

Methylation profiling report

General information

Sentrix ID: **203724130138_R06C01**
 Array type: **EPIC**
 Material type: **FFPE DNA**
 Gender: **male**

Medulloblastoma methylation classifier results (v1.0)

Methylation classes (MCs with score >= 0.3)	Calibrated score	Interpretation
medulloblastoma, subclass group 3/4, subtype II	0.48	no match ✘
medulloblastoma, subclass group 3/4, subtype III	0.31	no match ✘

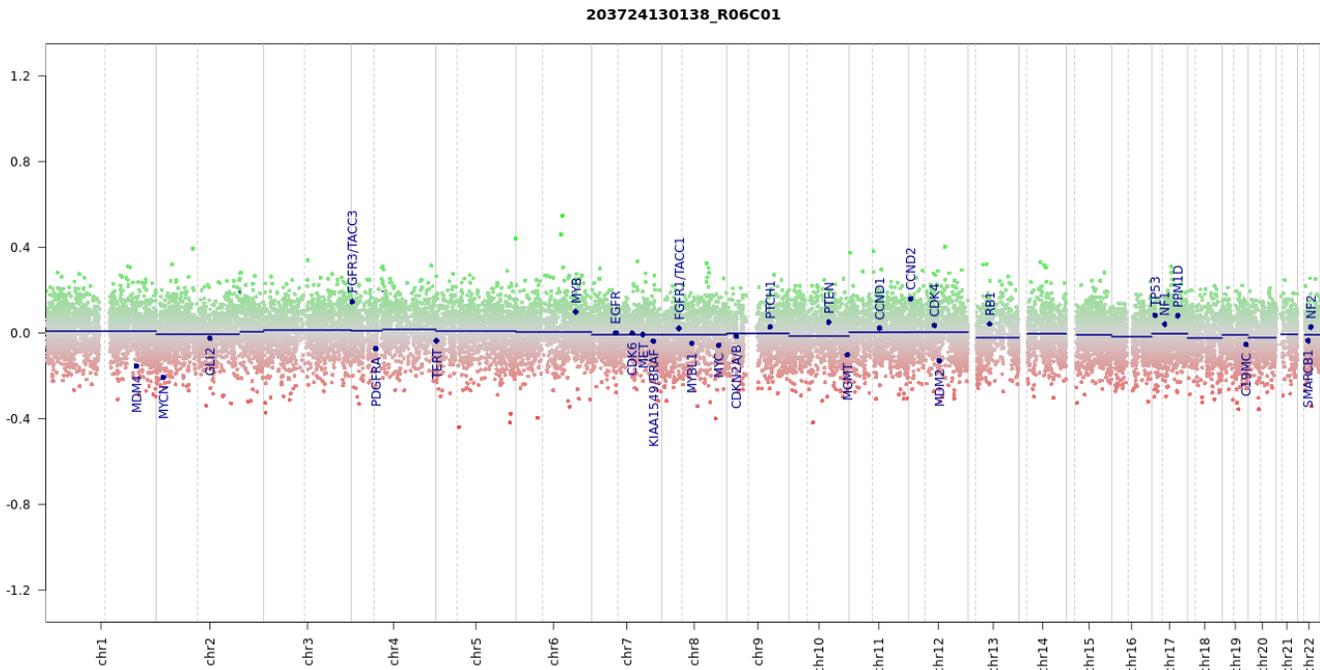
Legend: ✔ Match (score >= 0.9) ✘ No match (score < 0.9): possibly still relevant for low tumor content and low DNA quality cases. ● Match to MC family member (score >= 0.5)

Class descriptions

Medulloblastoma, subclass group 3/4, subtype II: The methylation class "medulloblastoma, subclass group 3/4, subtype II" is comprised of tumors with the diagnosis medulloblastoma. Histologically, most cases fall into the classic (50%) or large-cell/anaplastic group (45%) and 5% cases fall in the DN/MBEN group. Median age is 5 years (range 1 to 17). The majority (55%) are M+. Male:Female ratio is 3.3:1. Subtype II medulloblastomas are enriched for chr8 and chr17, isochromosome 17q (i17q), chr13q gain and chr 16 loss, and are enriched for MYC amplification (20% of cases). Subtype% in II is high-risk (5-year OS ~ 49% in retrospective series). This subtype is comprised of 100% Grp3 subgroup tumors.

Medulloblastoma, subclass group 3/4, subtype III: The methylation class "medulloblastoma, subclass group 3/4, subtype III" is comprised of tumors with the diagnosis medulloblastoma. Histologically, most cases fall into the classic (80%) or large-cell/anaplastic group (20%). Median age is 5 years (range 2 to 50). The majority (55%) are M+. Male:Female ratio is 3.6:1. Subtype III medulloblastomas are enriched for a characteristic 1q gain, and are enriched for MYC amplification (10% of cases). Subtype% in III is high-risk (5-year OS ~ 41 in retrospective series). This subtype is comprised of 100% Grp3 tumors.

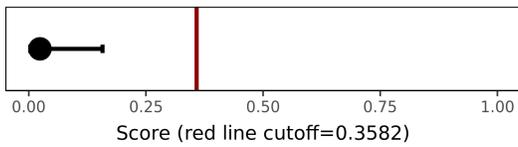
Copy number variation profile



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	0.02391	0.0032	0.15734

(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_reportMeduloblastoma_v1_0 Version 1.0

Task version:

Task	Version
idat_qc	2.0
idat_rs_gender	2.0
idat_predictMGMT	2.0
idat_cnvp	3.0
idat_predictMeduloblastoma	1.0