## Supplementary

## **Appendix 1**

In the supplementary, we present various visual and quantitative analyses: the k-space acceleration process in Figure S1, the distribution of the 5-fold split used for MGMT promoter methylation prediction in Figure S2, additional visual comparisons in Figure S3, ROC curves in Figure S4, and the scoring criteria provided to radiologists in Table S1.

Figure S1 depicts the acquisition process for undersampled MR images, which begins with transforming the original MR image into the k-space domain using a Fourier Transform (FFT). To simulate undersampling, an equi-spaced mask is created based on the k-space data dimensions, an acceleration factor (e.g., 4-fold or 32-fold), and a predefined center fraction (e.g., 0.05). This mask preserves a central portion of the k-space data, typically 5% of the total columns, while sampling the remaining columns at intervals determined by the acceleration factor (e.g., every 4th or 32nd column). As a result, two distinct k-space datasets corresponding to 4-fold and 32-fold accelerations are generated. These undersampled k-space datasets are then transformed back into the spatial domain via an Inverse Fourier Transform (IFFT), yielding undersampled MR images.



Figure S1 Depiction of the acceleration process utilizing undersampled k-space trajectories with an equi-spaced mask.



**Figure S2** Distribution of MGMT promoter methylation status across five random folds, illustrating the counts of non-methylated (MGMT value = 0) and methylated (MGMT value = 1) instances within each fold.



**Figure S3** Visualization of the comparative analysis between T1 and 4-fold accelerated T1 magnetic resonance images, along with their respective tumor masks, and the comparison between reconstructed 4-fold accelerated FLAIR images and their ground truth images.



Figure S4 Comparison of ROC curves for the prediction of O-6-methylguanine-DNA methyltransferase promoter methylation status between ground truth magnetic resonance images and reconstructed images.

Table S1	Criteria	for assessin	g the i	mage q	uality of	glioma N	IR images
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Scoring point	Description	Score range
Overall image quality	The overall clarity, contrast, and noise level of the image	1-5
Tumor margin clarity	The clarity of the tumor margins with respect to surrounding healthy brain tissue	1-5
Intratumoral heterogeneity	The heterogeneity within the tumor, including necrotic areas and angiogenesis	1-5
Gray-white matter contras	t The contrast between gray matter and white matter, aiding in the visualization of anatomical structures and detection of lesions	1-5
Ventricular system	The visualization and assessment of the ventricular system	1-5
Peritumoral edema	The presence and extent of edema around the tumor	1-5
Angiogenesis	The assessment of abnormal blood vessel formation within and around the tumor, especially as shown in contrast-enhanced scans	1-5

Score 5 represents the highest quality and 1 signifies the lowest.