Appendix 1: MR scanner settings

Parameters of the sequences were as follows:

T1WI: repetition time (TR) = 1750–1821 ms; echo time (TE) = 24–27 ms; slice thickness = 5.0–6.0 mm; slice gap = 1–2 mm; number of slices = 20–22; field of view (FOV) = 24 × 24 cm^2; matrix = 320 × 320; NEX = 1; T2WI: TR = 5741–4440 ms; TE = 93–102 ms; slice thickness = 5.0–6.0 mm; slice gap = 1–2 mm; number of slices =20–22; FOV = 24 × 24 cm^2; matrix = 320 × 320; NEX = 1; DWI: TR = 3000–6000 ms; TE = 110–90 ms; slice thickness = 5.0–6.0 mm; slice gap = 1–2 mm; number of slices = 20–22; FOV = 24 × 24 cm^2; matrix = 320 × 320; NEX = 1.

Appendix 2: Method of calculating the apparent diffusion coefficient maps

Based on the diffusion-weighted images (with b equal to 0 and 1000), the apparent diffusion coefficient (ADC) maps were calculated using the following formula:

$$S_{DWI} = S_0 e^{-b \cdot ADC} \rightarrow ADC = -\frac{1}{b} \ln\left(\frac{S_{DWI}}{S_0}\right) \quad [1]$$

where S_{DWI} is the value in a volume in the DWI with b equal to 1000; and S_0 is value in a volume in the DWI with b equal to 0. ADC is produced for the value in volume.

Appendix 3: Detailed results of the experiments

AUC, area under curve; ACC^1 represents accuracy on the training set, whereas ACC^2 represents accuracy on the testing set; SEN, sensitivity; SPE, specificity; P value, calculated from the permutation test. All the results are presented as the mean and 95% confidence interval.

Results of classifiers based on a single sequence

Table C.1. ACCs and AUCs of classifiers based on a single sequence

	Histological phenotype		IDH status		Ki-67 expression	
	ACC	AUC	ACC	AUC	ACC	AUC
T1WI	0.5213 (0.4805–0.5622)	0.5470 (0.5036–0.5903)	0.4920 (0.4548–0.5292)	0.5044 (0.4661–0.5427)	0.5556 (0.5166–0.5945)	0.5490 (0.5065–0.5914)
T2WI	0.6040 (0.5653–0.6427)	0.6326 (0.5855–0.6777)	0.5613 (0.5249–0.5978)	0.5524 (0.5148–0.5899)	0.6568 (0.6251–0.6884)	0.7032 (0.6639–0.7424)
ADC	0.6400 (0.6089–0.6711)	0.6909 (0.6538–0.7281)	0.6560 (0.6214–0.6906)	0.7034 (0.6644–0.7425)	0.6988 (0.6649–0.7326)	0.7556 (0.7128–0.7984)
T1C	0.6547 (0.6229–0.6864)	0.6876 (0.6553–0.7199)	0.6013 (0.5599–0.6427)	0.6336 (0.5962–0.6709)	0.6704 (0.6417–0.6990)	0.7077 (0.6561–0.7593)
DWI	0.5247 (0.5053–0.5800)	0.5507 (0.5108–0.5906)	0.5493 (0.5154–0.5833)	0.5439 (0.5014–0.5864)	0.6272 (0.5920–0.6624)	0.6573 (0.6069–0.7077)

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Results of the classifiers based on different sequence combinations

Table C.2. Histological phenotype (glioblastomas *vs.* LGG)

	A	B	C
AUC	0.7086 (0.6754–0.7418)	0.7181 (0.6825–0.7536)	0.7228 (0.6912–0.7543)
ACC[1]	0.8697 (0.8455–0.8938)	0.9210 (0.9002–0.9419)	0.9755 (0.9622–0.9887)
ACC[2]	0.6680 (0.6405–0.6954)	0.6733 (0.6439–0.7026)	0.6746 (0.6505–0.6988)
SEN	0.6377 (0.5837–0.6917)	0.6227 (0.5674–0.6780)	0.6168 (0.5651–0.6685)
SPE	0.6910 (0.6466–0.7354)	0.7079 (0.6670–0.7488)	0.7246 (0.6787–0.7705)
P value	0.0908 (0.0593–0.1222)	0.0955 (0.0601–0.1309)	0.0700 (0.0524–0.0877)

Note: A (ADC and T1C); B (ADC, T2, and T1C); and C (all five sequences).

