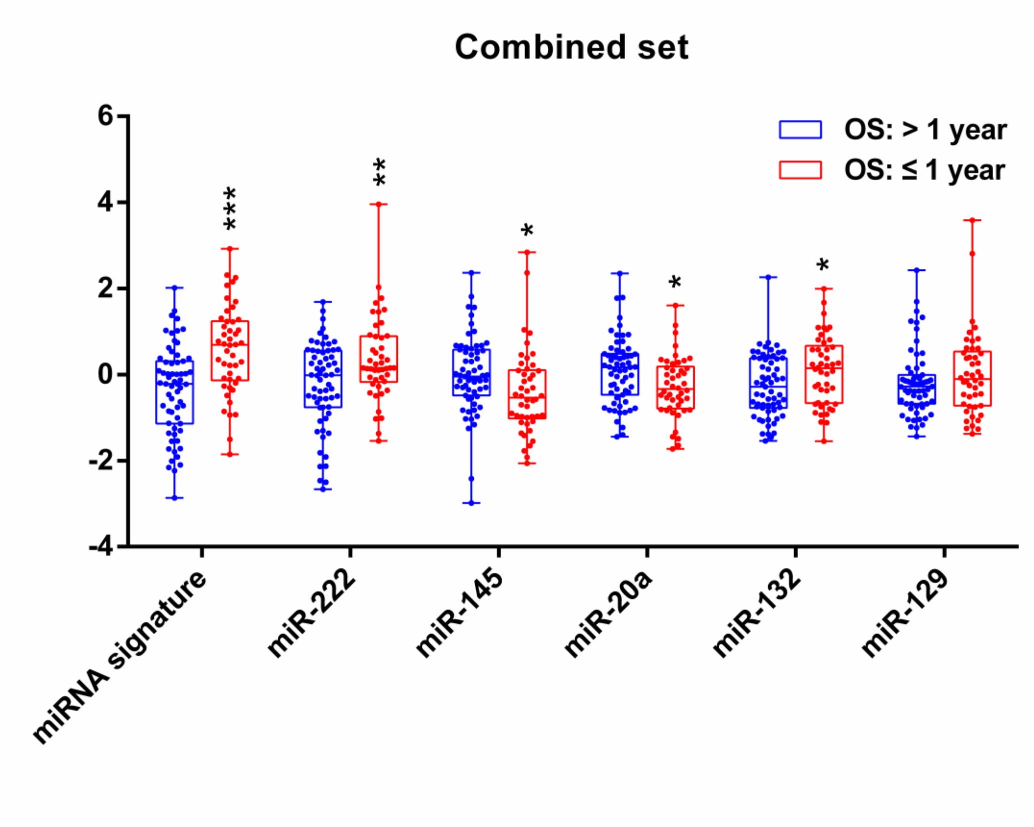


Figure S4. Comparison of the five-miRNA signature and its constituent miRNAs between cases with long and short survival time using a combined set. *P < 0.05, **P < 0.01, ***P < 0.001.

