

Table S1 Clinical data, pathology, and treatment plan information for the 58 glioma patients

n	Sex	Age (years)	Location	Pathology	WHO grade	IDH1 status	Treatment	Pretreatment
1	F	41	Frontal, right	Diffuse astrocytoma	II	Wild type	Total resection	None
2	M	63	Temporal, right	Diffuse astrocytoma	II	Wild type	Subtotal resection	None
3	M	48	Frontal, right	Oligodendroglioma, NOS	II	R132H mutation	Total resection	None
4	M	30	Brain stem	Astrocytoma	II	Wild type	Stereotactic biopsy	None
5	F	36	Frontal, left	Diffuse astrocytoma	II	R132H mutation	Subtotal resection	None
6	F	35	Frontal, left	Diffuse astrocytoma	II	Wild type	Subtotal resection	None
7	F	60	Frontal, left	Oligodendroglioma, NOS	II	R132H mutation	Total resection	None
8	F	49	Temporal, left	Diffuse astrocytoma	II	Wild type	Partial resection	None
9	F	49	Cerebellum, left	Diffuse astrocytoma	II	Wild type	Stereotactic biopsy	None
10	M	56	Frontal, left	Oligodendroglioma, NOS	II	R132H mutation	Subtotal resection	None
11	F	29	Frontal, left	Diffuse astrocytoma	II	R132H mutation	Total resection	None
12	F	35	Frontal, left	Oligodendroglioma, NOS	II	R132H mutation	Total resection	None
13	M	49	Frontal, left	Oligodendroglioma, NOS	II	R132H mutation	Subtotal resection	None
14	F	51	Frontal, left	Diffuse astrocytoma	II	Wild type (twice)	Total resection	None
15	M	51	Temporal, left	Diffuse astrocytoma	II	Wild type	Subtotal resection	None
16	M	29	Temporal, right	Oligodendroglioma, NOS	II	R132H mutation	Subtotal resection	None
17	F	32	Frontal-parietal, right	Diffuse astrocytoma	II	Wild type	Subtotal resection	None
18	M	24	Frontal, left	Diffuse astrocytoma	II	Wild type	Total resection	None
19	M	52	Parietal, right	Oligodendroglioma, NOS	II	R132H mutation	Subtotal resection	None
20	F	29	Frontal, left	Oligodendroglioma, NOS	II	R132H mutation	Total resection	None
21	F	31	Frontal, left	Diffuse astrocytoma	II	R132H mutation	Total resection	None
22	M	28	Thalamus, left	Diffuse astrocytoma	II	Wild type	Stereotactic biopsy	None
23	F	51	Frontal, left	Oligodendroglioma, NOS	II	R132H mutation	Total resection	None
24	M	54	Frontal, right	Diffuse astrocytoma	II	Wild type	Stereotactic biopsy	None
25	F	45	Parietal, right	Diffuse astrocytoma	II	Wild type (twice)	Stereotactic biopsy	None
26	M	39	Temporal, right	Oligodendroglioma, NOS	II	R132H mutation	Total resection	None
27	F	44	Temporal-insular, right	Oligodendroglioma, NOS	II	R132H mutation	Subtotal resection	None
28	M	28	Frontal, left	Diffuse astrocytoma	II	R132H mutation	Stereotactic biopsy	None
29	M	39	Frontal, right	Diffuse astrocytoma	II	R132H mutation	Total resection	None
30	M	42	Frontal, left	Oligodendroglioma, NOS	II	R132H mutation	Total resection	None
31	M	52	Frontal-temporal-insular, right	Oligodendroglioma, NOS	II	R132H mutation	Subtotal resection	None
32	M	24	Frontal-temporal, left	Diffuse astrocytoma	II	R132H mutation	Total resection	None
33	F	45	Frontal, left	Diffuse astrocytoma	II	Wild type	Stereotactic biopsy	None
34	M	29	Frontal-temporal-insular, left	Anaplastic astrocytoma	III	Wild type	Partial resection	None
35	M	66	Brain stem	Anaplastic astrocytoma	III	Wild type	Stereotactic biopsy	None
36	M	63	Frontal, right	Anaplastic astrocytoma	III	Wild type	Subtotal resection	None
37	M	52	Frontal, left	Anaplastic astrocytoma	III	Wild type	Total resection	None
38	M	38	Corpus callosum	Anaplastic astrocytoma	III	Wild type	Stereotactic biopsy	None
39	M	55	Frontal, left	Anaplastic astrocytoma	III	R132H mutation	Stereotactic biopsy	None
40	F	67	Temporal-insular, left	Anaplastic astrocytoma	III	Wild type	Total resection	None
41	M	31	Thalamus, right	Anaplastic astrocytoma	III	Wild type	Stereotactic biopsy	None
42	F	20	Basal ganglia, left	Anaplastic astrocytoma	III	Wild type	Stereotactic biopsy	None
43	F	30	Thalamus bilateral	Anaplastic astrocytoma	III	Wild type	Stereotactic biopsy	None
44	M	68	Frontal, right	Anaplastic astrocytoma	III	R132H mutation	Total resection	None
45	M	62	Basal ganglia, right	Anaplastic astrocytoma	III	Wild type	Stereotactic biopsy	None
46	F	24	Frontal, left	Anaplastic astrocytoma	III	Wild type	Stereotactic biopsy	None
47	M	17	Cerebellum, right	Glioblastoma	IV	Wild type	Partial resection	None
48	F	70	Frontal, left	Glioblastoma	IV	Wild type	Total resection	None
49	M	46	Temporal, right	Glioblastoma	IV	Wild type	Total resection	None
50	M	29	Thalamus, right	Diffuse midline glioma, H3K27M mutant	IV	Wild type	Stereotactic biopsy	None
51	M	30	Thalamus, left	Glioblastoma	IV	Wild type	Stereotactic biopsy	None
52	M	57	Basal ganglia, left	Glioblastoma	IV	Wild type	Subtotal resection	None
53	M	51	Basal ganglia, right	Glioblastoma	IV	Wild type	Stereotactic biopsy	None
54	M	19	Frontal, right	Glioblastoma	IV	Wild type	Total resection	None
55	M	61	Frontal, right	Glioblastoma	IV	Wild type	Subtotal resection	None
56	M	29	Frontal, left	Glioblastoma	IV	Wild type	Total resection	None
57	M	18	Basal ganglia, right	Glioblastoma	IV	Wild type	Stereotactic biopsy	None
58	M	27	Temporal, right	Glioblastoma	IV	Wild type	Partial resection	None

