Supplementary

Table S1 The Detailed Molecular Information of 9 Cases with Gliomas of *IDH*-wildtype, NOS

ID	sex	age	*IDH*	1p19q	*EGFR* amplification	+7/−10 cytogenetic signature	*CDKN2A/B* homozygously deletion	necrosis	microvascular proliferation	original histologic diagnosis	original histologic WHO grade	OS (m)	survival status
1	male	47	wild-type	non-codeletion			no deletion			diffuse astrocytomas	III	24.00	dead
2	male	50	wild-type							diffuse astrocytomas	II	92.80	alive
3	male	51	wild-type			no +7/−10				gemistocytic astrocytoma	II	-	lost to follow-up
4	female	43	wild-type	codeletion				no	no	oligodendrogliomas	II	39.10	alive
5	male	65	wild-type	non-codeletion	no amplification	no +7/−10		no		diffuse astrocytomas	II	2.40	alive
6	female	40	wild-type		no amplification	no +7/−10			not obvious	diffuse astrocytomas	II	74.60	dead
7	female	48	wild-type							anaplastic astrocytoma	III		
8	male	31	wild-type	non-codeletion			no deletion			low-grade glioma	II	31.60	dead
9	female	37	wild-type		no amplification	no +7/−10		no		oligoastrocytoma	II	72.70	alive

A blank in the table indicates that the attribute was not mentioned or not tested. The following tables show the results of the univariate statistical analysis. Initially, non-parametric univariate analysis was performed to evaluate whether any significant difference was presented in different groups. Then, for statistically significant parameters, receiver operating characteristic (ROC) curve analysis was performed to assess the discriminant capacity, describing the area under the ROC curves (AUCs), sensitivity, specificity, and cut-offs. The following additional abbreviations have been used in the following tables. Unless otherwise indicated, "*" indicates that $p < 0.05$, "**" indicates that $p < 0.01$, "***" indicates that $p<0.001$, "ns" indicates that $p>0.05$. p1, p value of the non-parametric test (two-tailed); p2, asymptotic p value of the ROC curve; 95% CI, 95% CI of AUC; Y, optimal Youden's index. In addition, the units of DCE parameters such as Ktans and Ve throughout the following tables are shown below, not displayed in the tables: The unit of Ktrans: min $^{-1}$. The unit of Kep: min^{-1}. The unit of iAUC: mM/sec. There is no unit for the DCE parameter of Ve and iAUC. WHO, World Health Organization; OS, overall survival; NOS, not otherwise specified.

Table S2 The Partial Representative Results of Non-parametric Tests and ROC Analysis of Useful Metrics for Diagnosing LGGs and HGGs

parameter	group (median)		p1	AUC	p2	95% CI	Y	SE	SP	cut-off
	HGG (n=61)	LGG (n=40)								
tumor.Ktrans.min	0.010	0.000	**	0.666	**	0.571 ~ 0.749	0.357	0.557	0.800	0.010
tumor.Ktrans.max	0.530	0.330	*	0.625	*	0.494 ~ 0.745	0.321	0.721	0.600	0.360
tumor.Ktrans.mean	0.150	0.060	***	0.777	***	0.683 ~ 0.842	0.444	0.869	0.575	0.080
tumor.Ve.min	0.030	0.000	***	0.748	***	0.656 ~ 0.827	0.520	0.770	0.750	0.010
tumor.Ve.max	2.480	2.030	ns	0.607	ns	0.497 ~ 0.716	0.266	0.541	0.725	2.370
tumor.Ve.mean	0.440	0.090	***	0.805	***	0.713 ~ 0.887	0.611	0.836	0.775	0.180
tumor.Kep.max	16.300	63.340	***	0.758	***	0.638~ 0.843	0.464	0.775	0.689	30.450
tumor.Kep.mean	1.580	5.235	***	0.800	***	0.670 ~ 0.898	0.610	0.725	0.885	4.320
tumor.iAUC.min	0.000	0.000	*	0.600	ns	0.486 ~ 0.708	0.195	0.295	0.900	0.000
tumor.iAUC.max	0.660	0.170	***	0.802	***	0.708 ~ 0.871	0.529	0.754	0.775	0.360
tumor.iAUC.mean	0.240	0.025	***	0.853	***	0.763 ~ 0.920	0.602	0.902	0.700	0.080
peritumoral.iAUC.max	0.020	0.010	ns	0.609	ns	0.493 ~ 0.724	0.254	0.754	0.500	0.000
peritumoral.iAUC.mean	0.010	0.000	ns	0.591	ns	0.476 ~ 0.707	0.215	0.590	0.625	0.000

ROC, receiver operating characteristic; LGG, low-grade glioma; HGG, high-grade glioma; AUC, area under the curve; CI, confidence interval; SE, sensitivity; SP, specificity; iAUC, initial area under the curve for the first 60 seconds.

