

Methylation profiling report

Supplier information

Sample identifier: GCGR-E25_p13
Sentry ID: 205715840058_R04C01
Material type: DNA-KRYO
Gender: NA
Supplier diagnosis: GBM

Automatic prediction			
Array type:	EPIC		
Material type:	DNA-KRYO		✓
Gender:	male		!
Legend:	✓ Ok	! Supplier information or prediction not available	✗ Warning, mismatch of prediction and supplier information

Brain tumor classifier results (11b4)

Methylation classes (MCs with score ≥ 0.3)

	Score	Interpretation
methylation class family Glioblastoma, IDH wildtype	0.59	no match ✗

MC family members with score ≥ 0.1

methylation class glioblastoma, IDH wildtype, subclass RTK I	0.56	match ●
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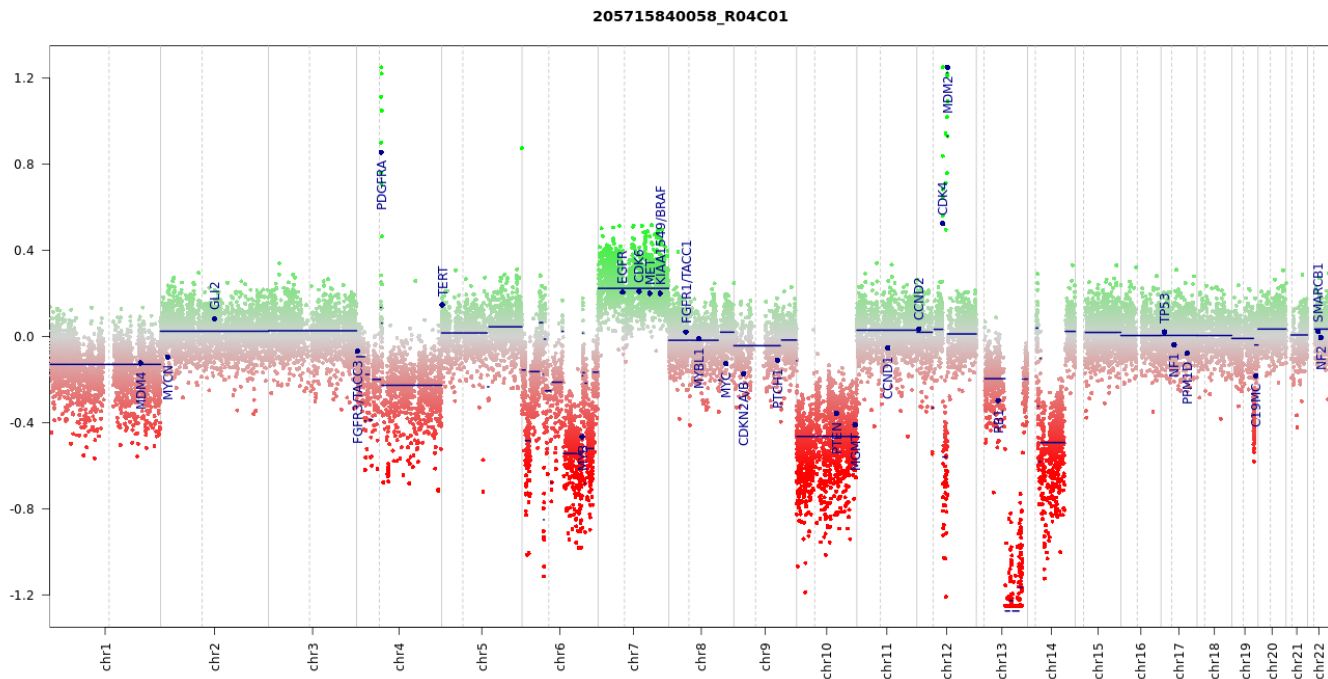
Legend: ✓ Match (score ≥ 0.9) ✗ No match (score < 0.9): possibly still relevant for low tumor content and low DNA quality cases. ● Match to MC family member (score ≥ 0.5)

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.

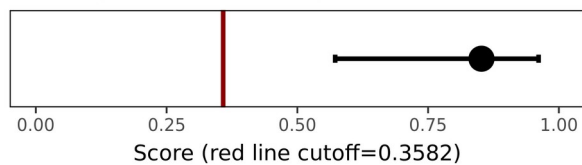
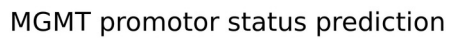
Methylation class glioblastoma, IDH wildtype, subclass RTK I: The methylation class "glioblastoma, IDH wildtype, subclass RTK I" is comprised of tumors with a histological diagnosis of glioblastoma, IDH wildtype. The tumors are located in the cerebral hemispheres. Median age is 64 years (range 29 to 84). Recurrent chromosomal alterations are gain of chromosome 7 with or without EGFR amplification ($>80\%$), loss of 9p21 (CDKN2A/B; $>50\%$) and chromosome 10 loss ($>70\%$). Amplifications of the PDGFRA oncogene are enriched in this class (present in 20-30% of cases). Expression profiles often resemble the 'Proneural' 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)



Status	Estimated	CI lower	CI upper
methyalted	0.85206	0.57230	0.96122

(see Bady et al, J Mol Diagn 2016; 18(3):350-61)

Disclaimer

Classification using methylation profiling is a tool/website for research use only, it is not verified and has not been clinically validated and, therefore, must not be used for diagnostic purposes. This tool/website is not HIPAA compliant.

Run information

Report: report_website_mnp_brain_v11b4_sample (Version 2.1)

Task version:

Task	Version
idat_preprocess	2.0.1
idat_qc	2.0.1
idat_predictBrain	2.0.1
idat_rs_gender	2.0.1
idat_cnv	3.0.1
idat_mgmt	2.0.1
report_website_mnp_brain_v11b4_research	2.1
report_website_mnp_brain_v11b4_sample	2.1
idat_predictBrain	12.5