

# Methylation profiling report

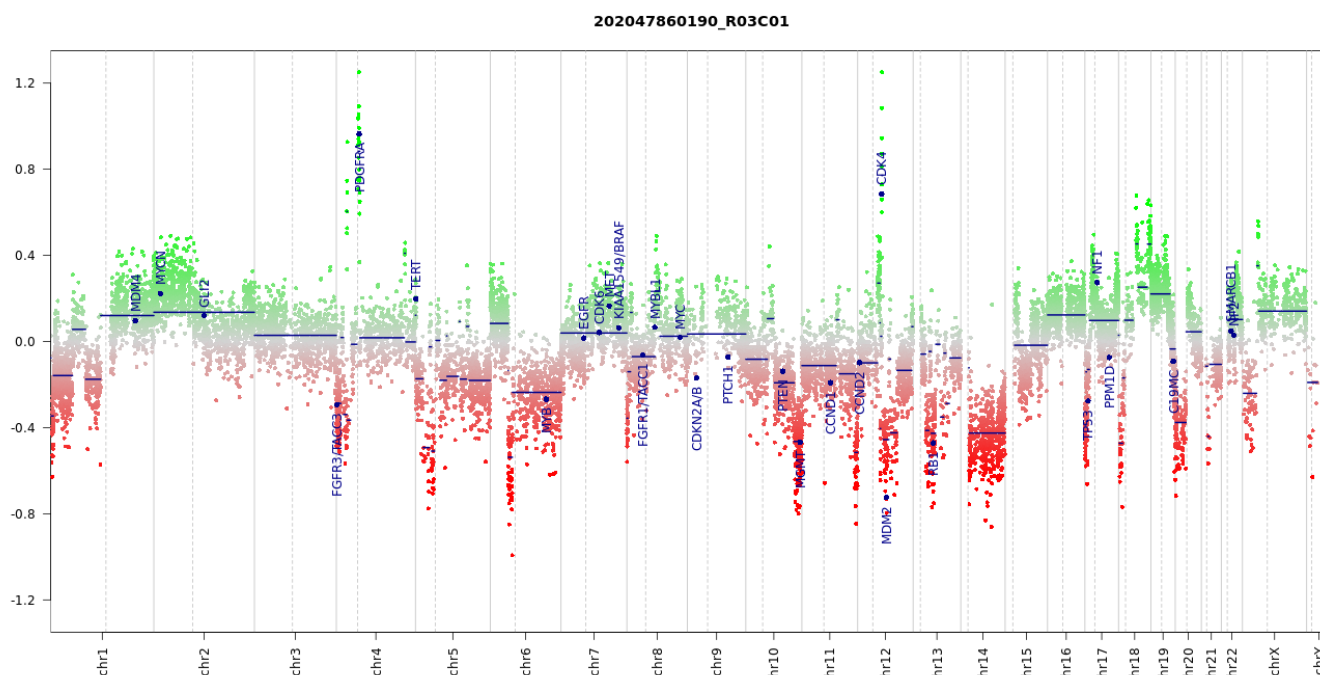
## Supplier information

Sample identifier: **sampleName1527692606**  
Sentrix ID: **202047860190\_R03C01**  
Material type: **FFPE DNA**  
Gender: **NA**  
Supplier diagnosis: **-**

| Automatic prediction   |          |   |
|--|----------|---|
| Array type:  | EPIC     |   |
| Material type:   | KRYO DNA | ✗ |
| Gender:  | male     | ! |
| Legend: ✓ OK   ! Supplier information or prediction not available   ✗ Warning, mismatch of prediction and supplier information |          |   |

## Brain tumor methylation classifier results (v11b4) - No matching methylation classes with calibrated score $\geq 0.3$

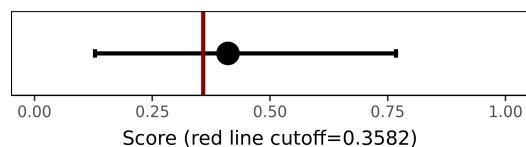
## Copy number variation profile



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



| Status    | Estimated | CI lower | CI upper |
|-----------|-----------|----------|----------|
| methyated | 0.41078   | 0.12828  | 0.7676   |

(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     |