Methylation profiling report

GERMAN CANCER RESEARCH CENTER IN THE HELMHOLTZ ASSOCIATION

Heidelberg University Hospital

MolecularNeuropathology.org

Supplier information

Sample identifier:	**sampleName1527692141**
Sentrix ID:	**202273260007_R06C01**
Material type:	**FFPE DNA**
Gender:	**NA**
Supplier diagnosis:	**-**

Automatic prediction		
Array type:	**EPIC**	
Material type:	**KRYO DNA**	✗
Gender:	**female**	!

Legend: ✓ OK ! Supplier information or prediction not available ✗ Warning, missmatch of prediction and supplier information

Brain tumor methylation classifier results (v11b4)

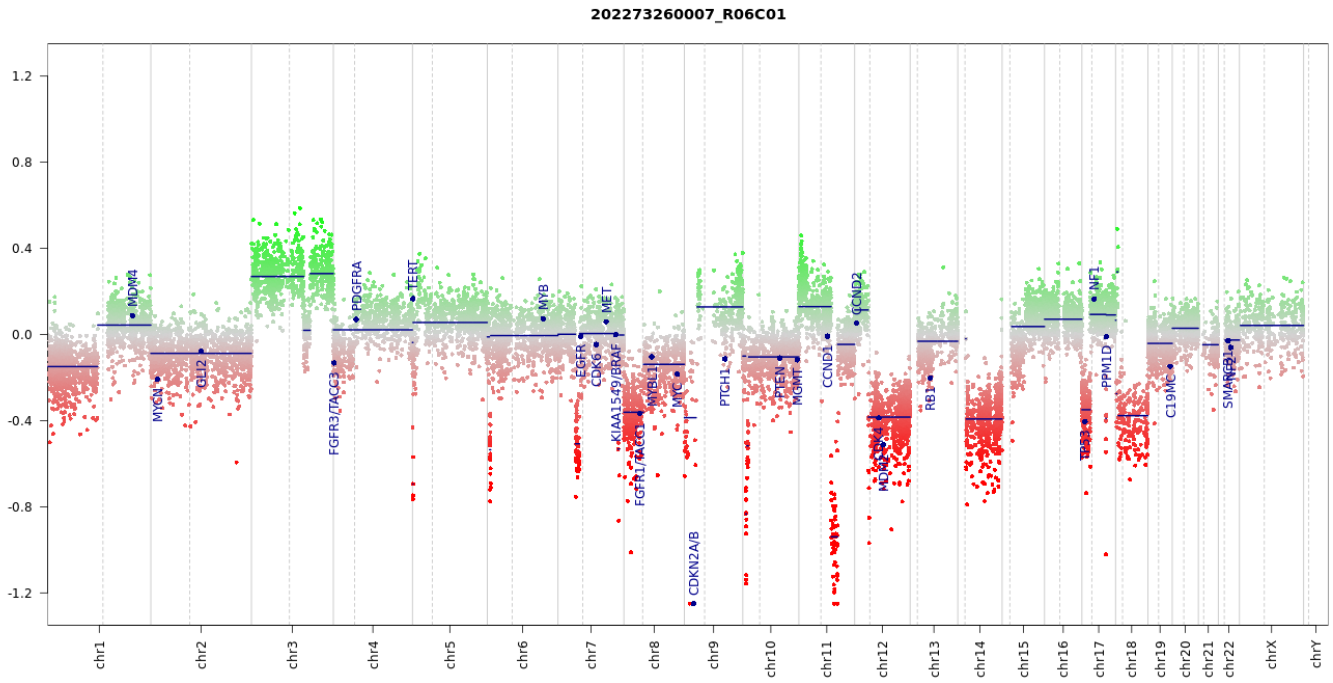
Methylation classes (MCs with score >= 0.3)	Calibrated score	Interpretation	
methylation class (anaplastic) pleomorphic xanthoastrocytoma	0.35	no match	✗

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

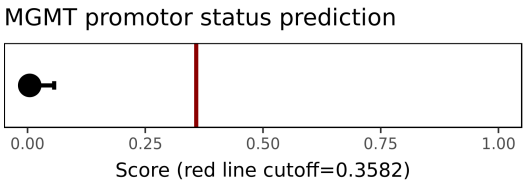
Methylation class (anaplastic) pleomorphic xanthoastrocytoma: The methylation class "(anaplastic) pleomorphic xanthoastrocytoma" mainly comprises tumors with the histological diagnosis of pleomorphic xanthoastrocytoma or anaplastic pleomorphic xanthoastrocytoma and to lesser extent IDH wildtype glioblastomas. Tumors in this class may also show a ganglion cell-like differentiation and may then histologically appear as anaplastic ganglioglioma. Tumors appearing as epithelioid glioblastoma, IDH wildtype may also fall into this class. Distinction of WHO grade II and III pleomorphic xanthoastrocytoma is currently not possible by methylation profiling. Location is typically supratentorial and frequently the temporal lobe is affected; median age is 19 years (range 7 to 51). Tumors of this class frequently harbor BRAF V600E mutations and deletions of chromosome 9 including the CDKN2A/B locus (>70%).

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
unmethylated	0.00459	3.5E-4	0.05655

(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