






Methylation profiling report

General information

Sentrix ID: 202010290105_R01C01
Array type: EPIC
Material type: KRYO DNA
Gender: male

Brain tumor methylation classifier results (v11b4)

| Methylation classes (MCs with score ≥ 0.3) | Calibrated score | Interpretation |
|--------------------------------------------------------------|------------------|-------------------------------------------------------------------------------------------|
| methylation class family Glioblastoma, IDH wildtype | 0.99 | match  |
| MC family members with score ≥ 0.1 | | |
| methylation class glioblastoma, IDH wildtype, subclass RTK I | 0.95 | match  |

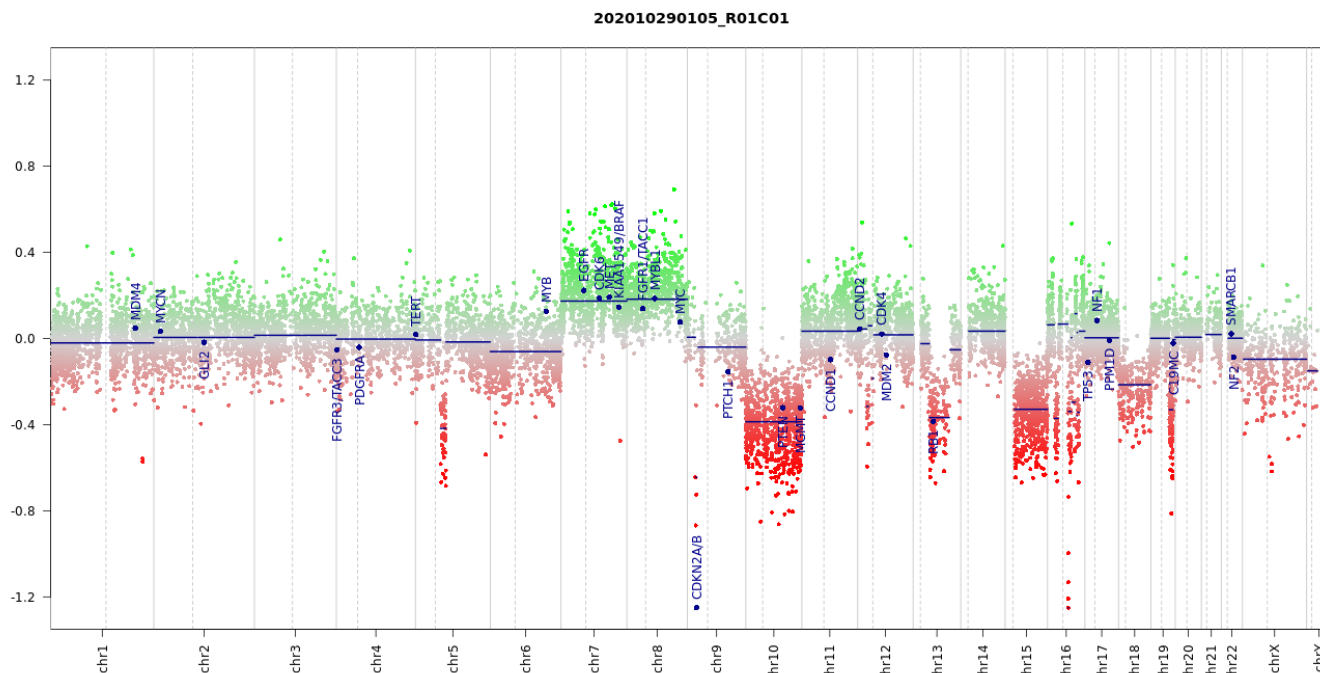
Legend:  Match (score ≥ 0.9)  No match (score < 0.9): possibly still relevant for low tumor content and low DNA quality cases.  Match to MC family member (score ≥ 0.5)

Class descriptions

Methylation class 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.

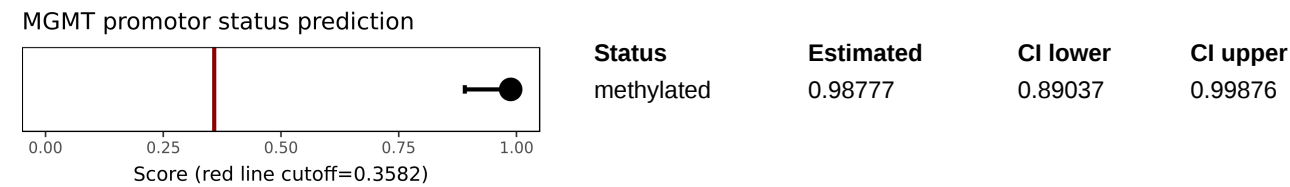
Copy number variation profile



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)



(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 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 |