Table S3 The Partial Representative Results of Non-parametric Tests and Post Hoc Pairwise Comparisons for Diagnosing Different Grades

parameter	grade (median)			p	p for WHO grade 2 *vs.* WHO grade 3	p for WHO grade 2 *vs.* WHO grade 4	p for WHO grade 3 *vs.* WHO grade 4
	WHO grade 2 (n=29)	WHO grade 3 (n=11)	WHO grade 4 (n=61)				
tumor-Ktrans-min	0.00	0.01	0.01	**	ns	***	ns
tumor-Ktrans-mean	0.06	0.11	0.15	***	ns	***	ns
tumor-Ve-min	0.00	0.04	0.03	***	**	***	ns
tumor-Ve-mean	0.08	0.46	0.44	***	**	***	ns
tumor-Kep-max	75.01	28.58	16.30	***	**	***	ns
tumor-Kep-mean	5.89	1.69	1.58	***	***	***	ns
tumor-iAUC-min	0.00	0.00	0.00	*	*	*	ns
tumor-iAUC-max	0.15	0.43	0.66	***	*	***	ns
tumor-iAUC-mean	0.01	0.16	0.24	***	*	***	ns
peritumoral-iAUC-max	0.00	0.05	0.02	*	ns	ns	ns
peritumoral-iAUC-mean	0.00	0.03	0.01	*	ns	ns	ns

WHO, World Health Organization; iAUC, initial area under the curve for the first 60 seconds.

Table S4 The partial representative AUC, Sensitivity, and Specificity Values, and Optimal Threshold for Useful Metrics for Diagnosing WHO Grade 2 gliomas

parameter	AUC	p2	95% CI	Y	SE	SP	cut-off
tumor-Ktrans-min	0.71	**	0.604 ~ 0.816	0.438	0.542	0.897	0
tumor-Ktrans-mean	0.789	***	0.677 ~ 0.878	0.516	0.861	0.655	0.06
tumor-Ve-min	0.813	***	0.737 ~ 0.879	0.598	0.736	0.862	0
tumor-Ve-mean	0.858	***	0.763 ~ 0.928	0.695	0.764	0.931	0.19
tumor-Kep-max	0.827	***	0.739 ~ 0.912	0.557	0.724	0.833	54.68
tumor-Kep-mean	0.872	***	0.788 ~ 0.942	0.689	0.828	0.861	4.86
tumor-iAUC-min	0.605	ns	0.491 ~ 0.720	0.209	0.278	0.931	0
tumor-iAUC-max	0.84	***	0.748 ~ 0.916	0.619	0.722	0.897	0.34
tumor-iAUC-mean	0.886	***	0.810 ~ 0.950	0.702	0.806	0.897	0.1
peritumoral-iAUC-max	0.643	*	0.523 ~ 0.744	0.239	0.722	0.517	0
peritumoral-iAUC-mean	0.64	*	0.532 ~ 0.750	0.273	0.583	0.69	0

ROC, receiver operating characteristic; AUC, area under the curve; CI, confidence interval; SE, sensitivity; SP, specificity; iAUC, initial area under the curve for the first 60 seconds.

