Methylation profiling report

Supplier information

Sample identifier:	FR-22-0277-206522890058_R06C01
Sentrix ID:	206522890058_R06C01
Material type:	DNA-KRYO
Gender:	NA
Supplier diagnosis:	High-grade glioma, H3 and IDH-wildtype

Automatic prediction		
Array type:	EPIC	
Material type:	DNA-FFPE	✗
Gender:	unknown	!

Legend: ✓ Ok ! Supplier information or prediction not available ✗ Warning, missmatch of prediction and supplier information

Version 12.8 of the brain classifier results (12.8)

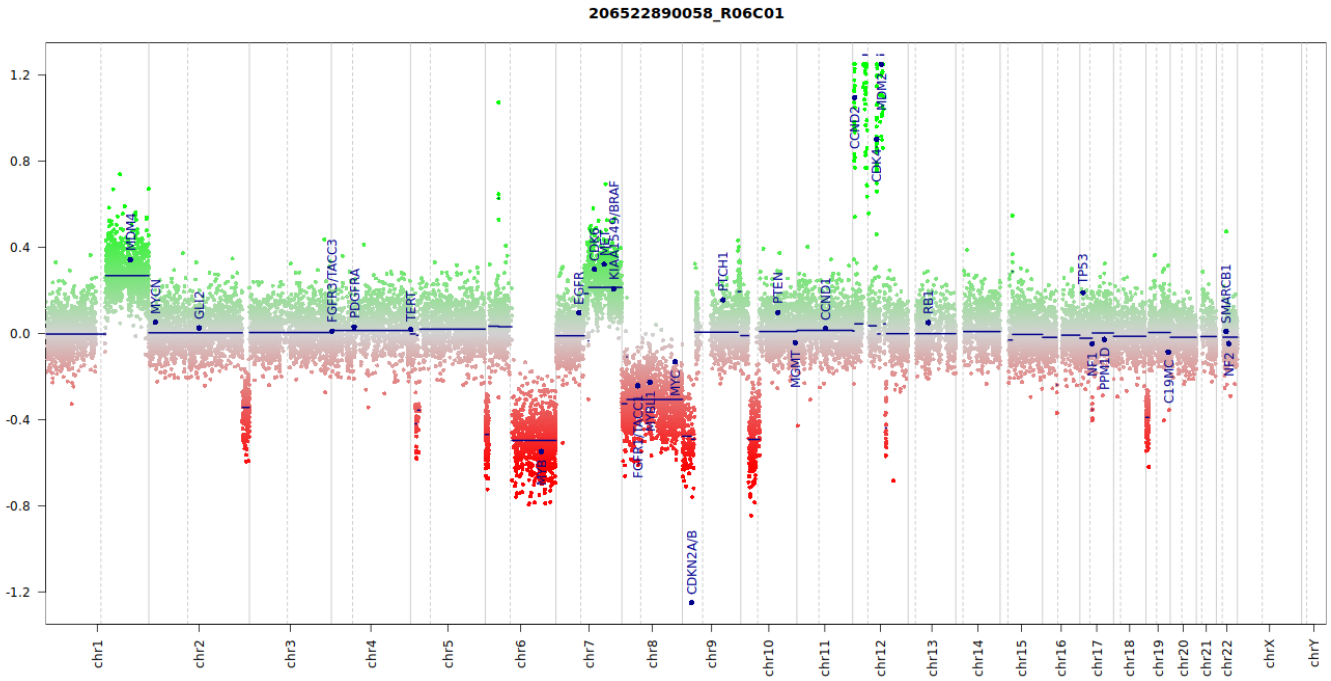
Methylation classes (Highest level >= 0.3, lower levels >= 0.1, all of lowest level)	Calibrated score	Interpretation	
Paediatric Type Diffuse High Grade Gliomas	0.99	match	✓
Diffuse Midline Glioma, H3 K27 Altered	0.99	match	✓
Diffuse Midline Glioma, H3 K27 Altered, Subtype Egfr Altered	0.99	match	✓
Mc Diffuse Midline Glioma, H3 K27 Altered, Subtype Egfr Altered	0.99	match	✓

Legend: ✓ Match (score >= 0.9) ✗ No match (score < 0.9): possibly still relevant for low tumor content and low DNA quality cases.

Class descriptions

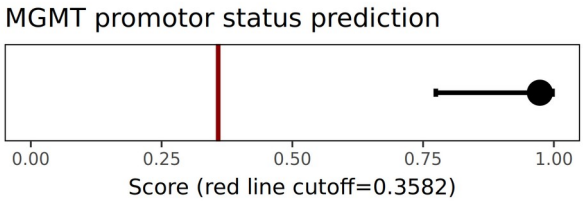
MC Diffuse midline glioma, H3 K27-altered, subtype EGFR-altered: The "mc Diffuse midline glioma, H3 K27-altered, subtype EGFR-altered" is comprised of infiltrative midline gliomas with loss of H3 p.K28me3 (K27me3) and an EGFR mutation (CNS WHO grade 4). The EGFR-mutant subtype most often occurs during childhood, with a median patient age of 7–8 years and typically unilaterally or bilaterally in the thalamus. Most tumours harbour small in-frame insertions/duplications within exon 20, which encodes the intracellular tyrosine kinase domain (TKD), whereas others harbour missense mutations in exons encoding parts of the extracellular domain, most commonly p.A289T or p.A289V.

Copy number variation profile



Depiction of chromosome 1 to 22 (and X/Y if automatic prediction was successful). Gains/amplifications represent positive, losses negative deviations from the baseline. 29 brain tumor relevant gene regions are highlighted for easier assessment. (see Hovestadt & Zapatka, http://www.bioconductor.org/packages/devel/bioc/html/conumee.html)

MGMT promotor methylation (MGMT-STP27)



Status	Estimated	CI lower	CI upper
methylated	0.97324	0.77431	0.99741

(see Bady et al, J Mol Diagn 2016; 18(3):350-61)

Disclaimer

Classification using methylation profiling is a tool for research use only, it is not verified and has not been clinically validated and, therefore, must not be used for diagnostic purposes. This tool is not HIPAA compliant.

Run information

Report: report_website_mnp_brain_v12.8_sample (Version 1.1)

Task version:

Task	Version
idat_preprocess	3.1
idat_qc	4.1
idat_predictBrain	12.8
idat_mgmt	3.1
idat_rs_gender	3.2
idat_cnvp	5.2
report_website_mnp_brain_v12.8_sample	1.1