

Supplier information

|                     |                      |                                                                                                                                |          |   |
|---------------------|----------------------|--------------------------------------------------------------------------------------------------------------------------------|----------|---|
| Sample identifier:  | sampleName1573896538 | Automatic prediction                                                                                                           |          |   |
| Sentrix ID:         | 203057570155_R08C01  | Array type:                                                                                                                    | EPIC     |   |
| Material type:      | KRYO DNA             | Material type:                                                                                                                 | KRYO DNA | ✓ |
| Gender:             | NA                   | Gender:                                                                                                                        | female   | ! |
| Supplier diagnosis: | -                    | Legend: ✓ OK   ! Supplier information or prediction not available   ✗ Warning, mismatch of prediction and supplier information |          |   |

Brain tumor methylation classifier results (v11b4)

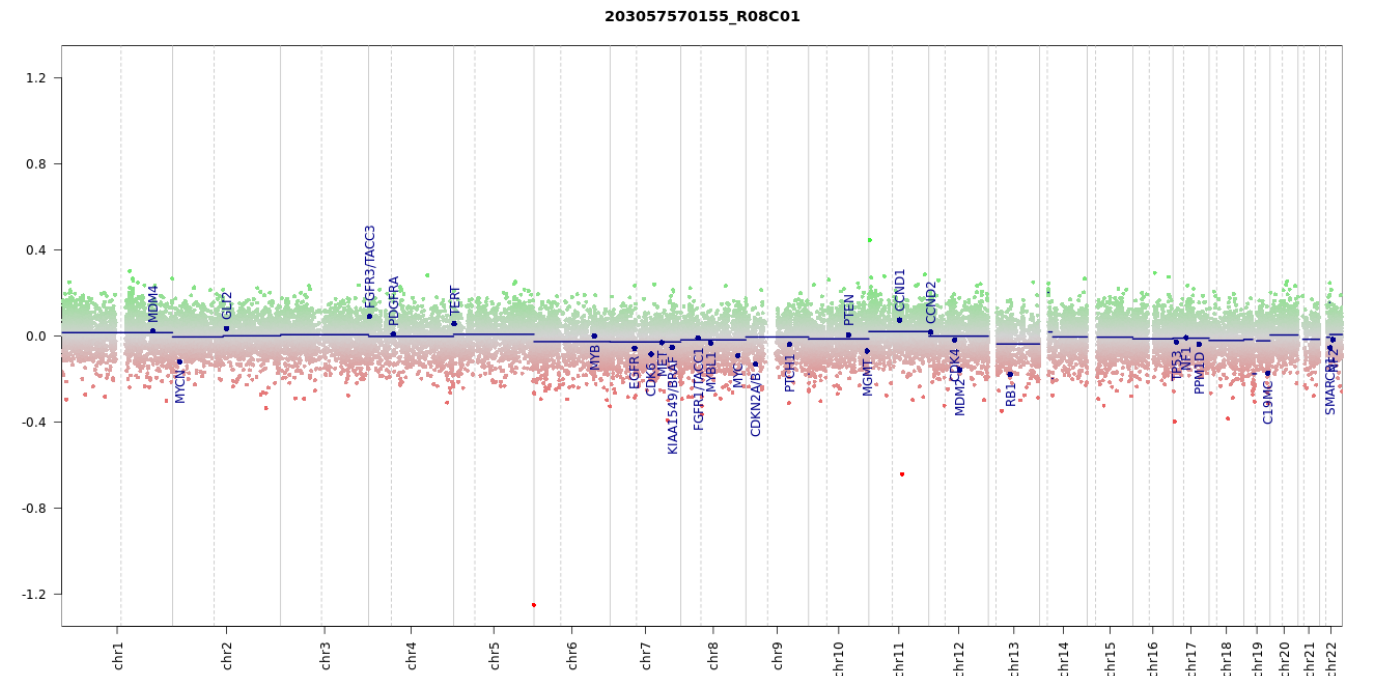
| Methylation classes (MCs with score >= 0.3)    | Calibrated score | Interpretation |
|------------------------------------------------|------------------|----------------|
| methylation class infantile hemispheric glioma | 0.44             | no match ✗     |

Legend: ✓ Match (score >= 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 >= 0.5)

Class descriptions

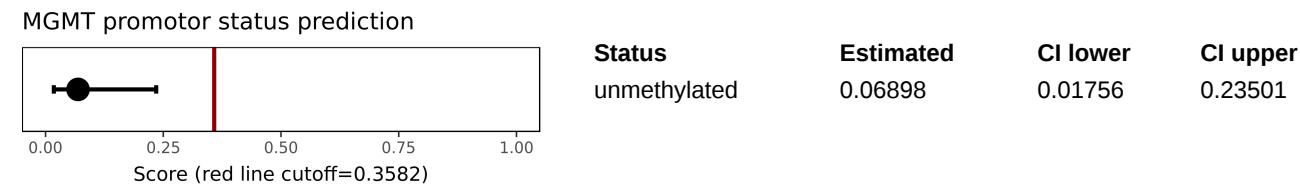
**Methylation class infantile hemispheric glioma:** The methylation class "infantile hemispheric glioma" comprises tumors with widely varying morphology, commonly including features more typical of higher grade lesions especially glioblastoma. These tumors are located supratentorially, all cases so far 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)



(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     |