Table S5 The Partial Representative AUC, Sensitivity, and Specificity Values, and Optimal Threshold for Useful Metrics for Diagnosing WHO grade 4 gliomas

parameter	AUC	p2	95% CI	Y	SE	SP	cut-off
tumor-Ktrans-min	0.666	**	0.557 ~ 0.774	0.357	0.557	0.8	0
tumor-Ktrans-mean	0.777	***	0.680 ~ 0.866	0.444	0.869	0.575	0.07
tumor-Ve-min	0.748	***	0.654 ~ 0.838	0.52	0.77	0.75	0
tumor-Ve-mean	0.805	***	0.709 ~ 0.889	0.611	0.836	0.775	0.17
tumor-Kep-max	0.758	***	0.650 ~ 0.845	0.464	0.775	0.689	27.99
tumor-Kep-mean	0.8	***	0.693 ~ 0.901	0.61	0.725	0.885	4.31
tumor-iAUC-min	0.597	ns	0.486 ~ 0.708	0.195	0.295	0.9	0
tumor-iAUC-max	0.802	***	0.701 ~ 0.888	0.529	0.754	0.775	0.34
tumor-iAUC-mean	0.853	***	0.768 ~ 0.925	0.602	0.902	0.7	0.07
peritumoral-iAUC-max	0.61	ns	0.496 ~ 0.714	0.254	0.754	0.5	0
peritumoral-iAUC-mean	0.591	ns	0.484 ~ 0.701	0.215	0.59	0.625	0

ROC, receiver operating characteristic; LGG, low-grade glioma; HGG, high-grade glioma; AUC, area under the curve; CI, confidence interval; SE, sensitivity; SP, specificity; iAUC, initial area under the curve for the first 60 seconds.

Table S6 The Partial Representative Results of Non-parametric tests and ROC Analysis of Useful Metrics for Diagnosing the Genotype of *IDH*

parameter	*IDH* (median)		p1	AUC	p2	95% CI	Y	SE	SP	cut-off
	wild-type (n=61)	mutation (n=36)								
tumor-Ktrans-min	0.010	0.000	*	0.629	*	0.540 ~ 0.714	0.272	0.516	0.757	0.000
tumor-Ktrans-mean	0.150	0.080	***	0.713	***	0.584 ~ 0.802	0.358	0.547	0.811	0.130
tumor-Ve-min	0.030	0.000	***	0.710	***	0.613 ~ 0.819	0.421	0.719	0.703	0.000
tumor-Ve-mean	0.420	0.090	***	0.738	***	0.643 ~ 0.828	0.467	0.656	0.811	0.340
tumor-Kep-max	21.630	54.680	***	0.705	***	0.559 ~ 0.815	0.370	0.730	0.641	27.990
tumor-Kep-mean	1.720	5.160	***	0.714	***	0.606 ~ 0.820	0.473	0.676	0.797	3.970
tumor-iAUC-max	0.590	0.240	***	0.710	***	0.601 ~ 0.788	0.476	0.719	0.757	0.340
tumor-iAUC-mean	0.220	0.050	***	0.770	***	0.690 ~ 0.868	0.459	0.594	0.865	0.170

ROC, receiver operating characteristicAUC, area under the curve; CI, confidence interval; SE, sensitivity; SP, specificity; iAUC, initial area under the curve for the first 60 seconds.

Table S7 The Partial Representative Results of Non-parametric Tests and ROC Analysis of Useful Metrics for Diagnosing the Genotype of 1p19q

parameter	1p19q (median)		p1	AUC	p2	95% CI	Y	SE	SP	cut-off
	codeletion (n=19)	non-codeletion (n=66)								
tumor-Ktrans-min	0.000	0.000	*	0.657	*	0.535 ~ 0.757	0.327	0.485	0.842	0.000
tumor-Ve-min	0.000	0.020	**	0.702	**	0.574 ~ 0.811	0.411	0.621	0.789	0.000
tumor-Ve-mean	0.110	0.375	*	0.687	*	0.541 ~ 0.837	0.388	0.652	0.737	0.160
tumor-Kep-max	70.650	27.510	**	0.705	**	0.575 ~ 0.828	0.388	0.737	0.652	42.040
tumor-Kep-mean	5.190	1.895	**	0.708	**	0.563 ~ 0.835	0.389	0.632	0.758	5.150
tumor-iAUC-mean	0.030	0.150	*	0.677	*	0.533 ~ 0.802	0.359	0.727	0.632	0.070

ROC, receiver operating characteristic; AUC, area under the curve; CI, confidence interval; SE, sensitivity; SP, specificity; iAUC, initial area under the curve for the first 60 seconds.

