

## Methylation profiling report

### Supplier information

Sample identifier: GCGR-NS9FB\_B-PTEN-TP53-PDGFR $\alpha$ -GFP-LUC  
Sentrix ID: 205715840020\_R02C01  
Material type: DNA-KRYO  
Gender: NA  
Supplier diagnosis: GBM

#### Automatic prediction

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

### Brain tumor classifier results (11b4)

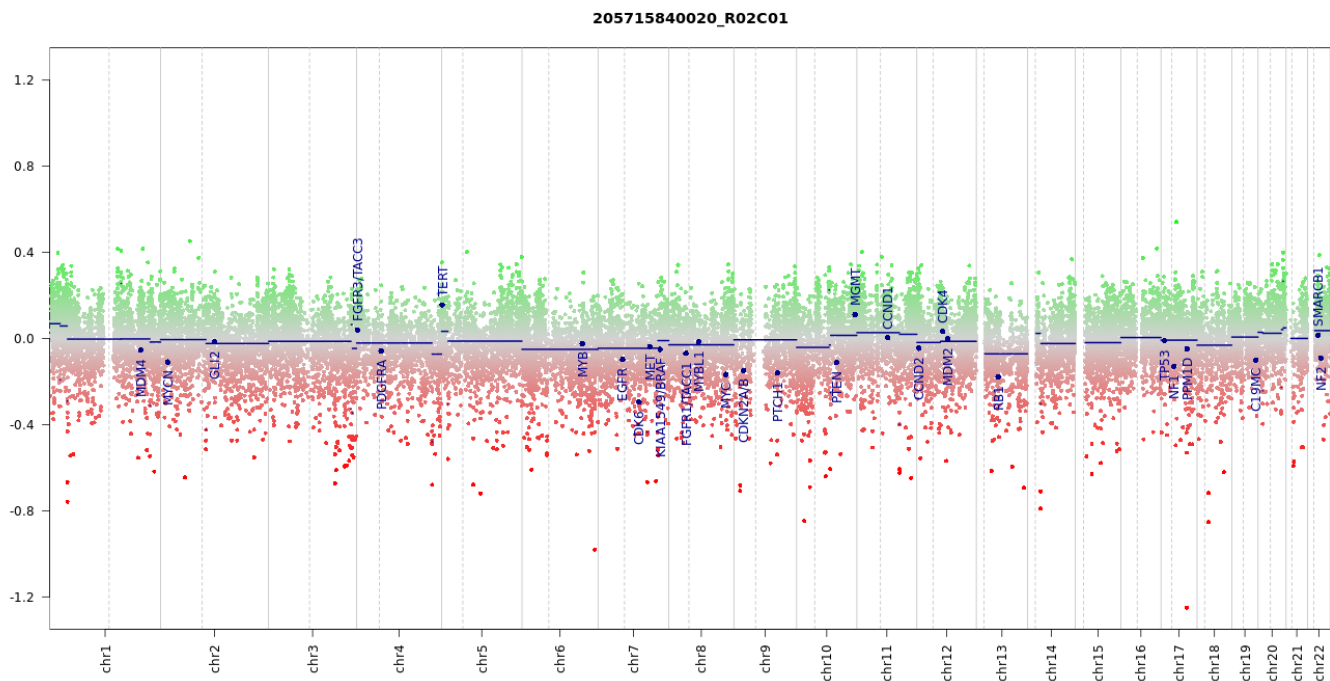
Not classifiable. No score is greater 0.3

Legend: ✓ Match (score  $\geq 0.9$ ) ✗ No match (score  $< 0.9$ ): possibly still relevant for low tumor content and low DNA quality cases. ● Match to MC family member (score  $\geq 0.5$ )

### Class descriptions

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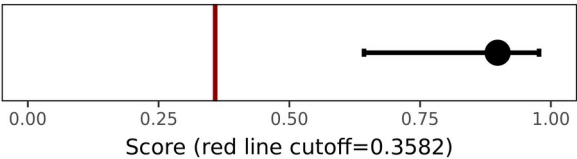
Copy number variation profile



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	0.89822	0.64275	0.97742

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

## Disclaimer

Classification using methylation profiling is a tool/website for research use only, it is not verified and has not been clinically validated and, therefore, must not be used for diagnostic purposes. This tool/website is not HIPAA compliant.

## Run information

**Report:** report\_website\_mnp\_brain\_v11b4\_sample (Version 2.1)

### Task version:

Task	Version
idat_preprocess	2.0.1
idat_qc	2.0.1
idat_predictBrain	2.0.1
idat_rs_gender	2.0.1
idat_cnvp	3.0.1
idat_mgmt	2.0.1
report_website_mnp_brain_v11b4_research	2.1
report_website_mnp_brain_v11b4_sample	2.1
idat_predictBrain	12.5