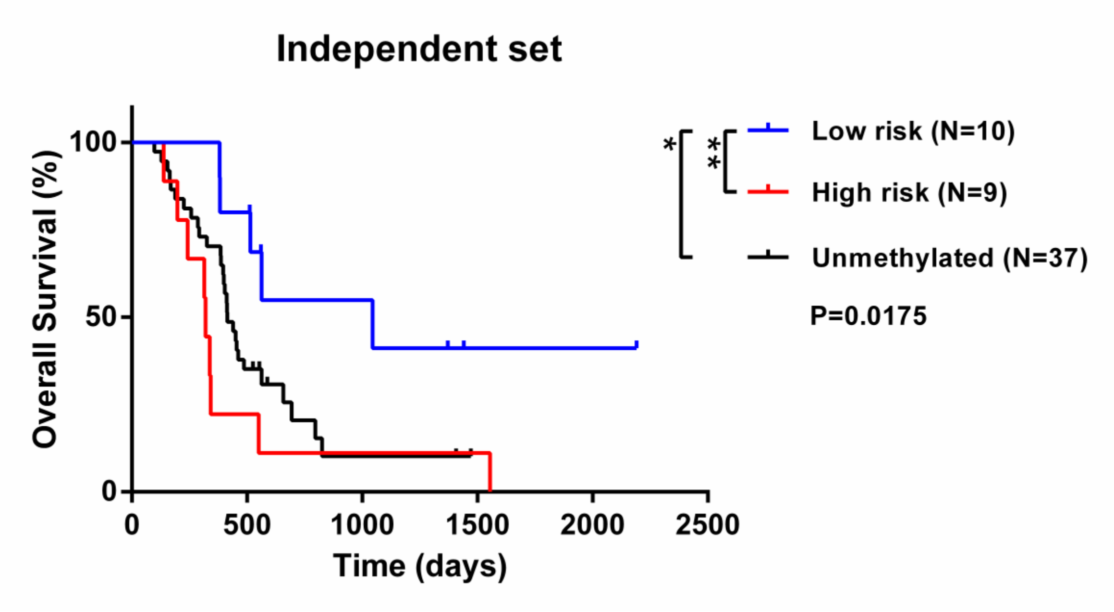


Figure S5. Prognosis of unmethylated GBM samples and high- and low-risk GBM patients with *MGMT* promoter methylation using an independent set. *P < 0.05, **P < 0.01, ***P < 0.001.

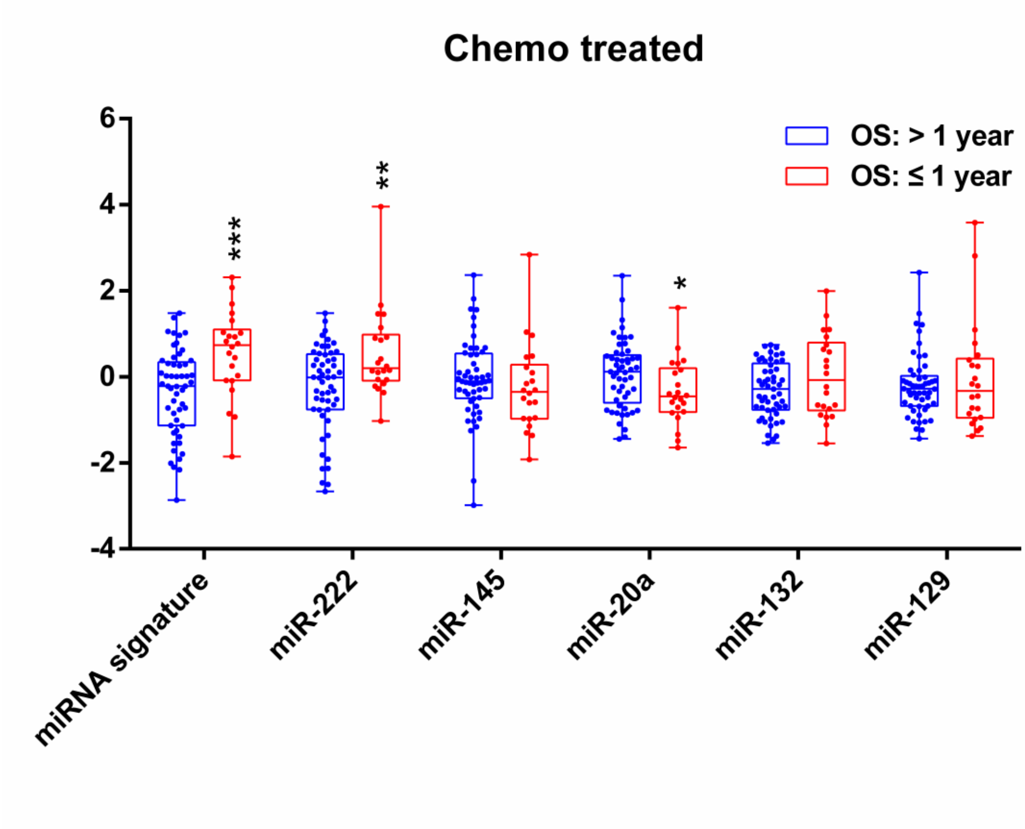
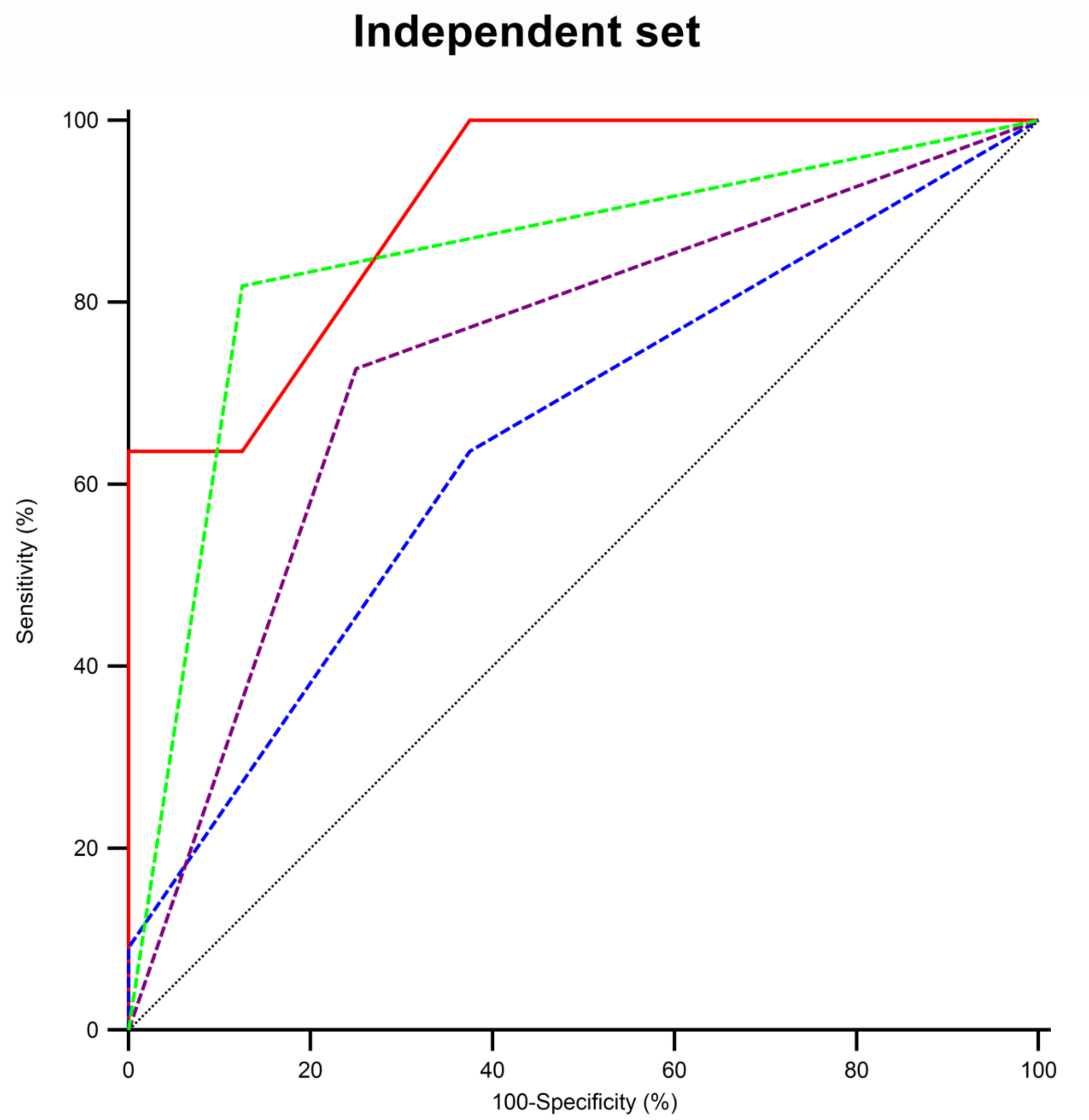


