Classification of brain tumors using pseudobulk spatial transcriptomics
Brain Tumor Pathology
Sze Jet Aw, Chuan Keng Goh, Jian Yuan Goh, Debbra Yi Xin Chong, Enrica Ee Kar Tan, Sharon Yin Yee Low
Corresponding author: Sze Jet Aw, Department of Pathology and Laboratory Medicine, KK Women's and Children's Hospital, 100 Bukit Timah Road, Singapore 229899. aw.sze.jet@singhealth.com.sg

Online Resource 3 Confusion matrices for the three classifiers. Rows give the reference diagnostic category and columns the predicted category after harmonization (Online Resource 2). Cells show the number of cases with the row percentage in parentheses; percentages may not sum to 100 owing to rounding. Color intensity encodes the row percentage; concordant assignments lie on the diagonal and are outlined in black. "Other" denotes a confident prediction of an entity not represented among the five harmonized categories; these were scored discordant. Denominators differ between classifiers: the six control tissue cases were excluded from M&M, which has no non-neoplastic reference class and therefore cannot predict that category, and eight glioma cases for which OTTER returned an indeterminate hierarchical node were excluded from OTTER. EPD, ependymoma; GNT, glioneuronal tumor; HGG, high-grade glioma; kNN, k-nearest neighbor; LGG, low-grade glioma; MB, medulloblastoma.

