

Histological classification of gliomas guides treatment decisions. Because of the high interobserver variability, we aimed to improve classification by performing gene expression profiling on a large cohort of glioma samples of all histological subtypes and grades. The seven identified intrinsic molecular subtypes are different from histological subgroups and correlate better to patient survival. Our data indicate that distinct molecular subgroups clearly benefit from treatment. Specific genetic changes (EGFR amplification, IDH1 mutation, 1p/19q LOH) segregate in -and may drive- the distinct molecular subgroups. Our findings were validated on three large independent sample cohorts (TCGA, REMBRANDT, and GSE12907). We provide compelling evidence that expression profiling is a more accurate and objective method to classify gliomas than histology.

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