






Methylation profiling report

General information

Sentrix ID:	202013790036_R04C01
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 family Glioma, IDH mutant	0.98	match 
MC family members with score >= 0.1		
methylation class IDH glioma, subclass 1p/19q codeleted oligodendroqlioma	0.94	match 

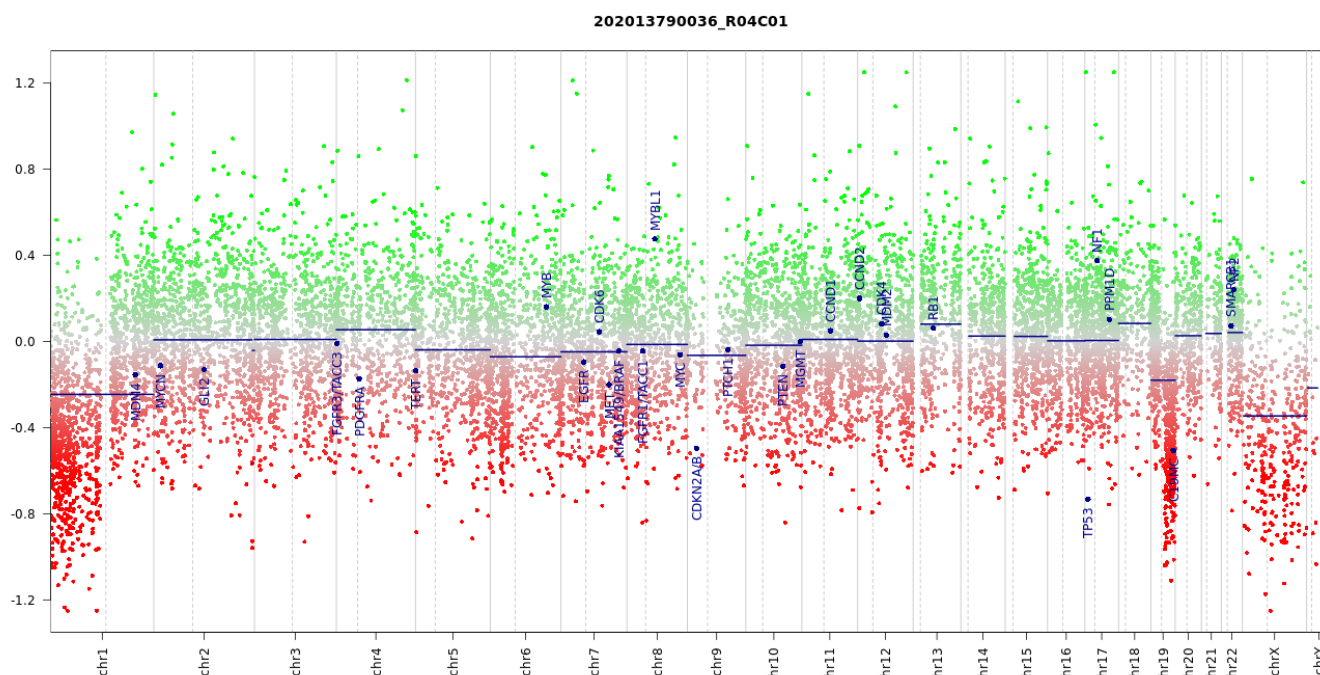
Legend:  Match (score ≥ 0.9)  No match (score < 0.9): possibly still relevant for low tumor content and low DNA quality cases.  Match to MC family member (score ≥ 0.5)

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.

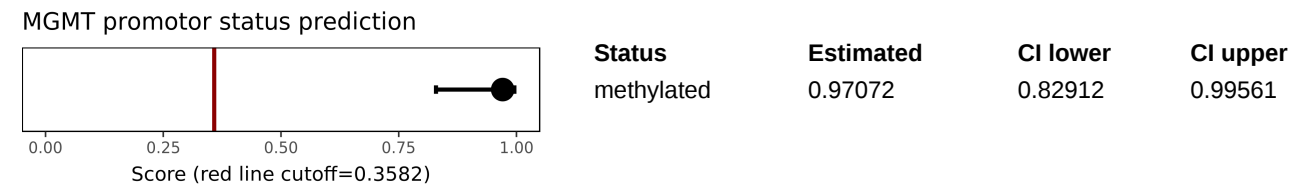
Copy number variation profile



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