F, female; IDH1, isocitrate dehydrogenase gene 1; M, male; NOS, not otherwise specified; WHO, World Health Organization.

Table S2 Efficacy comparisons between top models in glioma grade prediction

Model	Observations (n)	ROC area	Standard error	95% CI
TLU	58	0.8406	0.0548	0.73309–0.94807
TBRpeak	58	0.8315	0.0625	0.70903–0.95402
HI	58	0.8261	0.0642	0.70022–0.95195
Com1	58	0.8496	0.0576	0.7368–0.96244
Com2	58	0.8478	0.0588	0.7325–0.96306
Com3	58	0.8478	0.0589	0.7323–0.96330

χ^2 -test [5]=2.66 Prob> χ^2 -test=0.7516. CI, confidence interval; Com1, the combined model of TBRmax, SUVsd, and TBRmean; Com2, the combined model of HI, SUVsd, and MTV; Com3, the combined model of HI, SUVsd, and TLU; HI, heterogeneity index; MTV, metabolic tumor volume; ROC, receiver-operating characteristic; SUVsd, standard deviation of lesion standardized uptake value; TBRmax, maximal tumor-to-background ratio; TBRmean, mean tumor-to-background ratio; TBRpeak, peak tumor-to-background ratio; TLU, total lesion tracer standardized uptake.

Table S3 Hosmer-Lemeshow goodness-of-fit test results for models in glioma grade prediction

Parameters	Observations (n)	Groups (n)	Hosmer-Lemeshow χ^2 -test	P value
TBRmax	58	10	5.74	0.676
TBRpeak	58	10	7.44	0.490
TBRmean	58	10	11.89	0.156
COV	58	10	8.44	0.392
HI	58	10	4.48	0.812
SUVsd	58	10	8.55	0.382
MTV	58	10	8.10	0.423
TLU	58	10	7.79	0.454
Com1	58	10	6.21	0.624
Com2	58	10	7.83	0.450
Com3	58	10	8.02	0.432

Com1, the combined model of TBRmax, SUVsd, and TBRmean; Com2, the combined model of HI, SUVsd, and MTV; Com3, the combined model of HI, SUVsd, and TLU; COV, coefficient of variation; HI, heterogeneity index; MTV, metabolic tumor volume; SUVsd, standard deviation of lesion standardized uptake value; TBRmax, maximal tumor-to-background ratio; TBRmean, mean tumor-to-background ratio; TBRpeak, peak tumor-to-background ratio; TLU, total lesion tracer standardized uptake.

Table S4 Efficacy comparisons between top models in isocitrate dehydrogenase gene 1 status prediction

Model	Observations (n)	ROC area	Standard error	95% CI
SUVsd	58	0.7098	0.0701	0.57247–0.84710
TLU	58	0.6976	0.0737	0.55303–0.84208
HI	58	0.6757	0.0729	0.53286–0.81849
Com1	58	0.8211	0.0596	0.70430–0.93792
Com2	58	0.8044	0.0623	0.68234–0.92641
Com3	58	0.7992	0.0613	0.67901–0.91945

χ^2 -test [5]=8.03 Prob> χ^2 -test=0.1547. CI, confidence interval; Com1, the combined model of TBRmax, SUVsd, and TBRmean; Com2, the combined model of SUVsd and TBRmean; Com3, the combined model of SUVsd, HI, and TBRmean; HI, heterogeneity index; ROC, receiver-operating characteristic; SUVsd, standard deviation of lesion standardized uptake value; TBRmax, maximal tumor-to-background ratio; TBRmean, mean tumor-to-background ratio; TLU, total lesion tracer standardized uptake.

Table S5 Hosmer-Lemeshow goodness-of-fit test results for models in isocitrate dehydrogenase gene 1 status prediction

Parameter	Observations (n)	Groups (n)	Hosmer-Lemeshow χ^2 -test	P value
TBRmax	58	10	7.12	0.524
TBRpeak	58	10	10.53	0.230
TBRmean	58	10	9.75	0.283
COV	58	10	9.06	0.337
HI	58	10	7.53	0.481
MTV	58	10	9.57	0.297
TLU	58	10	9.21	0.325
SUVsd	58	10	12.24	0.141
Com1	58	10	12.38	0.135
Com2	58	10	8.59	0.378
Com3	58	10	7.71	0.463

Com1, the combined model of TBRmax, SUVsd, and TBRmean; Com2, the combined model of SUVsd, and TBRmean; Com3, the combined model of SUVsd, HI, and TBRmean; COV, coefficient of variation; HI, heterogeneity index; MTV, metabolic tumor volume; SUVsd, standard deviation of lesion standardized uptake value; TBRmax, maximal tumor-to-background ratio; TBRmean, mean tumor-to-background ratio; TBRpeak, peak tumor-to-background ratio; TLU, total lesion tracer standardized uptake.