Methylation profiling report

GERMAN CANCER RESEARCH CENTER IN THE HELMHOLTZ ASSOCIATION

Heidelberg University Hospital

MolecularNeuropathology.org

Supplier information

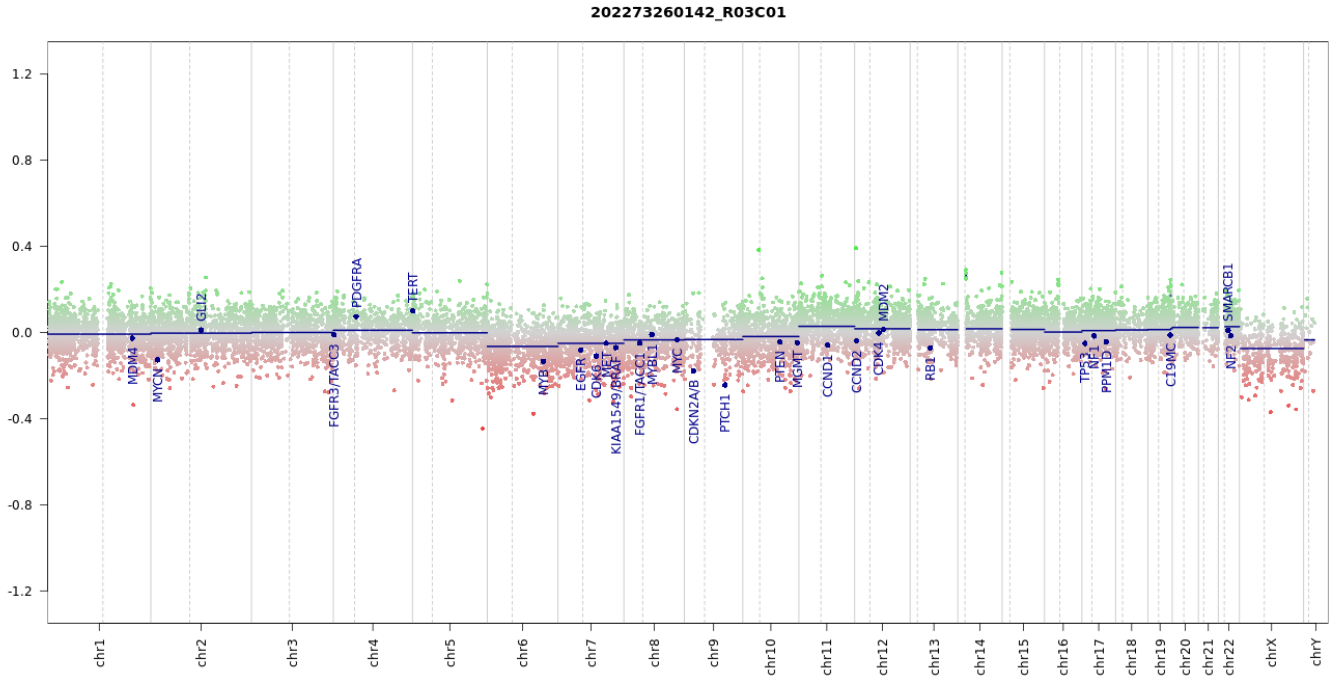
Sample identifier:	**sampleName1540574293**
Sentrix ID:	**202273260142_R03C01**
Material type:	**KRYO DNA**
Gender:	**NA**
Supplier diagnosis:	**-**

Automatic prediction		
Array type:	**EPIC**	
Material type:	**KRYO DNA**	✔
Gender:	**male**	!

Legend: ✔ OK ! Supplier information or prediction not available ✘ Warning, missmatch of prediction and supplier information

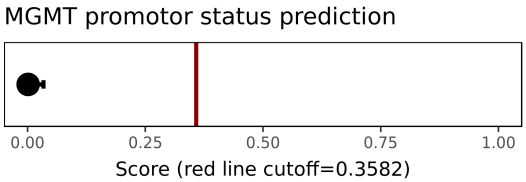
Brain tumor methylation classifier results (v11b4) - No matching methylation classes with calibrated score >= 0.3

Copy number variation profile



Depiction of chromosome 1 to 22 (and 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
unmethylated	0.00122	4.0E-5	0.03389

(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