Methylation profiling report

General information

Sentrix ID:	**202273260034_R08C01**
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 astrocytoma	0.5	match	●
methylation class IDH glioma, subclass high grade astrocytoma	0.35		
methylation class IDH glioma, subclass 1p/19q codeleted oligodendroglioma	0.11		

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

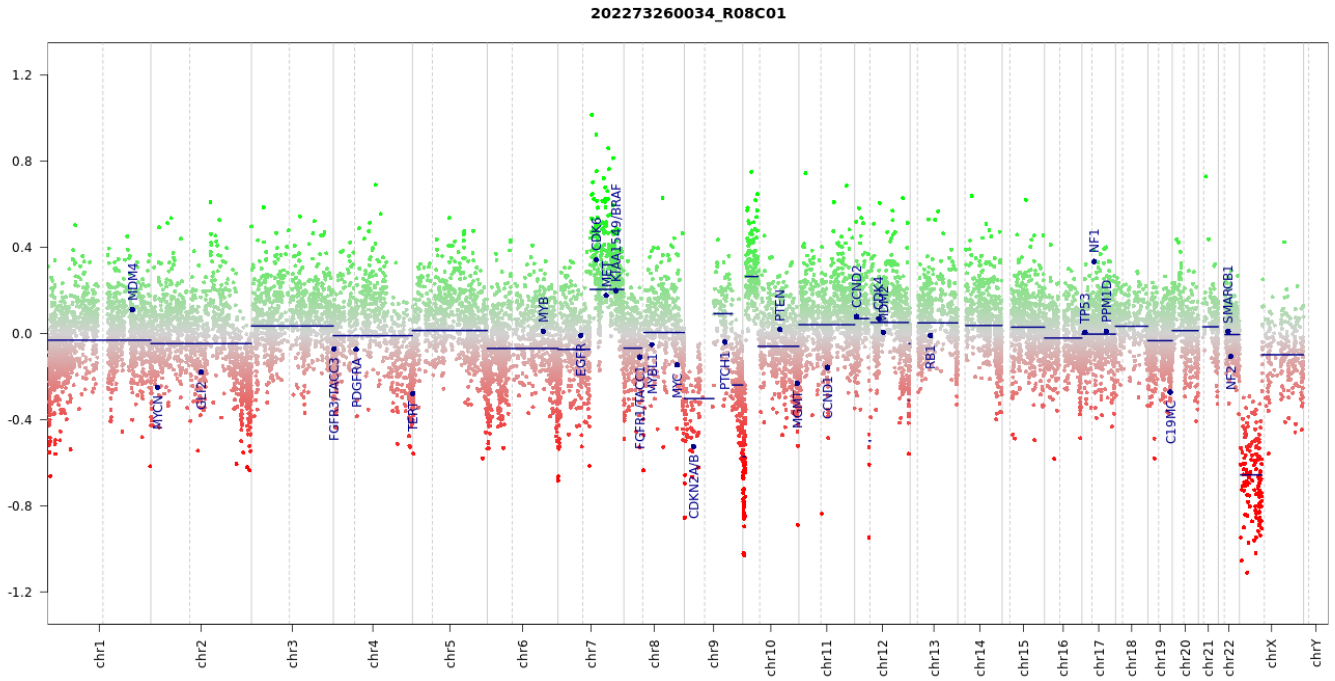
Methylation class family Glioma, IDH mutant: The methylation class family "Glioma, IDH mutant" comprises the methylation classes astrocytoma, IDH mutant, astrocytoma, IDH mutant, subtype high grade and oligodendroglioma, IDH mutant and 1p/19q codeleted.

Methylation class IDH glioma, subclass astrocytoma: The methylation class "IDH glioma, subclass astrocytoma" mainly comprises tumors with astrocytic histology of WHO grades II and III. Distinction of WHO grade II and III is not possible by DNA methylation profiling. This class is a member of the ? methylation-class-family Glioma, IDH mutant?. All tumors of this class have a supratentorial location; median age is 35 years (range 16 to 71). Complete 1p/19q codeletion is not compatible with "IDH glioma, subclass astrocytoma" and if present should lead to diagnosis of an "IDH glioma, subclass 1p/19q codeleted oligodendroglioma" despite a possibly higher classifier score for astrocytoma. This class universally harbors mutations of either IDH1 or IDH2 and the associated glioma CIMP phenotype.

Methylation class IDH glioma, subclass high grade astrocytoma : The methylation class "IDH glioma, subclass high grade astrocytoma" is mainly comprised of glioblastoma, IDH mutant and anaplastic astrocytoma, IDH mutant. Many of the cases in this class represent progressed tumors (i.e. secondary glioblastoma, IDH mutant). Primary location is generally supratentorial but posterior fossa spread in the course of disease is possible. Median age is 38 years (range 17 to 72). Complete 1p/19q codeletion is not compatible with "IDH glioma, subclass high grade astrocytoma" and if present should lead to diagnosis of an "IDH glioma, subclass 1p/19q codeleted oligodendroglioma". This class universally harbors mutations of either IDH1 or IDH2 and the associated glioma CIMP phenotype. Copy number changes are numerous and frequently complex.

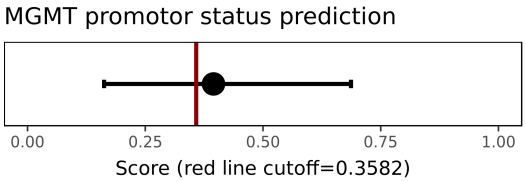
Methylation class IDH glioma, subclass 1p/19q codeleted oligodendroglioma: The methylation class "IDH glioma, subclass 1p/19q codeleted oligodendroglioma" exclusively comprises tumors with the diagnosis anaplastic oligodendroglioma, IDH-mutant and 1p/19q-codeleted and oligodendroglioma, IDH-mutant and 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)



Status	Estimated	CI lower	CI upper
methylated	0.39488	0.16258	0.68685

(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