

Methylation profiling report

Supplier information

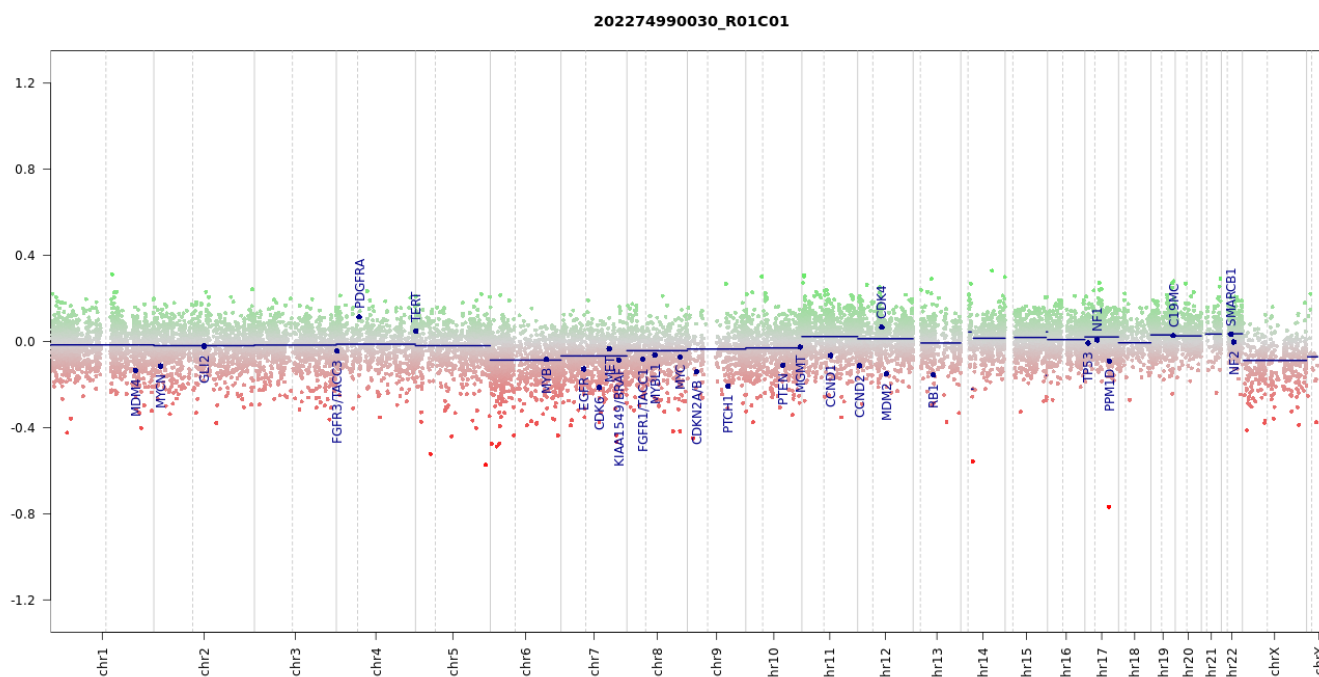
| | |
|---------------------|----------------------|
| Sample identifier: | sampleName1540553378 |
| Sentrix ID: | 202274990030_R01C01 |
| Material type: | KRYO DNA |
| Gender: | NA |
| Supplier diagnosis: | - |

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 ≥ 0.3

Copy number variation profile

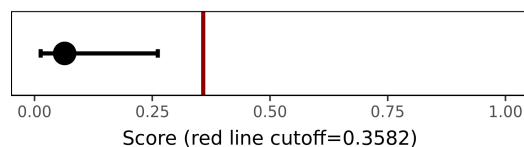


Depiction of chromosome 1 to 22 (and XY if automatic prediction was successful). Gains/amplifications represent positive, losses negative deviations from the baseline. 29 brain tumor relevant gene regions are highlighted for easier assessment.

(see Hovestadt & Zapatka, <http://www.bioconductor.org/packages/devel/bioc/html/conumee.html>)

MGMT promotor methylation (MGMT-STP27)

MGMT promotor status prediction



(see Bady et al, J Mol Diagn 2016; 18(3):350-61)

| Status | Estimated | CI lower | CI upper |
|--------------|-----------|----------|----------|
| unmethylated | 0.06397 | 0.013 | 0.26173 |

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 |