**Methylation profiling report**

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## Supplier information

| | | | Automatic prediction | | |
|---|---|---|---|---|---|
| Sample identifier: | **sampleName1527692876** | | | | |
| Sentrix ID: | **202053820004_R01C01** | | Array type: | **EPIC** | |
| Material type: | **FFPE DNA** | | Material type: | **KRYO DNA** | ✗ |
| Gender: | **NA** | | Gender: | **male** | ❗ |
| Supplier diagnosis: | **-** | | | | |

Legend: ✔ OK   ❗ Supplier information or prediction not available   ✗ Warning, missmatch of prediction and supplier information

## Brain tumor methylation classifier results (v11b4)

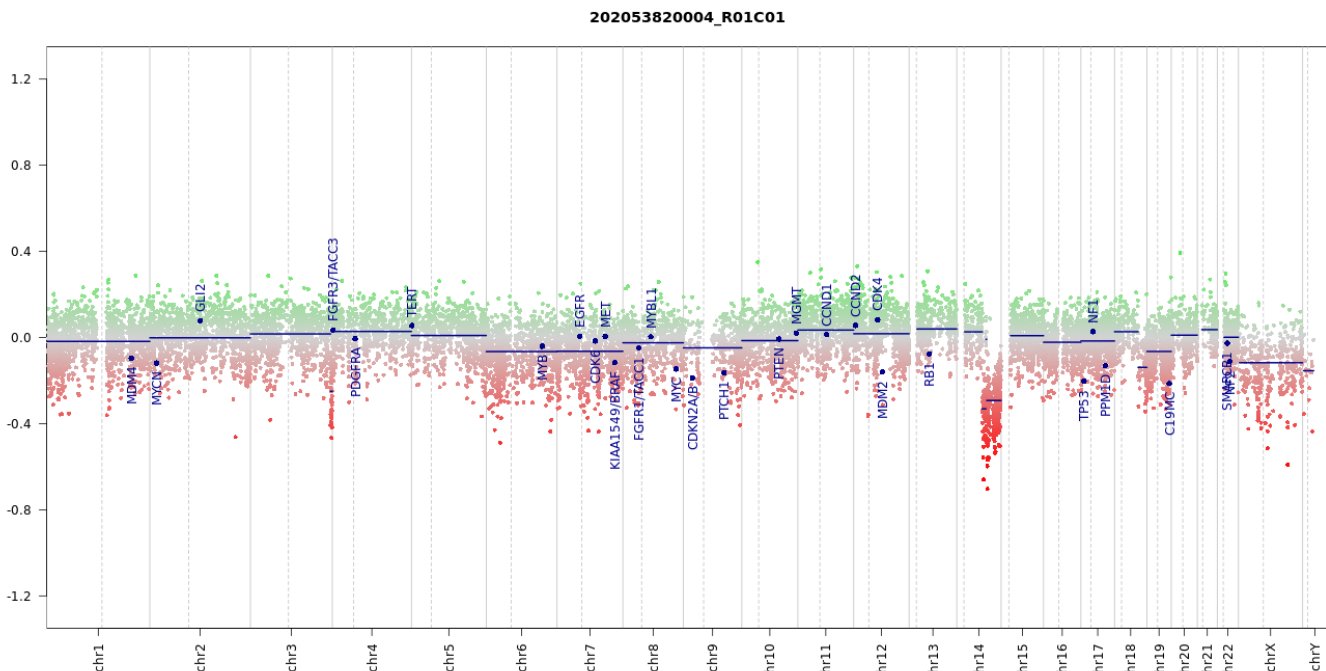| Methylation classes (MCs with score >= 0.3) | Calibrated score | Interpretation | |
|---|---|---|---|
| methylation class family Glioma, IDH mutant | 0.99 | match | ✔ |
| **MC family members with score >= 0.1** | | | |
| methylation class IDH glioma, subclass astrocytoma | 0.99 | match | ● |

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)
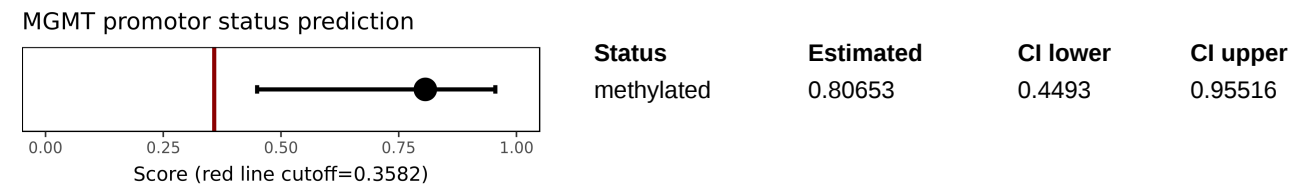
### Class descriptions

**Methylation class family Glioma, IDH mutant:** The methylation class family "Glioma, IDH mutant" comprises the methylation classes astrocytoma, IDH mutant, astrocytoma, IDH mutant, subtype high grade and oligodendroglioma, IDH mutant and 1p/19q codeleted.

**Methylation class IDH glioma, subclass astrocytoma:** The methylation class "IDH glioma, subclass astrocytoma" mainly comprises tumors with astrocytic histology of WHO grades II and III. Distinction of WHO grade II and III is not possible by DNA methylation profiling. This class is a member of the ? methylation-class-family Glioma, IDH mutant?. All tumors of this class have a supratentorial location; median age is 35 years (range 16 to 71). Complete 1p/19q codeletion is not compatible with "IDH glioma, subclass astrocytoma" and if present should lead to diagnosis of an "IDH glioma, subclass 1p/19q codeleted oligodendroglioma" despite a possibly higher classifier score for astrocytoma. This class universally harbors mutations of either IDH1 or IDH2 and the associated glioma CIMP phenotype.

## 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)

MGMT promotor status prediction



Score (red line cutoff=0.3582)

| Status | Estimated | CI lower | CI upper |
|---|---|---|---|
| methylated | 0.80653 | 0.4493 | 0.95516 |

(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 |