# Methylation profiling report

GERMAN CANCER RESEARCH CENTER IN THE HELMHOLTZ ASSOCIATION

Heidelberg University Hospital

MolecularNeuropathology.org

## Supplier information

| | |
|---|---|
| Sample identifier: | **sampleName1527692261** |
| Sentrix ID: | **202010290060_R01C01** |
| 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 family Glioblastoma, IDH wildtype | 0.35 | no match | ✗ |
| **MC family members with score >= 0.1** | | | |
| methylation class glioblastoma, IDH wildtype, subclass mesenchymal | 0.19 | | |
| methylation class glioblastoma, IDH wildtype, subclass RTK II | 0.12 | | |
| methylation class control tissue, inflammatory tumor microenvironment | 0.32 | 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

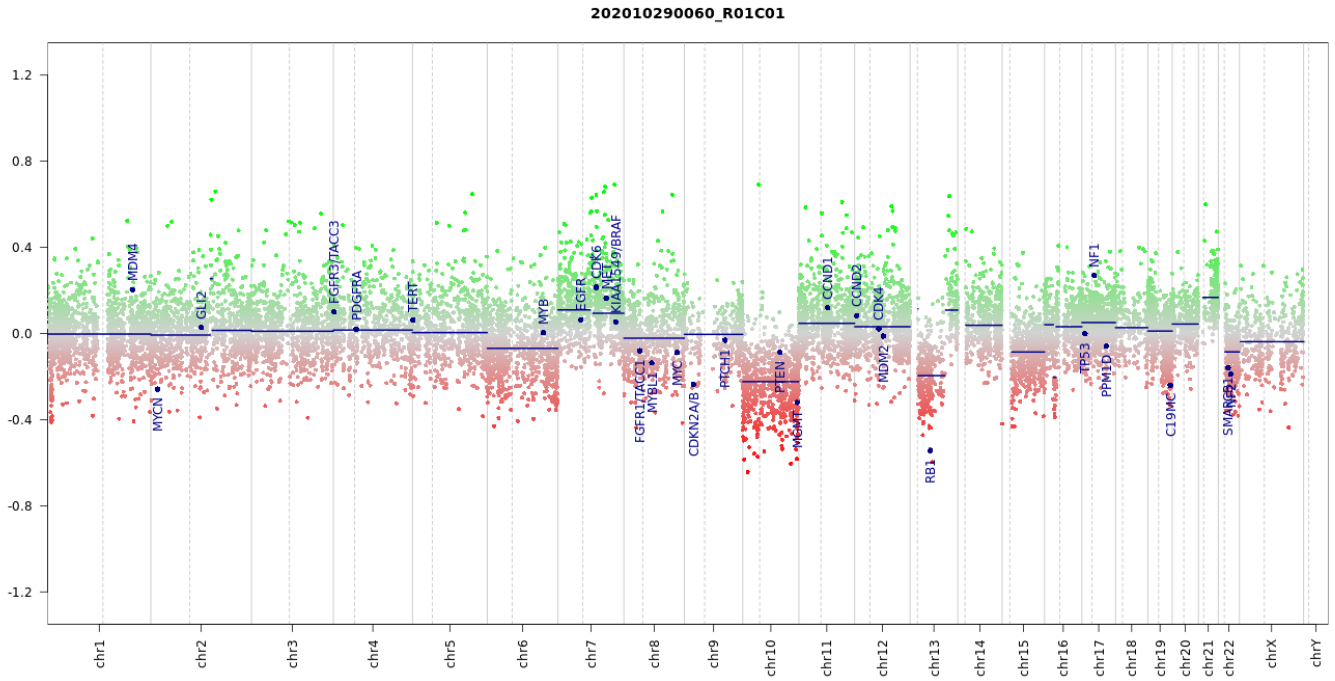
**Methylation class family Glioblastoma, IDH wildtype:** The methylation class family "Glioblastoma, IDH wildtype" comprises the methylation classes glioblastoma, IDH wildtype, subtype RTK I to III, glioblastoma, IDH wildtype, subtype mesenchymal, glioblastoma, IDH wildtype, subtype MYCN and glioblastoma,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

**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.

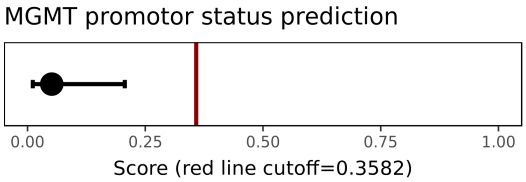
**Methylation class control tissue, inflammatory tumor microenvironment:** The methylation class "control tissue, inflammatory inflammatory tumor microenvironment" does not represent a distinct tumor class but rather a recurrently observed profile of mixed cell types with a high leukocyte fraction (often predominant granulocytic infiltrates). This is frequently observed in highly necrotic tumors, highly necrotic other tissues or when areas of extensive hemorrhage are sampled along with the tumor tissue of interest. Tumors with a pronounced granulocytic infiltrate due to other reasons can also get an elevated score for this class. Classification into this class is not diagnostic for a specific type of tumor. A score for this class indicates that the extracted DNA is likely not suitable for classification by methylation profiling. Depending on the degree, copy number alterations may also be masked by the high leukocyte infiltration. The reference class consists of glioblastomas only, but other tumors with high leukocyte infiltration are also expected to fall into this class.

## 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 | 0.05143 | 0.01117 | 0.20656 |

(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 |