Methylation profiling report

Supplier information

Sample identifier:	GCGR-E17_p13
Sentrix ID:	205715840058_R01C01
Material type:	DNA-KRYO
Gender:	NA
Supplier diagnosis:	GBM

Automatic prediction		
Array type:	EPIC	
Material type:	DNA-KRYO	✓
Gender:	female	!

Legend: ✓ Ok ! Supplier information or prediction not available ✗ Warning, missmatch 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	0.81	no match	✗

MC family members with score >= 0.1

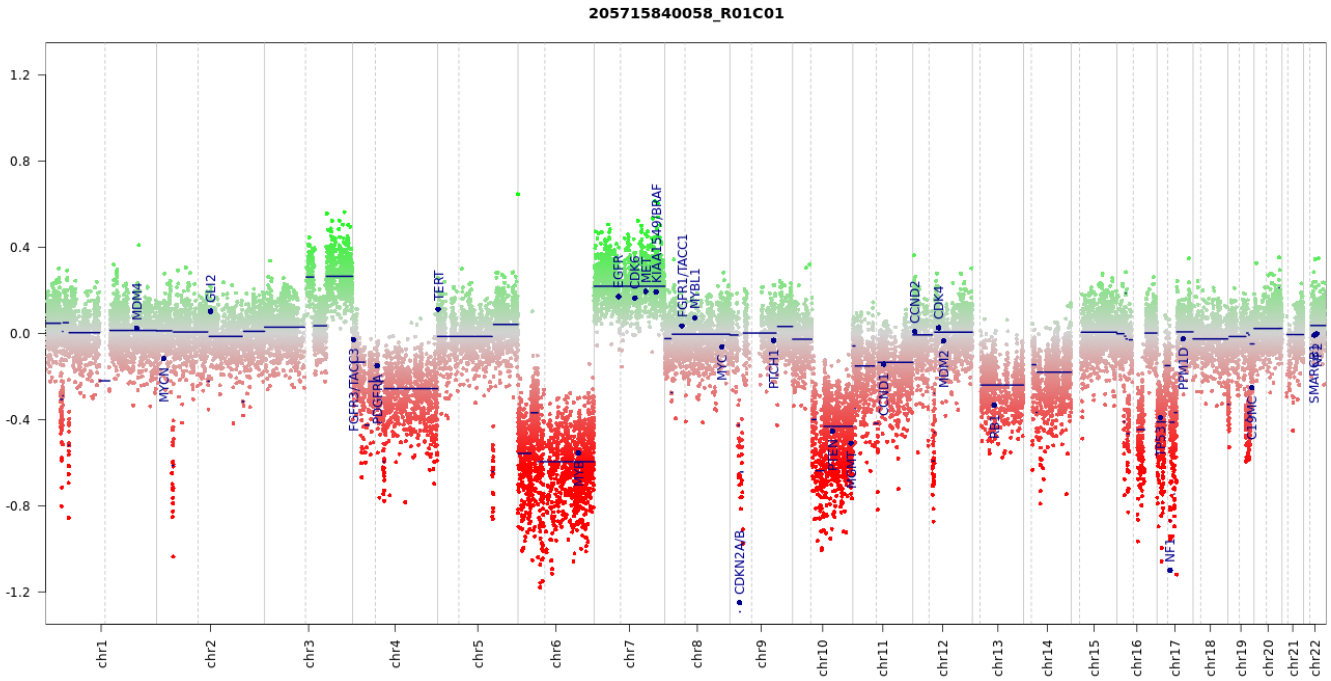
methylation class glioblastoma, IDH wildtype, subclass RTK I	0.52	match	●
methylation class glioblastoma, IDH wildtype, subclass RTK II	0.28		

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

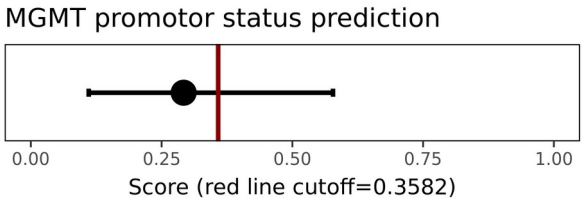
Methylation class family Glioblastoma, IDH wildtype: The methylation class family "Glioblastoma, IDH wildtype" comprises the methylation classes glioblastoma, IDH wildtype, subtype RTK I to III, glioblastoma, IDH wildtype, subtype mesenchymal, glioblastoma, IDH wildtype, subtype MYCN and glioblastoma, 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.
Methylation class glioblastoma, IDH wildtype, subclass RTK II: The methylation class "glioblastoma, IDH wildtype, subclass RTK II" is comprised of tumors with a histological diagnosis of glioblastoma, IDH wildtype and rarely gliosarcoma, IDH wildtype. These tumors are typically located in the cerebral hemispheres. Median age is 61 years (range 36 to 86). Recurrent chromosomal alterations are gain of chromosome 7 with or without EGFR amplification (>90%), loss of 9p21 (CDKN2A/B; >70%) and chromosome 10 loss (>90%). Gin of chromosome 19 and 20 is also recurrently observed (40% of cases). Expression profiles often resemble the 'Classical' 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
unmethylated	0.29216	0.11074	0.57772

(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_cnvp	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