Methylation profiling report

General information

Sentrix ID:	**203057570045_R07C01**
Array type:	**EPIC**
Material type:	**KRYO DNA**
Gender:	**male**

Brain tumor methylation classifier results (v11b4)

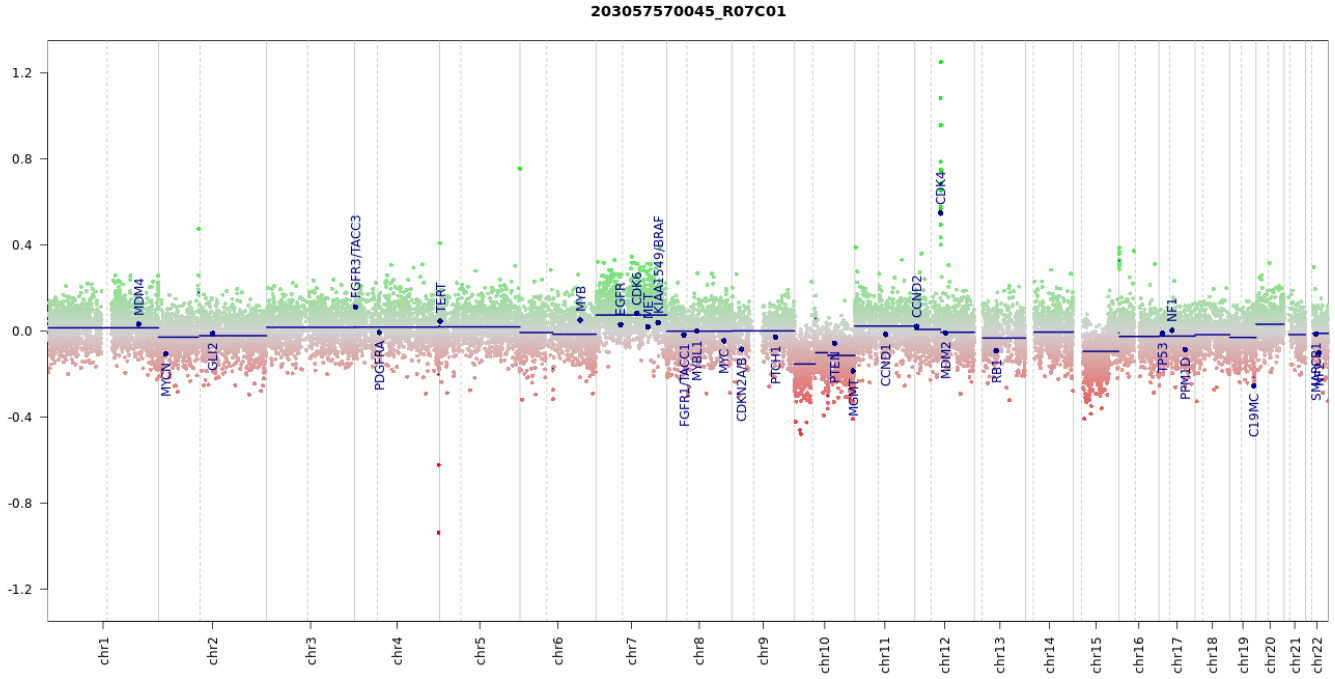
Methylation classes (MCs with score >= 0.3)	Calibrated score	Interpretation	
methylation class control tissue, hemispheric cortex	0.97	match	✔

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

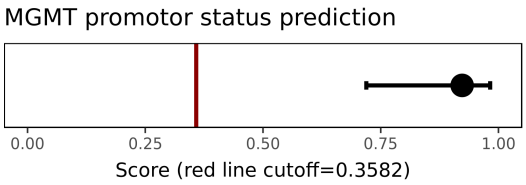
Methylation class control tissue, hemispheric cortex: The methylation class "control tissue, hemispheric cortex" is comprised of normal tissue samples from several different lobes of the cortex. In case tumor samples display this molecular pattern, it is typically an indication of low tumor cell content in the analyzed material and indicates that the extracted DNA is likely not suitable for classification by methylation profiling.

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	0.92289	0.71941	0.98241

(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 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