





Methylation profiling report

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Supplier information

Sample identifier: sampleName1527691879
Sentrix ID: 202273260034_R04C01

Material type: **FFPE DNA**

Gender: NA

Supplier diagnosis: -

Automatic prediction		
Array type:	EPIC	
Material type:	KRYO DNA	
Gender:	male	
Legend: ✔ OK Supplier information o prediction not available		

Brain tumor methylation classifier results (v11b4)

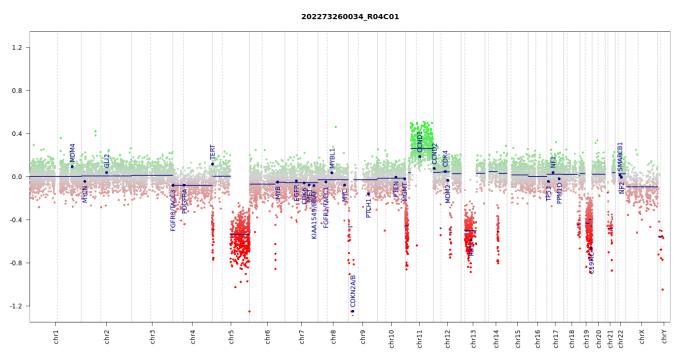
Methylation classes (MCs with score >= 0.3)	Calibrated score	Interpretation	n
methylation class family Glioma, IDH mutant	0.99	match	~
MC family members with score >= 0.1			
methylation class IDH glioma, subclass high grade astrocytoma	0.98	match	•
Legend: ✓ Match (score >= 0.9) X No match (score < 0.9): possibly still relevant for low tumor content ar quality cases.	d low DNA • Match to (score >=	MC family memb : 0.5)	er

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