Methylation profiling report

Supplier information

Sample identifier:	**sampleName1547111649**
Sentrix ID:	**203064760013_R04C01**
Material type:	**KRYO DNA**
Gender:	**NA**
Supplier diagnosis:	**-**

Automatic prediction		
Array type:	**EPIC**	
Material type:	**KRYO DNA**	✔
Gender:	**female**	!

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 Glioblastoma, IDH wildtype	0.99	match	✔
MC family members with score >= 0.1			
methylation class glioblastoma, IDH wildtype, subclass RTK II	0.91	match	●

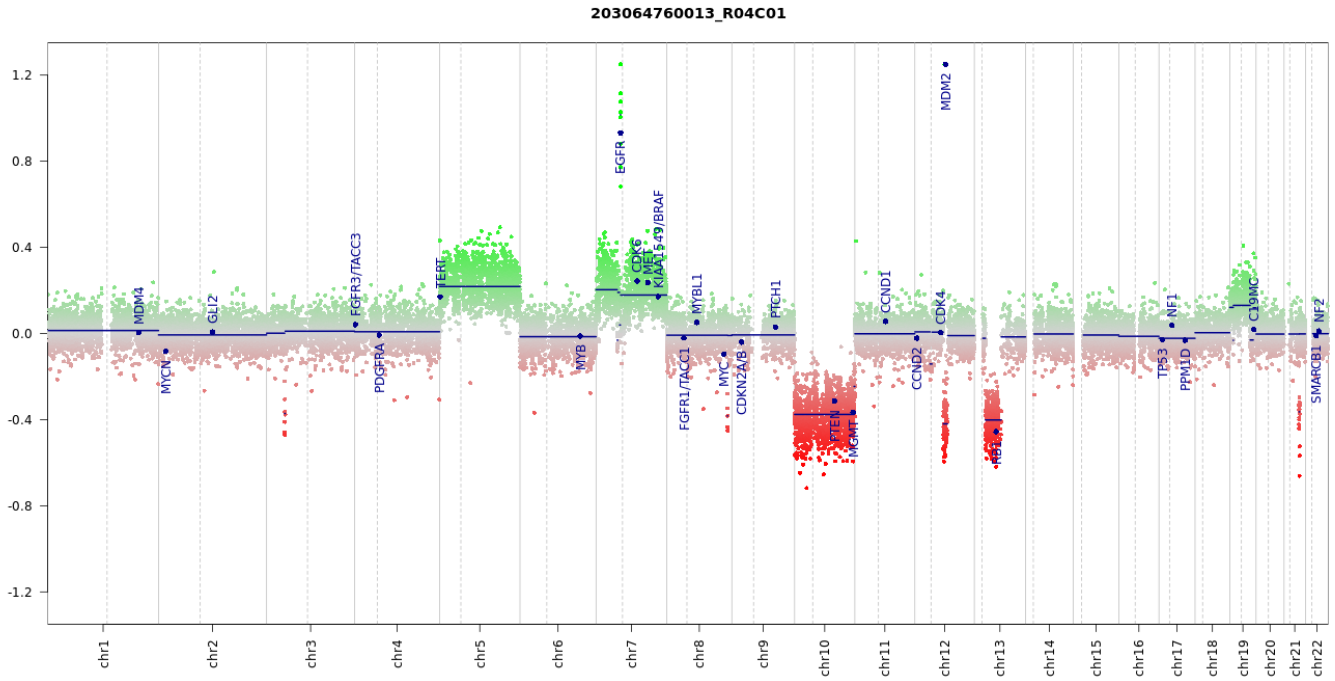
Legend: ✔ Match (score >= 0.9) ✘ No match (score < 0.9): possibly still relevant for low tumor content and low DNA quality cases. ● Match to MC family member (score >= 0.5)

Class descriptions

Methylation class family Glioblastoma, IDH wildtype: The methylation class family "Glioblastoma, IDH wildtype" comprises the methylation classes glioblastoma, IDH wildtype, subtype RTK I to III, glioblastoma, IDH wildtype, subtype mesenchymal, glioblastoma, IDH wildtype, subtype MYCN and glioblastoma, IDH wildtype, subtype midline.

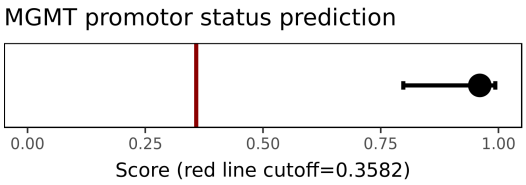
Methylation class glioblastoma, IDH wildtype, subclass RTK II: The methylation class "glioblastoma, IDH wildtype, subclass RTK II" is comprised of tumors with a histological diagnosis of glioblastoma, IDH wildtype and rarely gliosarcoma, IDH wildtype. These tumors are typically located in the cerebral hemispheres. Median age is 61 years (range 36 to 86). Recurrent chromosomal alterations are gain of chromosome 7 with or without EGFR amplification (>90%), loss of 9p21 (CDKN2A/B; >70%) and chromosome 10 loss (>90%). Gin of chromosome 19 and 20 is also recurrently observed (40% of cases). Expression profiles often resemble the 'Classical' subgroup according to the TCGA classification.

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)



Status	Estimated	CI lower	CI upper
methylated	0.96036	0.79794	0.99332

(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