



prediction not available



and supplier information

### **Methylation profiling report**

# Supplier information

Sample identifier: sampleName1527691945 **Automatic prediction** Sentrix ID: 202273260007\_R08C01 Array type: **EPIC KRYO DNA** Material type: **FFPE DNA** Material type: Gender: Gender: male NA Supplier diagnosis: Legend: ✓ OK Supplier information or Warning, missmatch of prediction

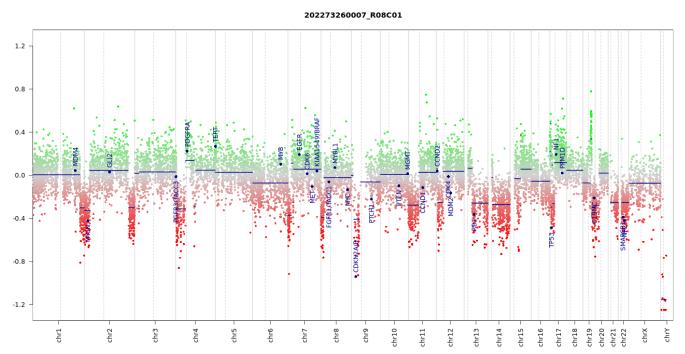
#### Brain tumor methylation classifier results (v11b4)

Methylation classes (MCs with score >= 0.3)		Calibrated score	Interpretation	
methylation class anaplastic pilocytic astrocytoma		0.33	no match	X
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 anaplastic pilocytic astrocytoma: The methylation class "anaplastic pilocytic astrocytoma" is mainly comprised of tumors with the histological diagnosis of anaplastic pilocytic astrocytoma or less commonly glioblastoma. The tumors mostly occur in the posterior fossa and rarely in the diencephalic/thalamic region; median age is 40 years (age range 24 to 75). Deletions of CDKN2A/B are very frequent (>70%). BRAF duplications are also observed in a fraction of cases. Around 50% of cases show an immunohistochemical loss of ATRX. Loss of chromosome 19q (total or partial) is observed in over 50% of cases.

#### 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, <a href="http://www.bioconductor.org/packages/devel/bioc/html/conumee.html">http://www.bioconductor.org/packages/devel/bioc/html/conumee.html</a>)

## 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