





Methylation profiling report

Sentrix ID: 203057710034_R03C01

Material type: KRYO DNA

Gender: NA

Supplier diagnosis: -

Supplier information

Sample identifier:

Automatic prediction	
Array type:	EPIC
Material type:	KRYO DNA
Gender:	male
Legend: ✔ OK Supplier information or prediction not available	★Warning, missmatch of prediction and supplier information

Brain tumor methylation classifier results (v11b4)

sampleName1573983806

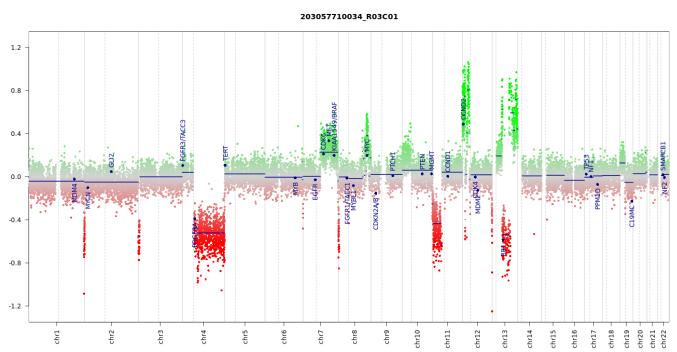
Methylation classes (MCs with score >= 0.3)	Calibrated score	Interpretati	on
methylation class family Glioma, IDH mutant	0.99	match	~
MC family members with score >= 0.1			
methylation class IDH glioma, subclass high grade astrocytoma	0.97	match	•
Legend: ✓ Match (score >= 0.9) × No match (score < 0.9): possibly still relevant for low tumor content at quality cases.	nd low DNA • Match to (score >=		ıber

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 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.

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



(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_sample 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
idat_reportBrain_v11b4	2.0