

Supplier information

Sample identifier:	sampleName1574006304	Automatic prediction		
Sentrix ID:	203057710116_R03C01	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		

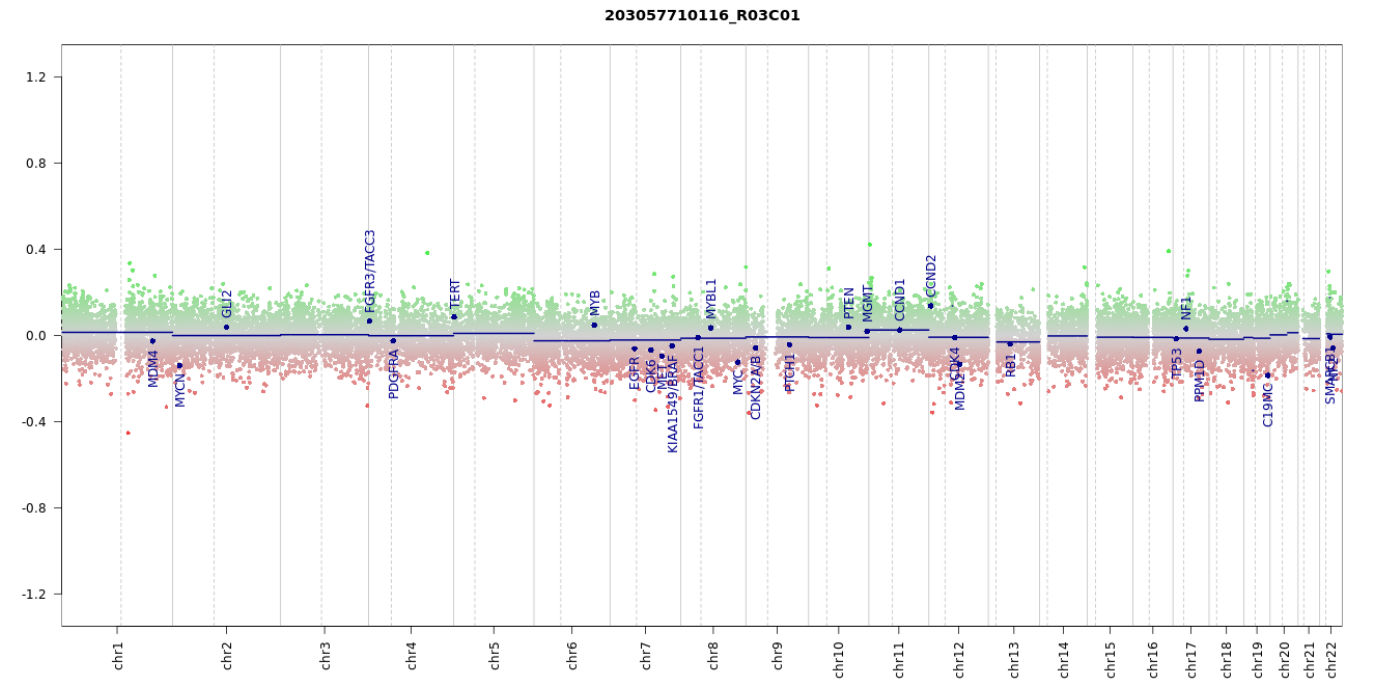
Brain tumor methylation classifier results (v11b4)

Methylation classes (MCs with score >= 0.3)	Calibrated score	Interpretation
methylation class diffuse midline glioma H3 K27M mutant	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

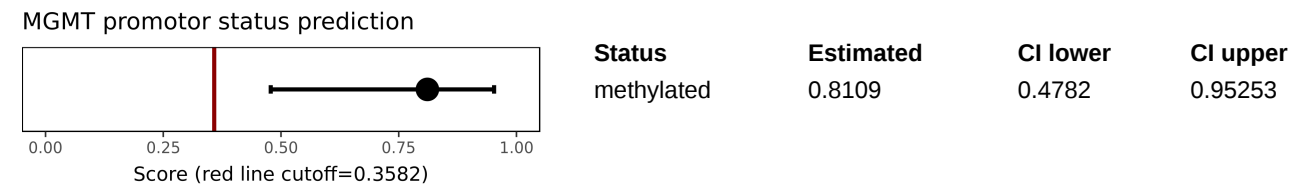
Methylation class diffuse midline glioma H3 K27M mutant: The methylation class "diffuse midline glioma H3 K27M mutant" is comprised of tumors with a histological diagnosis of diffuse midline glioma, H3 K27M mutant. The tumors are located in midline structures (thalamus, cerebellum, brainstem, spine). Median age is 12 years (range 1 to 54). Tumors of this class harbor mutations of codon 27 in one of the genes encoding histone 3 (most commonly H3F3A, but also the H3.1 genes HIST1H3A/B/C and very rarely H3.2). Additional mutations in ATRX and TP53/PPM1D are common. In brainstem tumors, ACVR1 mutations are also recurrently observed. Prognosis of this class is generally very poor, although rare lower grade lesions with K27M mutation have also been reported.

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