![dkfz. German Cancer Research Center in the Helmholtz Association] ![Heidelberg University Hospital] ![MolecularNeuropathology.org]

Methylation profiling report

Supplier information

Sample identifier:	**sampleName1527692956**
Sentrix ID:	**202047860190_R04C01**
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, missmatch of prediction and supplier information

Brain tumor methylation classifier results (v11b4)

| Methylation classes (MCs with score >= 0.3)	Calibrated score	Interpretation	
methylation class control tissue, inflammatory tumor microenvironment	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. ● Match to MC family member (score >= 0.5)

Class descriptions

Methylation class control tissue, inflammatory tumor microenvironment: The methylation class "control tissue, inflammatory inflammatory tumor microenvironment" does not represent a distinct tumor class but rather a recurrently observed profile of mixed cell types with a high leukocyte fraction (often predominant granulocytic infiltrates). This is frequently observed in highly necrotic tumors, highly necrotic other tissues or when areas of extensive hemorrhage are sampled along with the tumor tissue of interest. Tumors with a pronounced granulocytic infiltrate due to other reasons can also get an elevated score for this class. Classification into this class is not diagnostic for a specific type of tumor. A score for this class indicates that the extracted DNA is likely not suitable for classification by methylation profiling. Depending on the degree, copy number alterations may also be masked by the high leukocyte infiltration. The reference class consists of glioblastomas only, but other tumors with high leukocyte infiltration are also expected to fall into this class.
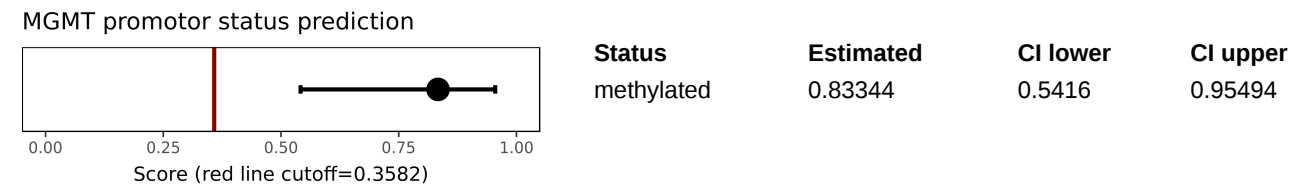
Copy number variation profile
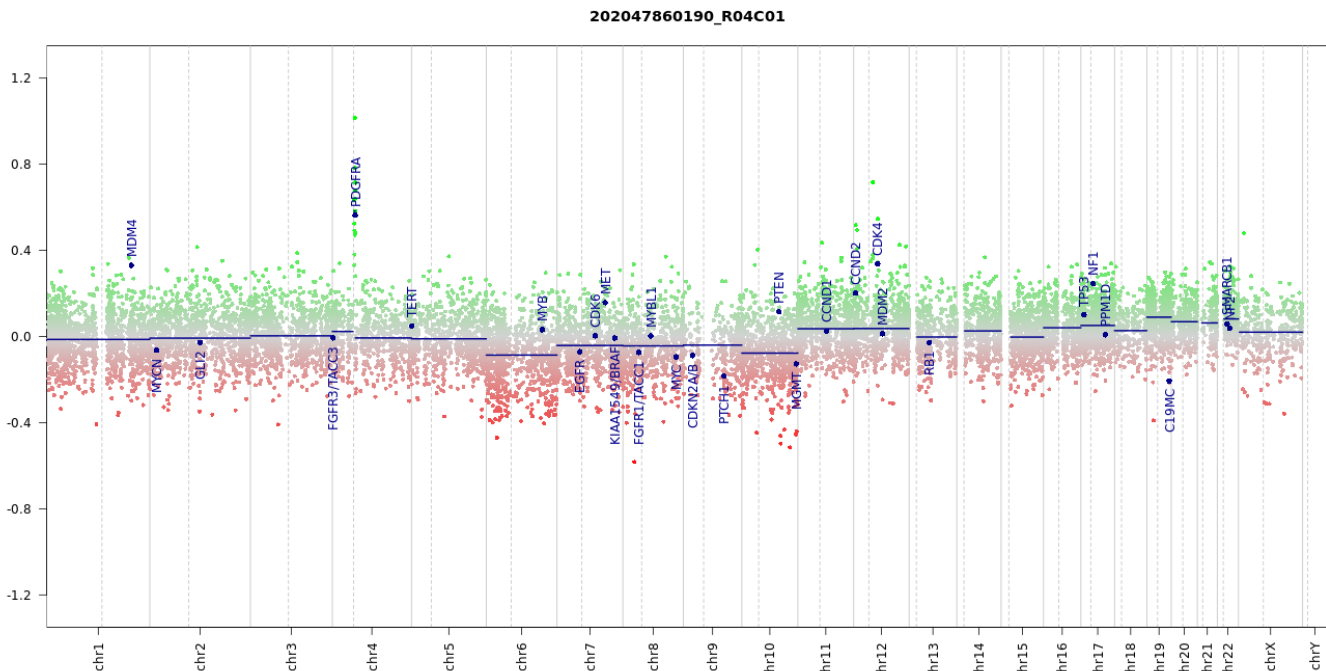
Depiction of chromosome 1 to 22 (and X/Y if automatic prediction was successful). Gains/amplifications represent positive, losses negative deviations from the baseline. 29 brain tumor relevant gene regions are highlighted for easier assessment.
(see Hovestadt & Zapatka, http://www.bioconductor.org/packages/devel/bioc/html/conumee.html)

MGMT promotor methylation (MGMT-STP27)

MGMT promotor status prediction

Score (red line cutoff=0.3582)

Status	Estimated	CI lower	CI upper
methylated	0.83344	0.5416	0.95494

(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