# Methylation profiling report

## Supplier information

| | |
|---|---|
| Sample identifier: | **sampleName1573983870** |
| Sentrix ID: | **203057710034_R01C01** |
| Material type: | **KRYO 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)

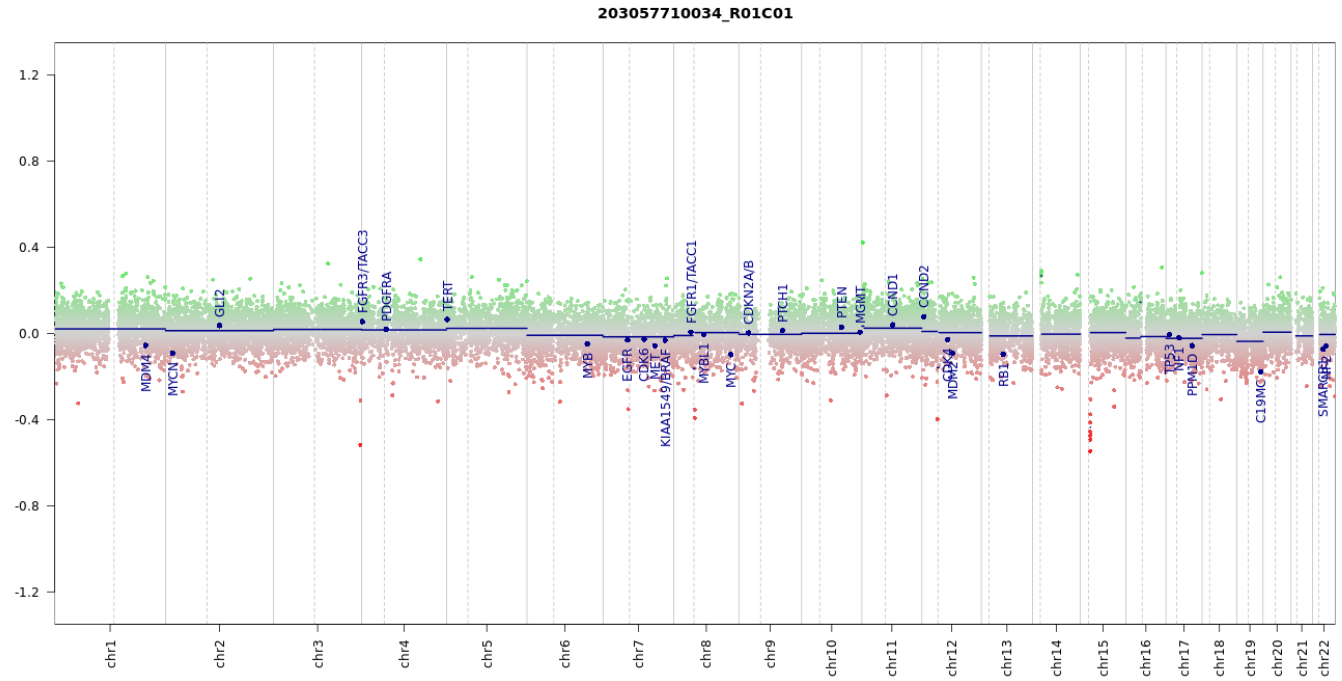
| Methylation classes (MCs with score >= 0.3) | Calibrated score | Interpretation | |
|---|---|---|---|
| methylation class diffuse midline glioma H3 K27M mutant | 0.42 | no match | ✘ |

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

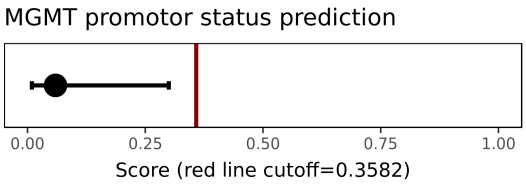
**Methylation class diffuse midline glioma H3 K27M mutant:** The methylation class "diffuse midline glioma H3 K27M mutant" is comprised of tumors with a histological diagnosis of diffuse midline glioma, H3 K27M mutant. The tumors are located in midline structures (thalamus, cerebellum, brainstem, spine). Median age is 12 years (range 1 to 54). Tumors of this class harbor mutations of codon 27 in one of the genes encoding histone 3 (most commonly H3F3A, but also the H3.1 genes HIST1H3A/B/C and very rarely H3.2). Additional mutations in ATRX and TP53/PPM1D are common. In brainstem tumors, ACVR1 mutations are also recurrently observed. Prognosis of this class is generally very poor, although rare lower grade lesions with K27M mutation have also been reported.

## 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 | 0.05938 | 0.00922 | 0.29993 |

(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 |