Table S8 The Partial Representative Results of Non-parametric Tests and ROC Analysis of Useful Metrics for Diagnosing the Genotype of *CDKN2A/B* Homozygous Deletion

parameter	*CDKN2A/B* homozygously deletion (median)		p1	AUC	p2	95% CI	Y	SE	SP	cut-off
	no deletion (n=43)	deletion (n=5)								
tumor-Ve-max	2.060	2.960	**	0.930	**	0.857 ~ 1.004	0.907	1.000	0.907	2.870
tumor-Ve-mean	0.090	0.700	*	0.830	*	0.719 ~ 0.942	0.744	1.000	0.744	0.190
tumor-Kep-min	0.030	0.000	*	0.784	*	0.645 ~ 0.922	0.674	0.674	1.000	0.010
tumor-Kep-mean	5.190	1.580	*	0.837	*	0.701 ~ 0.974	0.674	0.674	1.000	4.000
tumor-iAUC-max	0.220	0.440	*	0.777	*	0.597 ~ 0.956	0.581	1.000	0.581	0.240
tumor-iAUC-mean	0.030	0.140	*	0.791	*	0.644 ~ 0.937	0.628	1.000	0.628	0.070

ROC, receiver operating characteristic; AUC, area under the curve; CI, confidence interval; SE, sensitivity; SP, specificity; iAUC, initial area under the curve for the first 60 seconds.

Table S9 The Partial Representative Results of Non-parametric tests and ROC Analysis of Useful Metrics for Diagnosing the Genotype of *EGFR*

	EGFR amplification (median)		p1	AUC	p2	95% CI	Y	SE	SP	cut-off
	no amplification (n=37)	amplification (n=19)								
tumor-Ve-min	0.020	0.050	ns	0.649	ns	0.505 ~ 0.793	0.326	0.947	0.378	0.000
peritumoral-Ve-min	0.020	0.010	ns	0.649	ns	0.502 ~ 0.797	0.331	0.595	0.737	0.010
tumor-iAUC-mean	0.190	0.270	ns	0.648	ns	0.499 ~ 0.797	0.280	0.632	0.649	0.250

ROC, receiver operating characteristic; AUC, area under the curve; CI, confidence interval; SE, sensitivity; SP, specificity; iAUC, initial area under the curve for the first 60 seconds.

Table S10 The Partial Representative Results of Non-parametric Tests and ROC Analysis of Useful Metrics for Diagnosing the Genotype of +7/–10 Cytogenetic Signature

	+7/–10 cytogenetic signature (median)		p1	AUC	p2	95% CI	Y	SE	SP	cut-off
	no +7/–10 (n=18)	+7/–10 (n=2)								
peritumoral-Ktrans-max	0.090	0.035	ns	0.903	ns	0.728 ~ 1.078	0.778	0.778	1.000	0.050
peritumoral-Ve-max	0.210	0.020	ns	0.903	ns	0.758 ~ 1.048	0.778	0.778	1.000	0.030
peritumoral-Ve-mean	0.075	0.010	ns	0.917	ns	0.779 ~ 1.054	0.833	0.833	1.000	0.020

ROC, receiver operating characteristic; AUC, area under the curve; CI, confidence interval; SE, sensitivity; SP, specificity; iAUC, initial area under the curve for the first 60 seconds.

Table S11 The Partial Representative Results of Logistic Models for Predicting HGG, WHO Grade 2, WHO Grade 4, *IDH* Mutation, 1p19q Codeletion, and *CDKN2A/B* Homozygous Deletion

model	N	AUC	SE	SP	Y	cut-off	accuracy	PPV	NPV
pro-group	101	0.870	0.82	0.8	0.62	0.608	0.811	0.836	0.70
pro-grade2	101	0.893	0.793	0.903	0.696	0.494	0.861	0.759	0.903
pro-grade4	101	0.858	0.82	0.8	0.62	0.54	0.802	0.86	0.727
pro-IDH	101	0.85	0.892	0.703	0.595	0.264	0.762	0.627	0.9
pro-1p19q	85	0.705	0.652	0.737	0.388	0.798	0.659	0.894	0.368
pro-CDKN2A/B	48	0.93	1	0.907	0.907	0.315	0.896	0.5	0.975

AUC, area under the curve; CI, confidence interval; SE, sensitivity; SP, specificity; PPV, positive predictive value; NPV, negative predictive value.

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