

Methylation profiling report

Supplier information

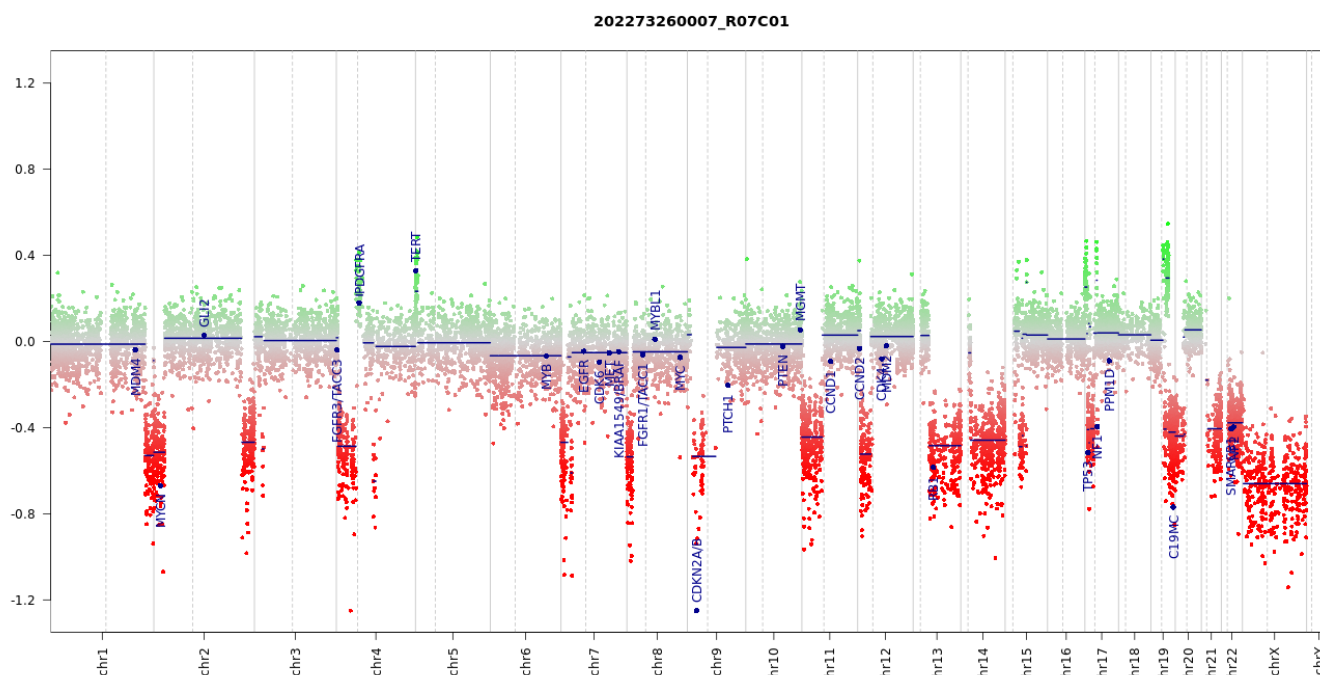
Sample identifier:	sampleName1527692823
Sentrix ID:	202273260007_R07C01
Material type:	FFPE DNA
Gender:	NA
Supplier diagnosis:	-

Automatic prediction

Array type:	EPIC	
Material type:	KRYO DNA	✗
Gender:	female	⚠
Legend: ✔ OK ⚠ Supplier information or prediction not available ✗ Warning, mismatch of prediction and supplier information		

Brain tumor methylation classifier results (v11b4) - No matching methylation classes with calibrated score ≥ 0.3

Copy number variation profile

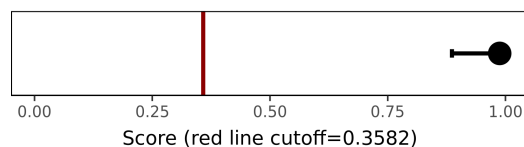


Depiction of chromosome 1 to 22 (and XY if automatic prediction was successful). Gains/amplifications represent positive, losses negative deviations from the baseline. 29 brain tumor relevant gene regions are highlighted for easier assessment.

(see Hovestadt & Zapatka, <http://www.bioconductor.org/packages/devel/bioc/html/conumee.html>)

MGMT promotor methylation (MGMT-STP27)

MGMT promotor status prediction



Status	Estimated	CI lower	CI upper
methyalted	0.9878	0.88638	0.99881

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

Disclaimer

Classification using methylation profiling is a research tool under development, it is not verified and has not been clinically validated. Implementation of the results in a clinical setting is in the sole responsibility of the treating physician.

Intended for non-commercial use only.

Run information

Report: idat_reportBrain_v11b4_sample Version 2.0
Task version:

Task	Version
idat_qc	2.0
idat_predictBrain	2.1
idat_rs_gender	2.0
idat_predictMGMT	2.0
idat_cnvp	3.0
idat_reportBrain_v11b4	2.0