





### **Methylation profiling report**

# Supplier information

Sample identifier: sampleName1573855888 **Automatic prediction** Sentrix ID: 203057570098\_R03C01 Array type: **EPIC KRYO DNA** Material type: Material type: **KRYO DNA** Gender: Gender: male NA Supplier diagnosis: Legend: ✓ OK Supplier information or Warning, missmatch of prediction prediction not available and supplier information

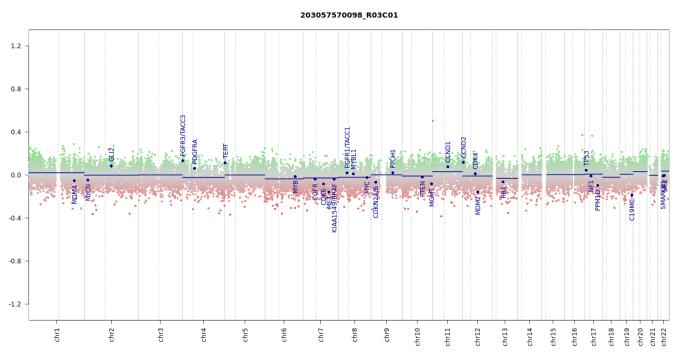
#### Brain tumor methylation classifier results (v11b4)

| Methylation classes (MCs with score >= 0.3)   |  | Calibrated score | Interpretation |          |  |
|---|--|------------------|----------------|----------|--|
| methylation class infantile hemispheric glioma  |  | 0.96             | match          | <b>~</b> |  |
| Legend: ✓ Match (score >= 0.9) X No match (score < 0.9): possibly still relevant for low tumor content and low DNA Match to MC family member (score >= 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.

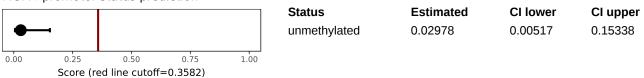
#### Copy number variation profile



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)

MGMT promotor status prediction



(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     |