Table C.3. IDH status (IDH mutation *vs.* IDH wild-type)

	A	B	C
AUC	0.7034 (0.6666–0.7402)	0.7098 (0.6782–0.7413)	0.6865 (0.6441–0.7289)
ACC[1]	0.7586 (0.7206–0.7967)	0.8966 (0.8729–0.9204)	0.9563 (0.9394–0.9731)
ACC[2]	0.6560 (0.6234–0.6885)	0.6733 (0.6432–0.7033)	0.6466 (0.6087–0.6845)
SEN	0.7277 (0.6771–0.7783)	0.7176 (0.6760–0.7592)	0.7366 (0.6936–0.7796)
SPE	0.5679 (0.4993–0.6364)	0.6065 (0.5428–0.6701)	0.5221 (0.4481–0.5960)
P value	0.1156 (0.0670–0.1641)	0.1239 (0.0822–0.1657)	0.1517 (0.0783–0.2250)

Note: A (ADC); B (ADC and T1C); and C (all five sequences).

Table C.4. Ki-67 expression level (high expression vs. low expression, threshold =0.1)

	A	B	C
AUC	0.7783 (0.7515–0.8050)	0.7899 (0.7559–0.8239)	0.7858 (0.7606–0.8111)
ACC[1]	0.9512 (0.9315–0.9709)	0.9888 (0.9831–0.9945)	0.9873 (0.9824–0.9922)
ACC[2]	0.7246 (0.6989–0.7504)	0.7333 (0.7040–0.7626)	0.7320 (0.7108–0.7533)
SEN	0.7914 (0.7579–0.8248)	0.8259 (0.7954–0.8586)	0.8085 (0.7722–0.8448)
SPE	0.6105 (0.5537–0.6672)	0.5662 (0.5092–0.6232)	0.6013 (0.5423–0.6603)
P value	0.0363 (0.0187–0.0539)	0.0549 (0.0367–0.0732)	0.0320 (0.0230–0.0410)

Note: A (ADC, T2, and T1C); B (ADC, T2, T1C, and DWI); and C (all five sequences).

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Results of the classifiers on Ki-67 expression level (threshold =0.25)

Table C.5. Predictive performance of classifiers under certain sequence combinations

	B (ADC, T2, T1C, and DWI)
AUC	0.6206 (0.5762–0.6650)
ACC^1	0.8686 (0.8367–0.9004)
ACC^2	0.5974 (0.5653–0.6295)
SEN	0.4904 (0.4308–0.5501)
SPE	0.6753 (0.6283–0.7224)
P value	0.3222 (0.2648–0.3795)

Note: B (ADC, T2, T1C, and DWI) is the final sequence combination used in the Ki-67 classification based on *threshold* =0.1.

Table C.6. Predictive performance of the ultimate classifier

	AUC	ACC^1	ACC^2	SEN	SPE	P value
Ki-67 expression level	0.899	0.883	0.846	0.769	0.923	0.03

Note: AUC, area under the curve; ACC^1 represents accuracy on the training set, whereas ACC^2 represents accuracy on the testing set; SEN, sensitivity; SPE, specificity; P_value, calculated from the permutation test.

