Methylation profiling report

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Supplier information

			Automatic prediction		
Sample identifier:	**sampleName1527692555**		Array type:	**EPIC**	
Sentrix ID:	**202053820004_R06C01**		Material type:	**KRYO DNA**	✗
Material type:	**FFPE DNA**		Gender:	**male**	❗
Gender:	**NA**				
Supplier diagnosis:	**-**				

Legend: ✔ OK ❗ Supplier information or prediction not available ✗ Warning, missmatch of prediction and supplier information

Brain tumor methylation classifier results (v11b4)

| Methylation classes (MCs with score >= 0.3)	Calibrated score	Interpretation	
methylation class family Pilocytic astrocytoma	0.96	match	✔
MC family members with score >= 0.1			
methylation class low grade glioma, subclass hemispheric pilocytic astrocytoma and ganglioglioma	0.96	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 family Pilocytic astrocytoma: The methylation class family "Pilocytic astrocytoma" comprises the methylation classes low grade glioma, subtype posterior fossa pilocytic astrocytoma, low grade glioma, subtype midline pilocytic astrocytoma and low grade glioma, subtype hemispheric pilocytic astrocytoma and ganglioglioma.
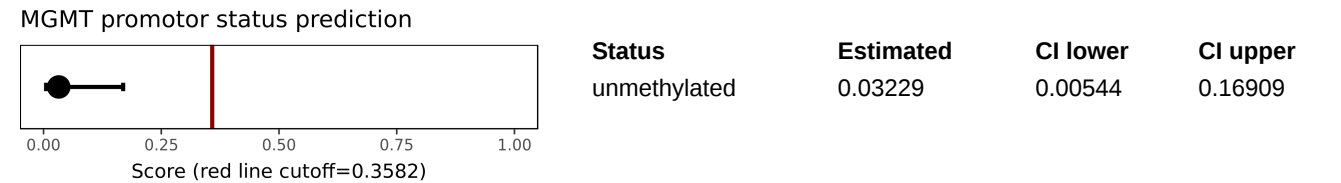
Methylation class low grade glioma, subclass hemispheric pilocytic astrocytoma and ganglioglioma: The methylation class "low grade glioma, subclass hemispheric pilocytic astrocytoma and ganglioglioma" is mainly comprised of tumors diagnosed as pilocytic astrocytoma, but also includes gangliogliomas and pilomyxoid astrocytomas. Tumors are located supratentorially (cerebral hemispheres). Median age is 19 years (range 4 to 32). These tumors typically carry MAPK pathway alterations, in particular BRAF V600E mutation or BRAF fusion, but also some others (NF1, KRAS etc.). The most frequent copy number alterations are gains of chromosome 5, 6 or 7 (20-30% of cases).

Copy number variation profile

202053820004_R06C01
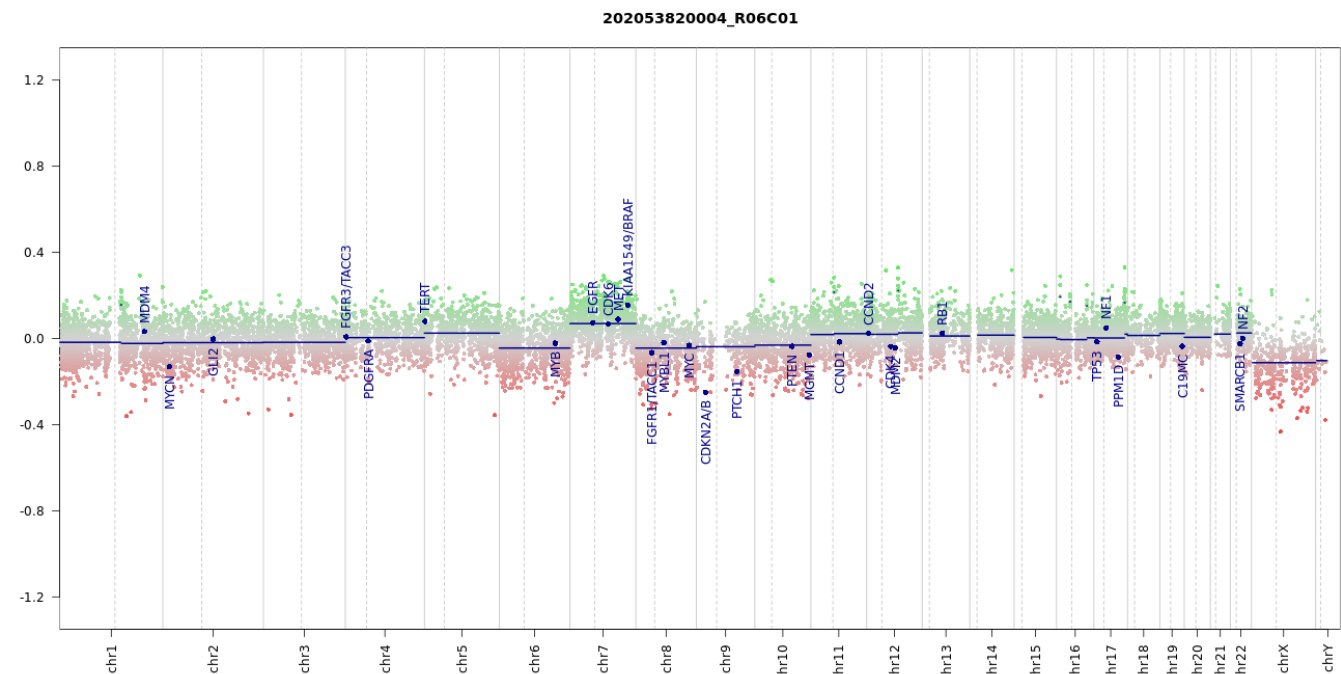
Depiction of chromosome 1 to 22 (and X/Y if automatic prediction was successful). Gains/amplifications represent positive, losses negative deviations from the baseline. 29 brain tumor relevant gene regions are highlighted for easier assessment.
(see Hovestadt & Zapatka, http://www.bioconductor.org/packages/devel/bioc/html/conumee.html)

MGMT promotor methylation (MGMT-STP27)

MGMT promotor status prediction

Score (red line cutoff=0.3582)

Status	Estimated	CI lower	CI upper
unmethylated	0.03229	0.00544	0.16909

(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