Methylation profiling report

General information

Sentrix ID:	**202047860190_R01C01**
Array type:	**EPIC**
Material type:	**KRYO DNA**
Gender:	**male**

Brain tumor methylation classifier results (v11b4)

Methylation classes (MCs with score >= 0.3)	**Calibrated score**	**Interpretation**	
methylation class family Glioblastoma, IDH wildtype	0.75	no match	✗
MC family members with score >= 0.1			
methylation class glioblastoma, IDH wildtype, subclass RTK I	0.46		
methylation class glioblastoma, IDH wildtype, subclass midline	0.28		

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)

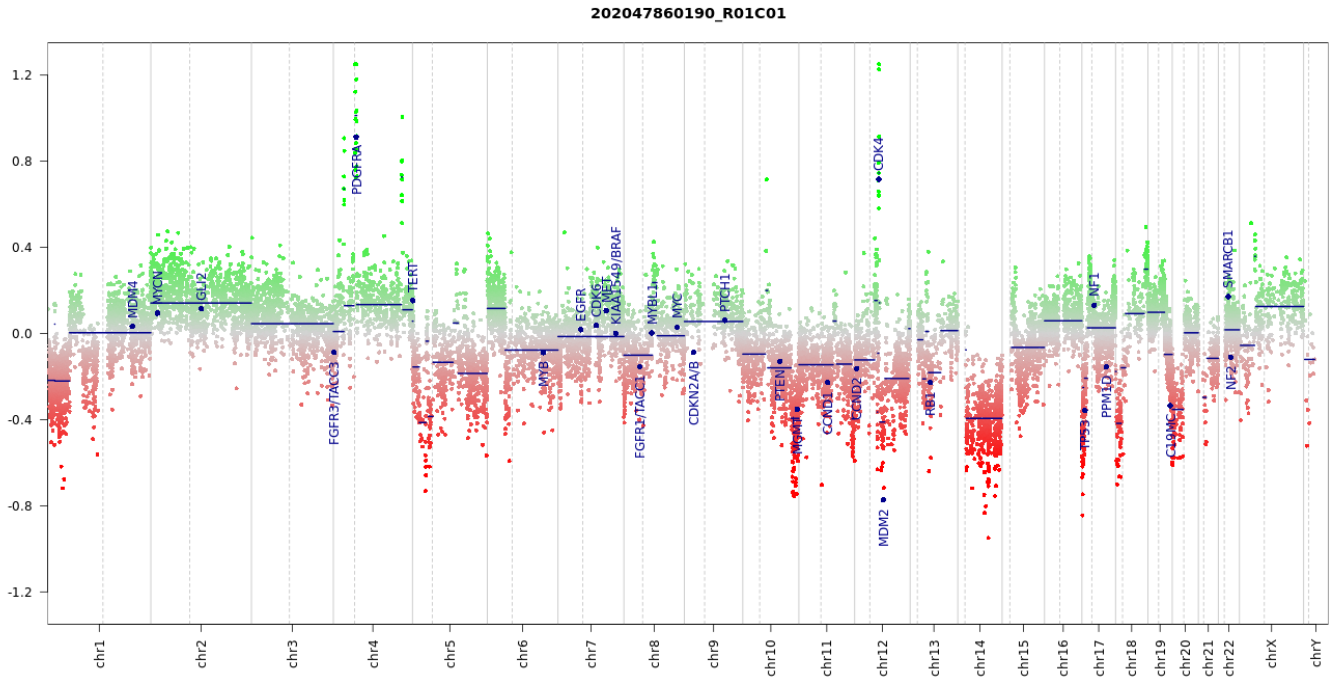
Class descriptions

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 I: The methylation class "glioblastoma, IDH wildtype, subclass RTK I" is comprised of tumors with a histological diagnosis of glioblastoma, IDH wildtype. The tumors are located in the cerebral hemispheres. Median age is 64 years (range 29 to 84). Recurrent chromosomal alterations are gain of chromosome 7 with or without EGFR amplification (>80%), loss of 9p21 (CDKN2A/B; >50%) and chromosome 10 loss (>70%). Amplifications of the PDGFRA oncogene are enriched in this class (present in 20-30% of cases). Expression profiles often resemble the 'Proneural' subgroup according to the TCGA classification.

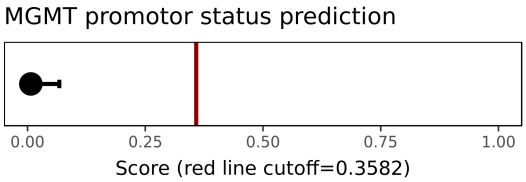
Methylation class glioblastoma, IDH wildtype, subclass midline : The methylation class "glioblastoma, IDH wildtype, subclass midline" is comprised of tumors with a histological diagnosis of glioblastoma, located in midline structures (thalamus, cerebellum, spine). Median age is 13 years (range 2 to 79). Tumors of this class share epigenetic similarities with histone 3 K27M-mutated tumors, but lack this mutation. Mutations of FGFR1 are relatively common, particularly in thalamic tumors. Copy number changes are numerous, the most frequent changes being gain/amplification of PDGFR-alpha and loss of CDKN2A/B (both in over 70% 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, http://www.bioconductor.org/packages/devel/bioc/html/conumee.html)

MGMT promotor methylation (MGMT-STP27)



Status	Estimated	CI lower	CI upper
unmethylated	0.00697	6.8E-4	0.06742

(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 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