

Methylation profiling report

Supplier information

Sample identifier:	sampleName1527692195	Automatic prediction	
Sentrix ID:	202010290174_R06C01	Array type:	EPIC
Material type:	FFPE DNA	Material type:	KRYO DNA ✗
Gender:	NA	Gender:	female !
Supplier diagnosis:	-	Legend: ✔ OK ! Supplier information or prediction not available ✗ Warning, mismatch of prediction and supplier information	

Brain tumor methylation classifier results (v11b4)

Methylation classes (MCs with score >= 0.3)	Calibrated score	Interpretation
methylation class family Glioblastoma, IDH wildtype	0.7	no match ✗
MC family members with score >= 0.1		
methylation class glioblastoma, IDH wildtype, subclass mesenchymal	0.67	

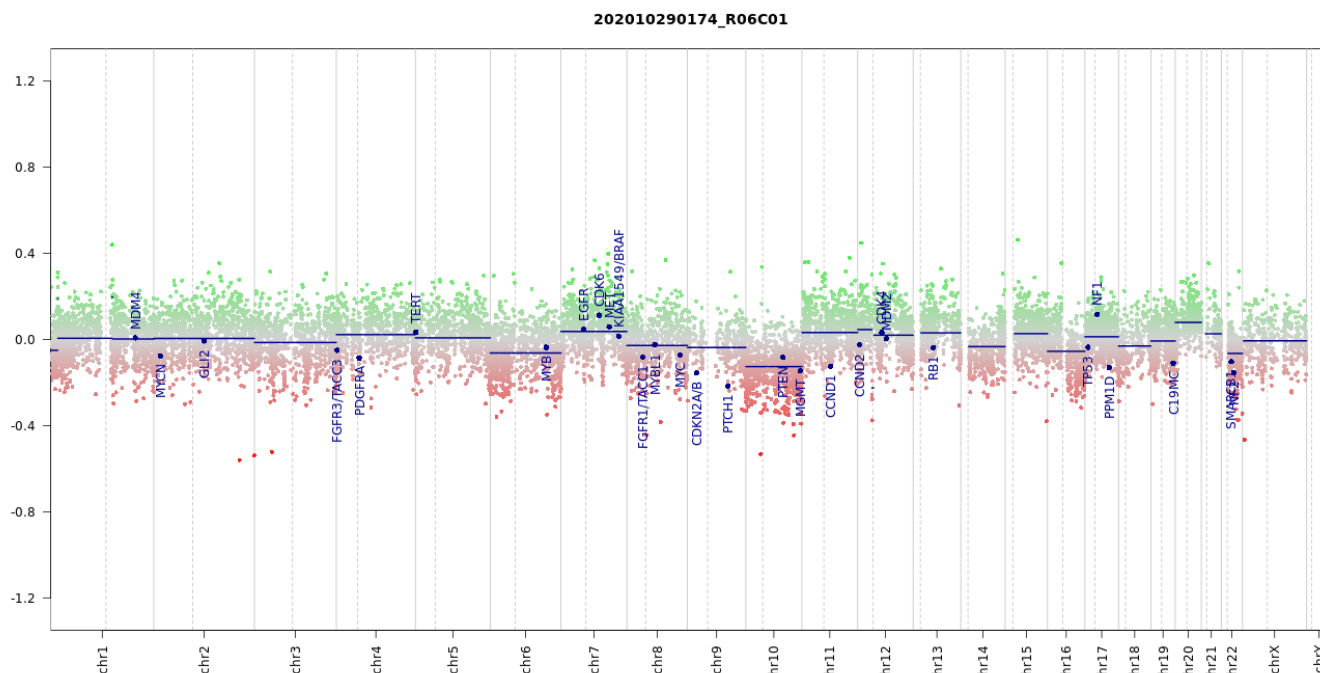
Legend: ✔ Match (score >= 0.9) ✗ No match (score < 0.9): possibly still relevant for low tumor content and low DNA quality cases. ● Match to MC family member (score >= 0.5)

Class descriptions

Methylation class family Glioblastoma, IDH wildtype: The methylation class family "Glioblastoma, IDH wildtype" comprises the methylation classes glioblastoma, IDH wildtype, subtype RTK I to III, glioblastoma, IDH wildtype, subtype mesenchymal, glioblastoma, IDH wildtype, subtype MYCN and glioblastoma, IDH wildtype, subtype midline.

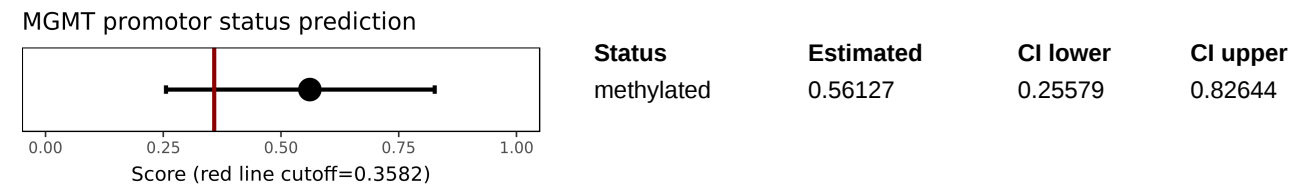
Methylation class glioblastoma, IDH wildtype, subclass mesenchymal: The methylation class "glioblastoma, IDH wildtype, subclass mesenchymal" is comprised of tumors with a histological diagnosis of glioblastoma or occasionally gliosarcoma. These tumors are typically located in the cerebral hemispheres. Median age is 59 years (range 40 to 86). Recurrent chromosomal alterations are gain of chromosome 7 with or without EGFR amplification (>80%), loss of 9p21 (CDKN2A/B; >60%) and chromosome 10 loss (>90%). Alterations of NF1 may also be enriched in this subtype, and expression profiles often resemble the 'Mesenchymal' subgroup according to the TCGA classification.

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_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