

# Methylation profiling report

## General information

Sentrix ID: **203724130138\_R05C01**  
 Array type: **EPIC**  
 Material type: **FFPE DNA**  
 Gender: **female**

## Brain tumor methylation classifier results (v11b4)

Methylation classes (MCs with score >= 0.3)	Calibrated score	Interpretation
methylation class family Medulloblastoma group 3 and 4	0.99	match <span style="color: green;">✔</span>
<b>MC family members with score &gt;= 0.1</b>		
methylation class medulloblastoma, subclass group 3	0.98	match <span style="color: green;">●</span>

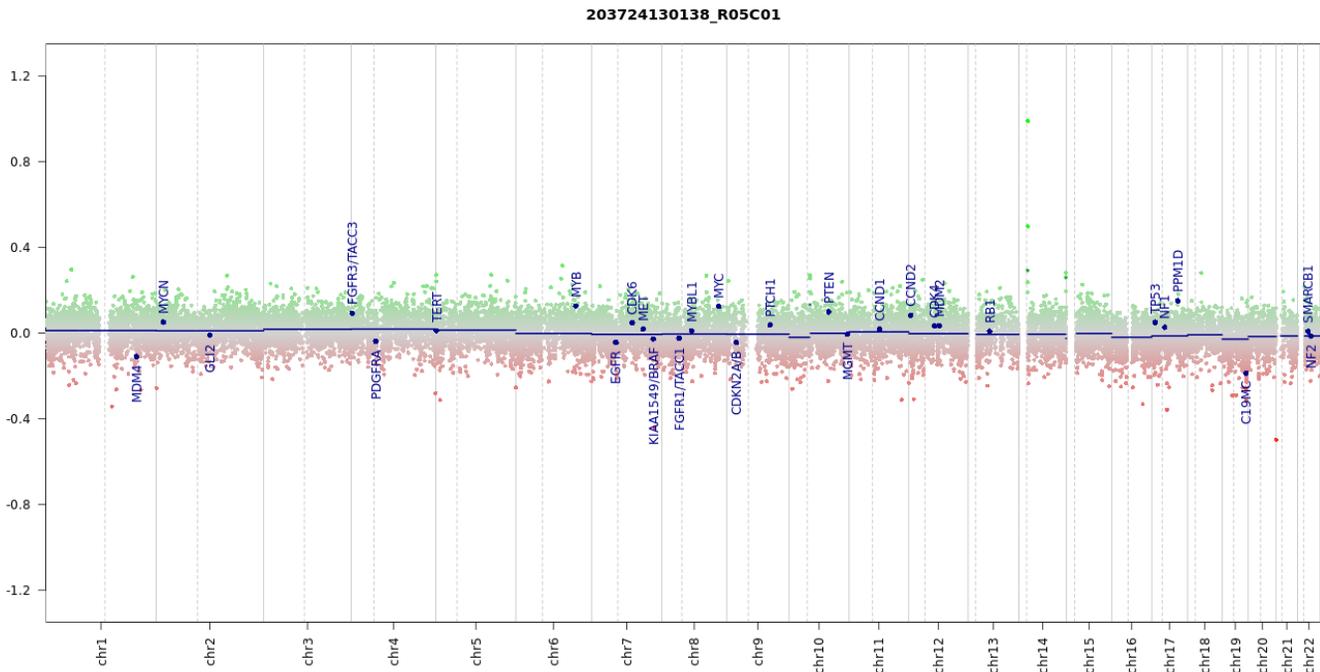
Legend: ✔ Match (score >= 0.9) ✘ No match (score < 0.9): possibly still relevant for low tumor content and low DNA quality cases. ● Match to MC family member (score >= 0.5)

## Class descriptions

**Methylation class family Medulloblastoma group 3 and 4:** The methylation class family "Medulloblastoma class 3 and 4" comprises the methylation classes medulloblastoma, class 3 and medulloblastoma, class 4.

**Methylation class medulloblastoma, subclass group 3:** The methylation class "medulloblastoma, subclass group 3" is comprised of tumors with the diagnosis medulloblastoma, genetically defined, group 3. Histologically most cases fall into the classical and large cell/anaplastic groups. Tumors are located in the cerebellum, typically in the vermis. Median age is 4 years (range 1 to 17). Group 3 medulloblastomas are more common in males than females. MYC amplification, aneuploidy, isochromosome 17q and GF11/1B activation by enhancer hijacking are recurrent features, but a fraction lack an obvious driving genetic change.

## Copy number variation profile

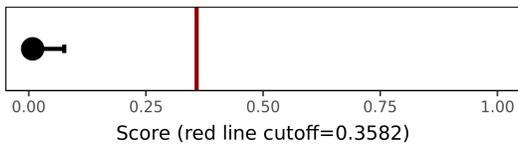


Depiction of chromosome 1 to 22 (and X/Y if automatic prediction was successful). Gains/amplifications represent positive, losses negative deviations from the baseline. 29 brain tumor relevant gene regions are highlighted for easier assessment.

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

## MGMT promotor methylation (MGMT-STP27)

MGMT promotor status prediction



Status	Estimated	CI lower	CI upper
unmethylated	0.00824	8.4E-4	0.07576

(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