

## Methylation profiling report

### Supplier information

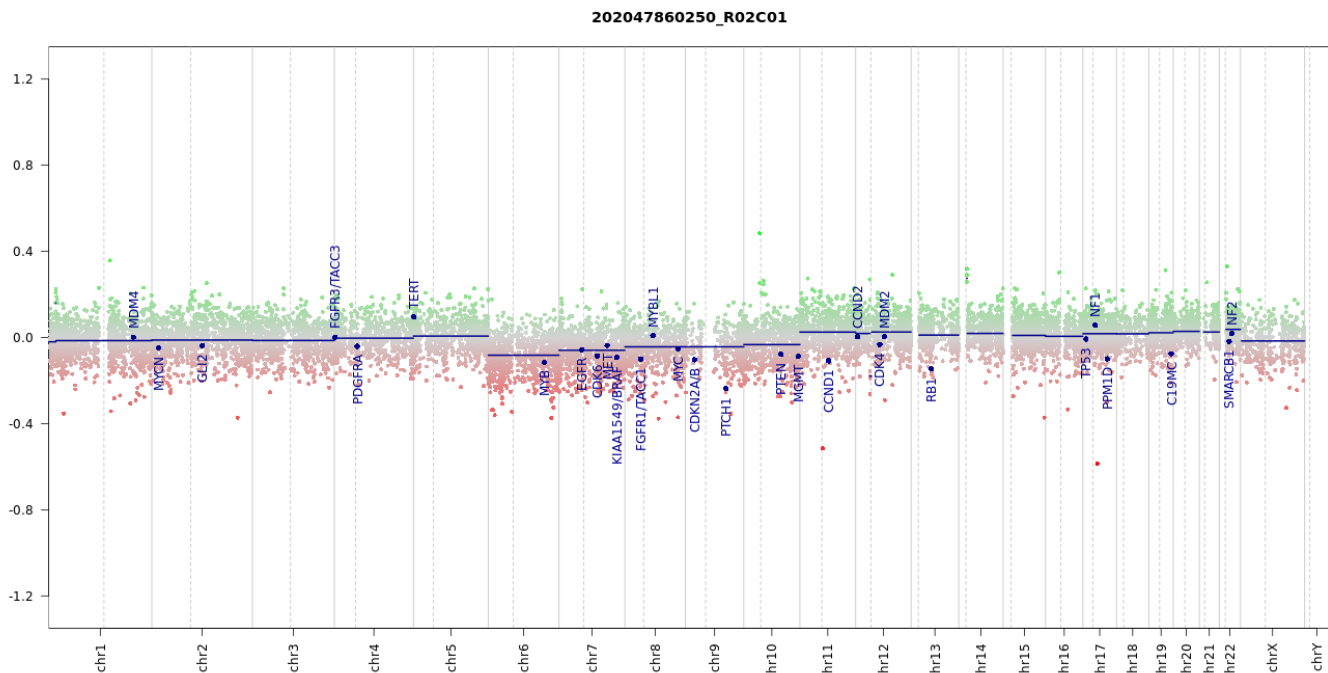
Sample identifier: **sampleName1527691856**  
Sentrix ID: **202047860250\_R02C01**  
Material type: **FFPE DNA**  
Gender: **NA**  
Supplier diagnosis: **-**

#### Automatic prediction

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

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

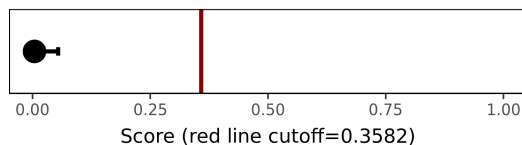
### Copy number variation profile



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
unmethylated	0.00413	3.0E-4	0.05437

(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