

Methylation profiling report



GERMAN
CANCER RESEARCH CENTER
IN THE HELMHOLTZ ASSOCIATION



Heidelberg University Hospital



General information

Sentrix ID: 202013790083_R01C01
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 Glioma, IDH mutant	0.97	match
MC family members with score ≥ 0.1		
methylation class IDH glioma, subclass 1p/19q codeleted oligodendroglioma	0.86	match

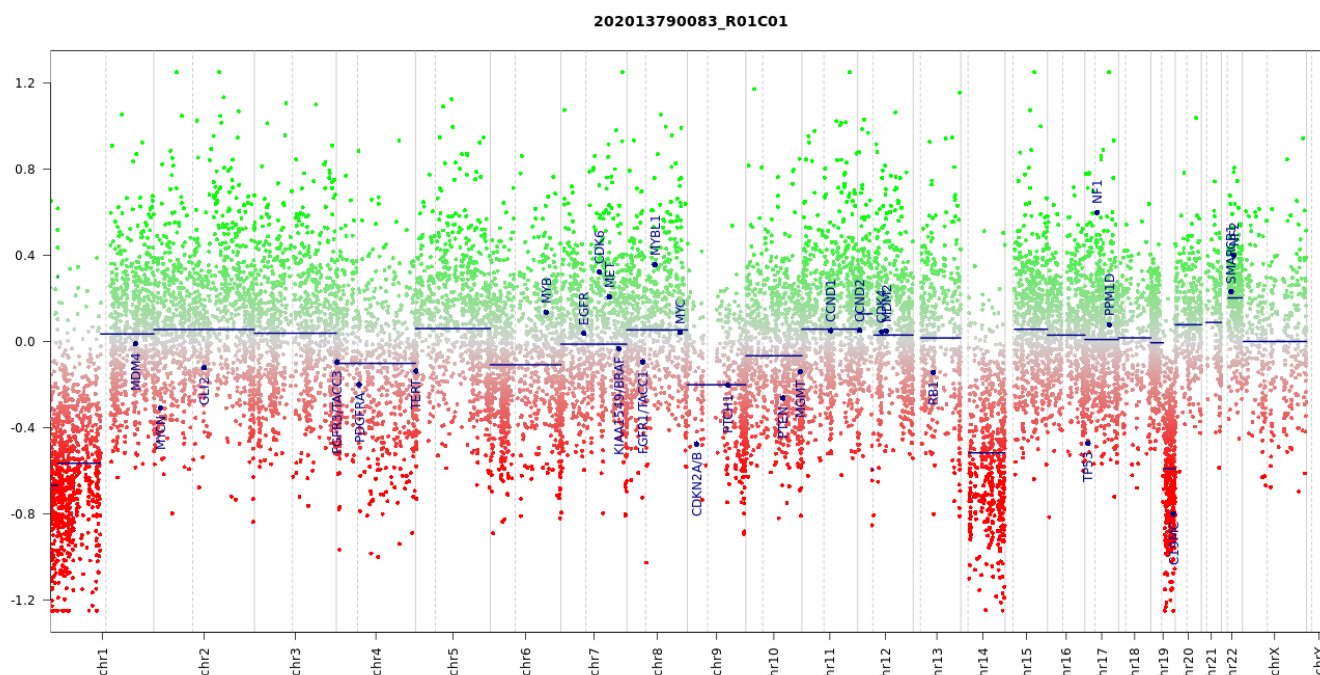
Legend: Match (score ≥ 0.9) No match (score < 0.9): possibly still relevant for low tumor content and low DNA quality cases. Match to MC family member (score ≥ 0.5)

Class descriptions

Methylation class family Glioma, IDH mutant: The methylation class family "Glioma, IDH mutant" comprises the methylation classes astrocytoma, IDH mutant, astrocytoma, IDH mutant, subtype high grade and oligodendroglioma, IDH mutant and 1p/19q codeleted.

Methylation class IDH glioma, subclass 1p/19q codeleted oligodendroglioma: The methylation class "IDH glioma, subclass 1p/19q codeleted oligodendroglioma" exclusively comprises tumors with the diagnosis anaplastic oligodendroglioma, IDH-mutant and 1p/19q-codeleted and oligodendroglioma, IDH-mutant and 1p/19q-codeleted. All tumors have a supratentorial location and frequently involve the frontal lobe; median age is 44 years (range 18 to 78). Molecularly, this class shares an IDH mutation-associated glioma CIMP, complete 1p/19q codeletion and TERT promoter mutation. A missing complete 1p/19q codeletion is not compatible with this diagnosis. Cases with elevated scores for this class but no complete 1p/19q codeletion likely represent "IDH glioma, subclass astrocytoma" or "IDH glioma, subclass high grade astrocytoma". Copy number analysis shows complete chromosome 1p and 19q loss in all cases. Around 30% of cases additionally show loss of chromosome 4.

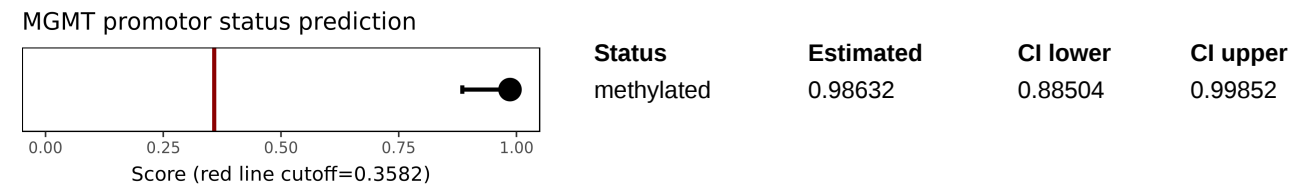
Copy number variation profile



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