Methylation profiling report

General information

Sentrix ID:	**202273260096_R02C01**
Array type:	**EPIC**
Material type:	**KRYO DNA**
Gender:	**female**

Brain tumor methylation classifier results (v11b4)

Methylation classes (MCs with score >= 0.3)	**Calibrated score**	**Interpretation**	
methylation class family Medulloblastoma, SHH	0.95	match	✔
MC family members with score >= 0.1			
methylation class medulloblastoma, subclass SHH A (children and adult)	0.95	match	●

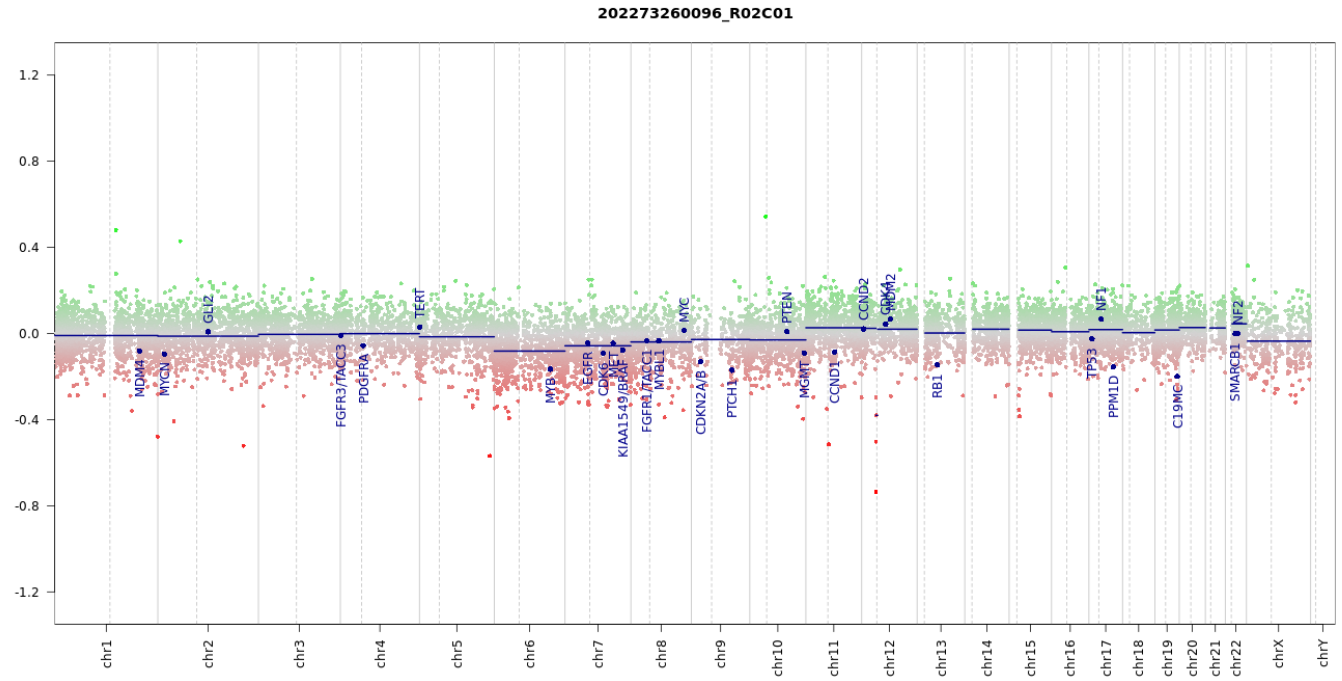
Legend: ✔ Match (score >= 0.9) ✘ No match (score < 0.9): possibly still relevant for low tumor content and low DNA quality cases. ● Match to MC family member (score >= 0.5)

Class descriptions

Methylation class family Medulloblastoma, SHH: The methylation class family "Medulloblastoma, SHH" comprises the methylation classes medulloblastoma, SHH subtype A (children and adult) and medulloblastoma, SHH subtype B (infant).

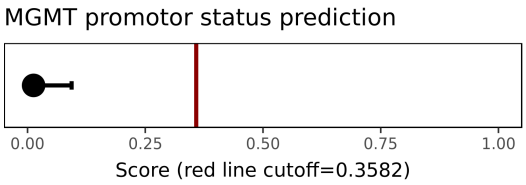
Methylation class medulloblastoma, subclass SHH A (children and adult): The methylation class "medulloblastoma, subclass SHH A (children and adult)" is comprised of tumors diagnosed as Medulloblastoma, genetically defined, SHH-activated occurring in non-infant patients. Histologically most cases fall into the desmoplastic variant, sometimes classic and occasionally large cell/anaplastic groups. Tumors are located in the cerebellum, usually laterally. Median age is 22 years (range 3 to 51). Upstream SHH pathway alterations (i.e. PTCH1 and SMO) are relatively common. Importantly, this methylation class also includes the majority of TP53-mutated SHH tumors (often Li-Fraumeni associated), which typically occur in children (~8-16 years) and often have large cell/anaplastic morphology, with dramatic copy number alterations (chromothripsis).

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
unmethylated	0.01281	0.00163	0.09359

(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