

## Methylation profiling report

### Supplier information

|                     |                                |                      |   |   |
|---------------------|--------------------------------|----------------------|---|---|
| Sample identifier:  | GCGR-NS17ST_A-NF1-PTEN-GFP-LUC | Automatic prediction |   |   |
| Sentrix ID:         | 205624860044_R01C01            | Array type:          | EPIC  |   |
| Material type:      | DNA-KRYO                       | Material type:       | DNA-KRYO  | ✓ |
| Gender:             | NA                             | Gender:              | female  | ! |
| Supplier diagnosis: | GBM                            | Legend:              | <div>✓ Ok</div> <div>! Supplier information or prediction not available</div> <div>✗ Warning, mismatch of prediction and supplier information</div> |   |

### Brain tumor classifier results (11b4)

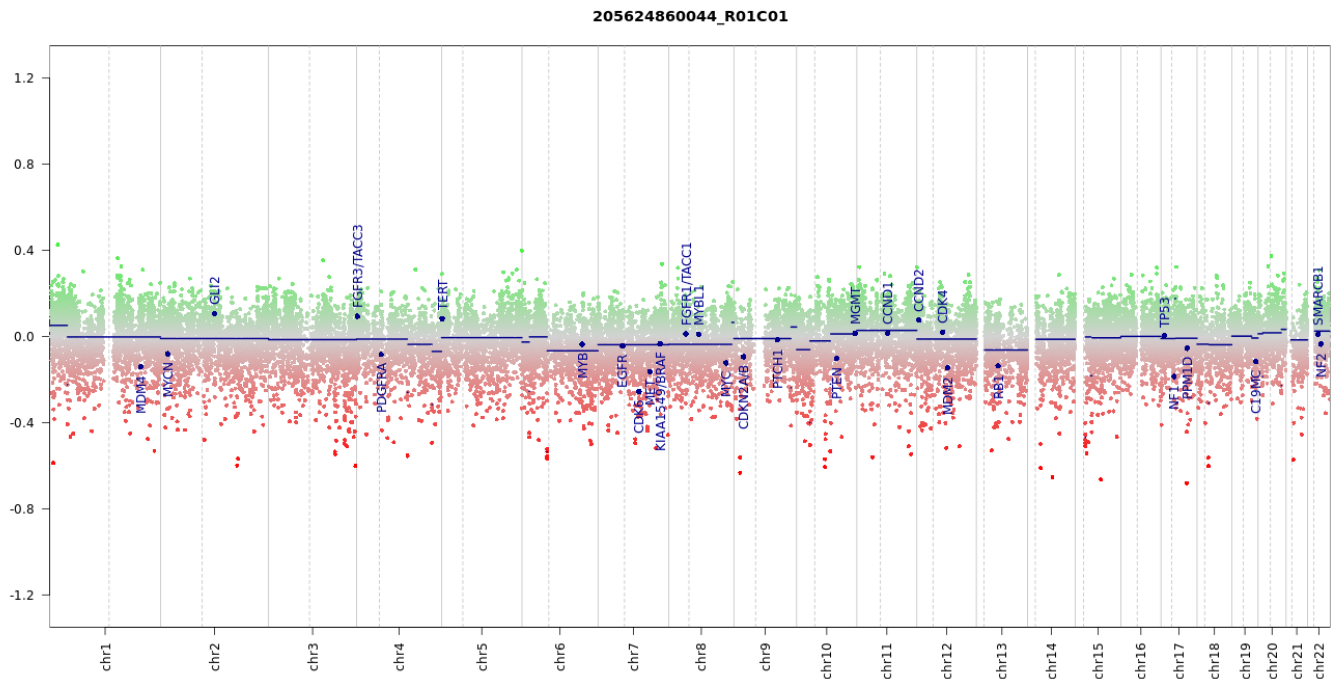
#### Methylation classes (MCs with score $\geq 0.3$ )

|   | Score | Interpretation                                |
|---|-------|---|
| methylation class infantile hemispheric glioma  | 0.55  | no match ✗                                    |
| 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

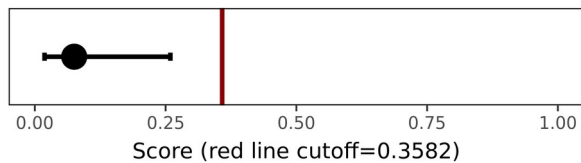
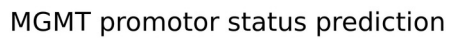
**Methylation class infantile hemispheric glioma:** The methylation class "infantile hemispheric glioma" comprises tumors with widely varying morphology, commonly including features more typical of higher grade lesions especially glioblastoma. These tumors are located supratentorially, all cases so far were observed in infants; median age is 0 years (age range 0 to 1). Copy number alterations are scarce, and typical molecular features of this class are not currently known. The name given here is provisional.

## 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)



| Status       | Estimated | CI lower | CI upper |
|--------------|-----------|----------|----------|
| unmethylated | 0.07528   | 0.01859  | 0.25918  |

(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_cnv                                | 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    |