The authors wish to thank Mrs. Amy Cossart from the Raymond and Beverly Sackler Center for Biomedical Imaging at Memorial Sloan Kettering Cancer Center for performing image segmentations. This work was supported in part by the National Cancer Institute Award Numbers (1P30CA008748-35 and 1R01CA151791-01). The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health. There are several advantages of using imaging features linked to genetic profiles, primarily molecular biomarkers, to study the tumor phenotype, i.e. to predict its behavior based on its genetic composition [12]. First, imaging-based evaluations may be used to complement the evaluation by biopsy. Second, imaging features can be evaluated through different modalities, including 2D and 3D modalities. This fact could be very valuable, as it may facilitate the analysis and interpretation of the results of the analyses performed by different modalities. Third, molecular biomarkers, being a direct measure of the tumor phenotype, can give valuable information for treatment and prognosis as well. Finally, molecular markers allow us to quantify the tumor phenotype, increasing its interpretation and actionability [13, 14]. Initial evidence suggests that a combination of ASL and perfusion-weighted contrast-enhanced (PWI) MRI produced promising results for the identification of metastasis (Table 2) [1], but further investigation is warranted. However, it is also postulated that GBM responds to hypoxia in a microenvironmental fashion, hence “microenvironmental MRI” that combines the simultaneous acquisition of multiple MRI-based parameters to identify microenvironmental alterations [13]. Such an approach may be crucial for the segmentation of images acquired from imaging protocols that lack the capability to differentiate tumor hypoxia from microenvironmental heterogeneity.

Gaw5.6T02-4-DL-R1B010-ME.EN Whole Image(0222163812) (1).en Whole Image

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