Figure S6. Comparison of the five-miRNA signature and its constituent miRNAs between chemotherapy responders and non-responders. *P < 0.05, **P < 0.01, ***P < 0.001.



	AUROC	95% CI	P-value
― Total points	0.909	0.687 to 0.991	
- - - Age	0.648	0.399 to 0.849	0.0085
- - - Chemotherapy	0.739	0.490 to 0.910	0.0402
- - - 5-miRNA signature	0.847	0.610 to 0.968	0.4524

Figure S7. Sensitivity and specificity of the risk model for predicting 1-year survival using the independent set.

Table S1. Univariate Cox regression of miRNAs for survival in training set.

Variable	P-value	HR	95%CI
hsa-miR-222	0.0112	1.6024	1.1129-2.3072
hsa-miR-145	0.0132	0.5809	0.3780-0.8925
hsa-miR-20a	0.0202	0.6175	0.4112-0.9274
hsa-miR-132	0.0218	1.6954	1.0797-2.6623
hsa-miR-129	0.0456	1.3948	1.0066-1.9328

Table S2. Cox hazard regression analysis of clinicopathologic factors and the five-miRNA signature for survival in the independent set

Variable	Univariate Cox		Multivariate Cox	
	P-value	HR	P-value	HR
Age				
(Per 20 years)	0.3845	1.4990		
Gender				
(Female vs. Male)	0.5433	0.7195		
KPS				
(≥80 vs. <80)	0.4431	0.5296		
IDH1 mutation				
(Mutation vs. Wild type)	0.0469	0.1137	0.0305	0.0753
Radiotherapy				
(Treated vs. Untreated)	0.0530	0.2504		
Chemotherapy				
(Treated vs. Untreated)	0.0937	0.3798		
Five-miRNA signature				
(High vs. Low risk)	**0.0082**	**4.5896**	**0.0090**	**6.4662**