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Appendix 4: Selected features in the ultimate classifiers

	IDH genotype	Histological phenotype	Ki-67 expression level
The selected features	ADC_wavelet-LLH_firstorder_Mean ADC_wavelet-LLH_glszm_SizeZoneNonUniformityNormalized ADC_wavelet-HHL_gldm_LowGrayLevelEmphasis ADC_wavelet-LLL_glszm_GrayLevelNonUniformity ADC_log-sigma-3-0-mm-3D_glcm_ClusterShade ADC_log-sigma-3-0-mm-3D_glszm_GrayLevelVariance ADC_squareroot_firstorder_InterquartileRange T1C_original_shape_Elongation T1C_original_firstorder_Skewness T1C_wavelet-LLH_glszm_SmallAreaLowGrayLevelEmphasis T1C_wavelet-LHL_firstorder_Kurtosis T1C_wavelet-LHL_glcm_Imc2 T1C_wavelet-LHL_glcm_MCC T1C_wavelet-HLL_firstorder_10Percentile T1C_wavelet-HLL_firstorder_MeanAbsoluteDeviation T1C_wavelet-HLL_firstorder_RootMeanSquared T1C_wavelet-HLH_glszm_ZonePercentage T1C_wavelet-LLL_glrlm_LongRunEmphasis T1C_log-sigma-3-0-mm-3D_firstorder_TotalEnergy T1C_log-sigma-3-0-mm-3D_glrlm_GrayLevelVariance T1C_logarithm_glrlm_LongRunEmphasis	ADC_original_firstorder_InterquartileRange ADC_wavelet-HLL_glszm_HighGrayLevelZoneEmphasis ADC_wavelet-HLL_glszm_LowGrayLevelZoneEmphasis ADC_wavelet-HLL_glszm_SmallAreaLowGrayLevelEmphasis ADC_wavelet-HLH_firstorder_Kurtosis ADC_wavelet-LLL_firstorder_InterquartileRange ADC_log-sigma-3-0-mm-3D_glcm_MaximumProbability ADC_log-sigma-3-0-mm-3D_glszm_LowGrayLevelZoneEmphasis ADC_log-sigma-3-0-mm-3D_ngtdm_Contrast ADC_square_firstorder_10Percentile ADC_logarithm_firstorder_InterquartileRange DWI_wavelet-HHH_firstorder_Kurtosis DWI_logarithm_firstorder_Median T1_wavelet-LHH_firstorder_Median T1_wavelet-HLL_glcm_DifferenceEntropy T1_wavelet-HLL_glcm_DifferenceVariance T1_wavelet-HHL_glszm_LowGrayLevelZoneEmphasis T1_logarithm_glrlm_ShortRunHighGrayLevelEmphasis T1C_wavelet-LLH_glcm_Imc1 T1C_wavelet-HHL_glcm_Autocorrelation T1C_wavelet-HHL_glcm_ClusterProminence T1C_wavelet-HHL_glcm_ClusterTendency T1C_wavelet-HHL_glcm_Correlation T1C_wavelet-HHH_glcm_ClusterTendency T1C_exponential_firstorder_MeanAbsoluteDeviation T1C_logarithm_glcm_ClusterShade T2_wavelet-HLL_firstorder_Kurtosis T2_wavelet-HHL_firstorder_Median T2_wavelet-HHL_glszm_LowGrayLevelZoneEmphasis T2_log-sigma-3-0-mm-3D_glszm_GrayLevelNonUniformityNormalized T2_log-sigma-3-0-mm-3D_glszm_GrayLevelVariance T2_log-sigma-3-0-mm-3D_glszm_SmallAreaHighGrayLevelEmphasis	ADC_wavelet-LHL_glcm_MaximumProbability ADC_wavelet-HLL_gldm_DependenceVariance ADC_exponential_firstorder_10Percentile ADC_logarithm_firstorder_InterquartileRange DWI_wavelet-LLH_gldm_DependenceNonUniformityNormalized DWI_wavelet-HHH_firstorder_MeanAbsoluteDeviation DWI_log-sigma-3-0-mm-3D_firstorder_Minimum DWI_log-sigma-3-0-mm-3D_firstorder_Skewness T1C_wavelet-LLH_glrlm_HighGrayLevelRunEmphasis T1C_square_firstorder_Range T2_wavelet-HLL_glszm_SmallAreaLowGrayLevelEmphasis T2_log-sigma-3-0-mm-3D_glszm_GrayLevelNonUniformityNormalized T2_square_firstorder_Minimum

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