

Table 1. Pediatric-type diffuse glioma in 2021 WHO classification and genome-wide DNA methylation profiling

	2021 WHO classification	Genome-wide DNA methylation profiling (v12.5)
Low-grade	Diffuse astrocytoma, MYB- or MYBL1-altered	Diffuse glioma, MYB(L1)-altered, subtype B [infratentorial-type] Diffuse glioma, MYB(L1)-altered, subtype C [isomorphic diffuse glioma-type] Diffuse glioma, MYB(L1)-altered, subtype D
	Angiocentric glioma	Diffuse glioma, MYB(L1)-altered, subtype A [angiocentric glioma-type]
	Polymorphous low-grade neuroepithelial tumor of the young	Polymorphous low-grade neuroepithelial tumor of the young
	Diffuse low-grade glioma, MAPK pathway-altered	
High-grade	Diffuse midline glioma, H3 K27-altered	Diffuse midline glioma, H3 K27-altered, subtype EGFR-altered Diffuse midline glioma, H3 K27-mutant / EZHIP overexpressing
	Diffuse hemispheric glioma, H3 G34-mutant	Diffuse hemispheric glioma, H3 G34-mutant
	Diffuse pediatric-type high-grade glioma; H3-wildtype and IDH-wildtype gliomas	Diffuse pediatric-type high-grade glioma, H3 wildtype and IDH wildtype, Subtype A&B Diffuse pediatric-type high-grade glioma, MYCN subtype Diffuse pediatric-type high-grade glioma, RTK1 subtype (subclass A–C) Diffuse pediatric-type high-grade glioma, RTK2 subtype (subclass A, B)
	Infant-type hemispheric glioma	Infant-type hemispheric glioma

Table 2. Representative larger cohorts of pediatric brain tumor patients analyzed by genome-wide DNA methylation profiling

Author, year	Patient number #	Calibrated score		Effect of methylation analysis on diagnosis	
Pickles JC et al., 2019	n = 306	≥ 0.9	48.7% (n = 149)	Confirmed diagnosis	12.6% (n = 39)
		0.3–0.9	29.7% (n = 91)	Refined diagnosis	32.0% (n = 99)
		< 0.3	21.6% (n = 66)	Changed diagnosis	1.6% (n = 5)
Priesterbach-Ackley L.P. et al., 2020	n = 223	≥ 0.9	71.7% (n = 160)	Confirmed diagnosis	41.7% (n = 93)
		0.3–0.9	21.5% (n = 48)	Refined diagnosis	19.7% (n = 44)
		< 0.3	16.9% (n = 15)	Changed diagnosis	8.5% (n = 19)
Schepke E et al., 2022	n = 240	≥ 0.84	77.9% (n = 187)	Confirmed diagnosis	44.2% (n = 106)
		0.3–0.84	16.7% (n = 40)	Refined diagnosis	24.6% (n = 59)
		< 0.3	5.4% (n = 13)	Changed diagnosis	5.8% (n = 14)
Ecker J et al., 2022 (PTT 2.0 registry)	n = 175	≥ 0.9	64.0% (n = 112)	Confirmed diagnosis	6.9% (n = 12)
				Refined diagnosis	52.0% (n = 91)
				Changed diagnosis	5.1% (n = 9)

Patient number indicates the number of pediatric brain tumor patients who received genome-wide DNA methylation profiling in the cohort.