

# Methylation profiling report

## General information

Sentrix ID:	202273260157_R01C01
Array type:	EPIC
Material type:	KRYO DNA
Gender:	male

## Brain tumor methylation classifier results (v11b4)

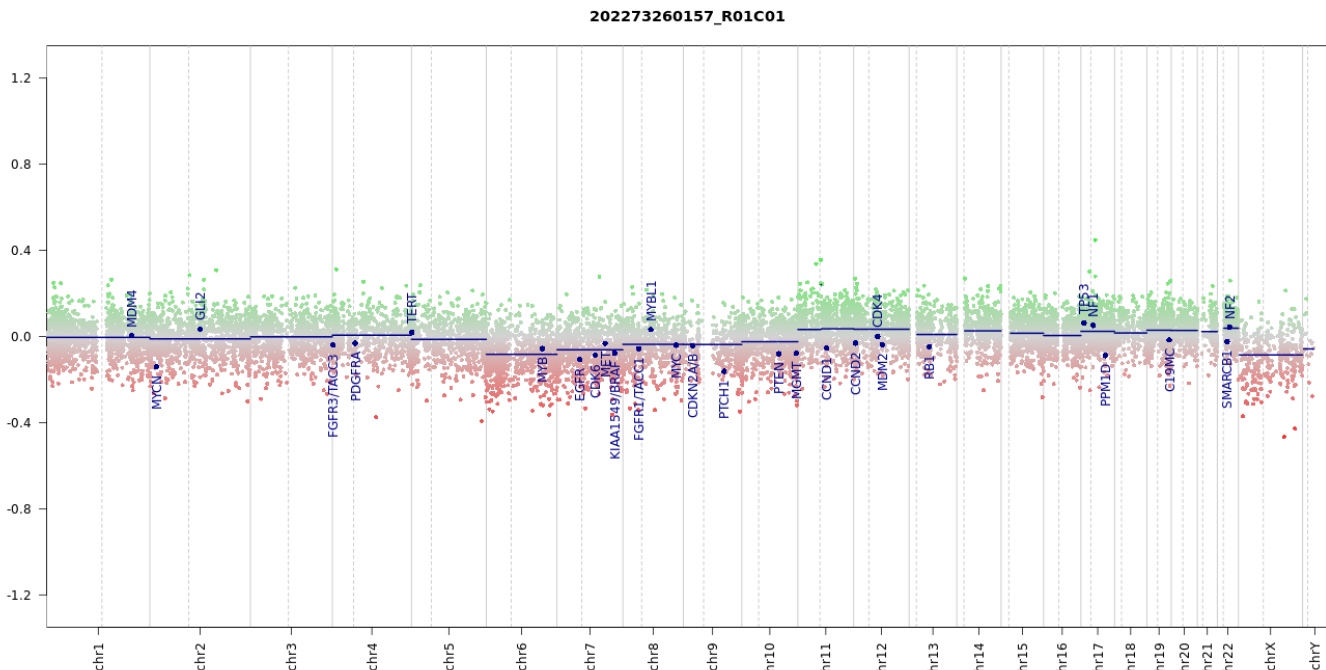
Methylation classes (MCs with score >= 0.3)	Calibrated score	Interpretation
methylation class meningioma	0.42	no match

Legend: ✔ Match (score  $\geq 0.9$ ) ✘ No match (score  $< 0.9$ ): possibly still relevant for low tumor content and low DNA quality cases. ● Match to MC family member (score  $\geq 0.5$ )

## Class descriptions

**Methylation class meningioma:** The methylation class "meningioma" mainly comprises tumors with the histological diagnosis meningioma WHO I but also tumors with the diagnosis of atypical meningioma WHO II and single cases of anaplastic meningioma WHO III. Location is typically with meningeal attachment; median age is 63 (range 29 to 93). This class likely consists of further subgroups which have not yet been precisely defined, some of which may show recurrent genetic alterations.

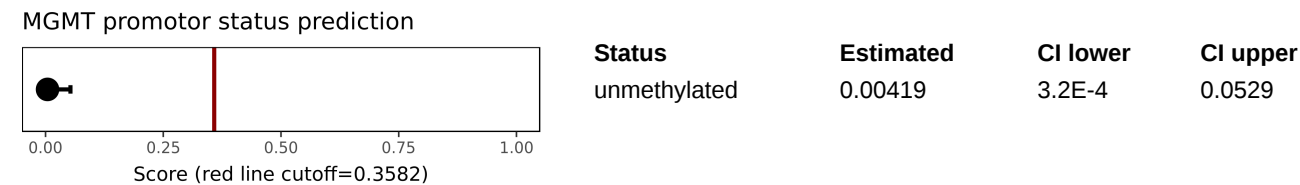
### Copy number variation profile



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)



(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