

Methylation profiling report

Supplier information

Sample identifier:	Sample 1	Automatic prediction	
Sentrix ID:	3999078080_R05C02	Array type:	450k
Material type:	FFPE DNA	Material type:	FFPE DNA ✓
Gender:	male	Gender:	male ✓
Supplier diagnosis:	Glioblastoma (WHO grade IV)	Legend: ✓ OK ⚠ Supplier information or prediction not available ✗ Warning, mismatch of prediction and supplier information	

Brain tumor methylation classifier results (v11b2)

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, subtype RTK II	0.78	match ●
methylation class glioblastoma, IDH wildtype, subtype RTK I	0.18	

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)

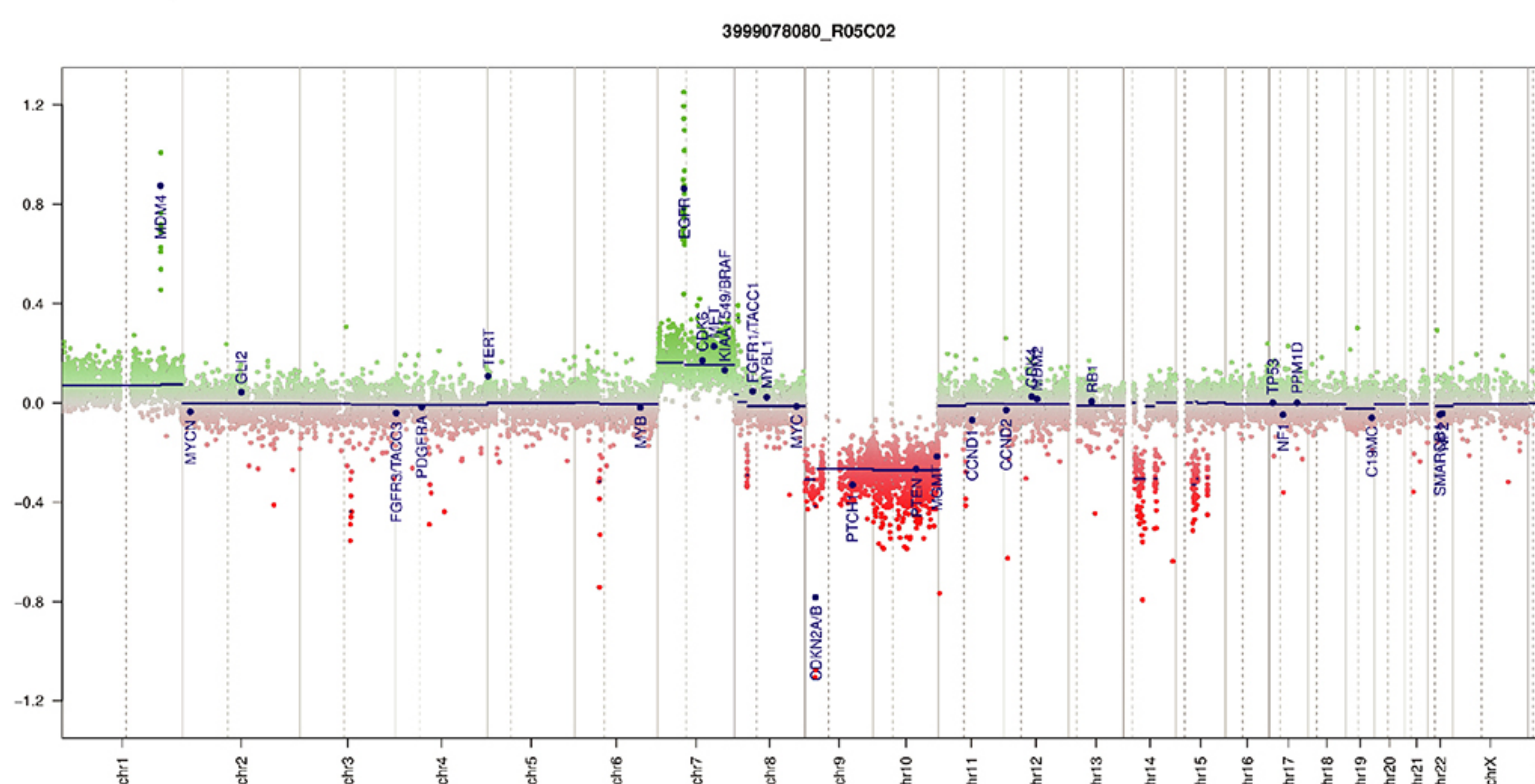
Class descriptions

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, subtype RTK II: The methylation class "glioblastoma, IDH wildtype, subtype 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%). Gain of chromosome 19 and 20 is also recurrently observed (40% of cases). Expression profiles often resemble the "Classical" subgroup according to the TCGA classification.

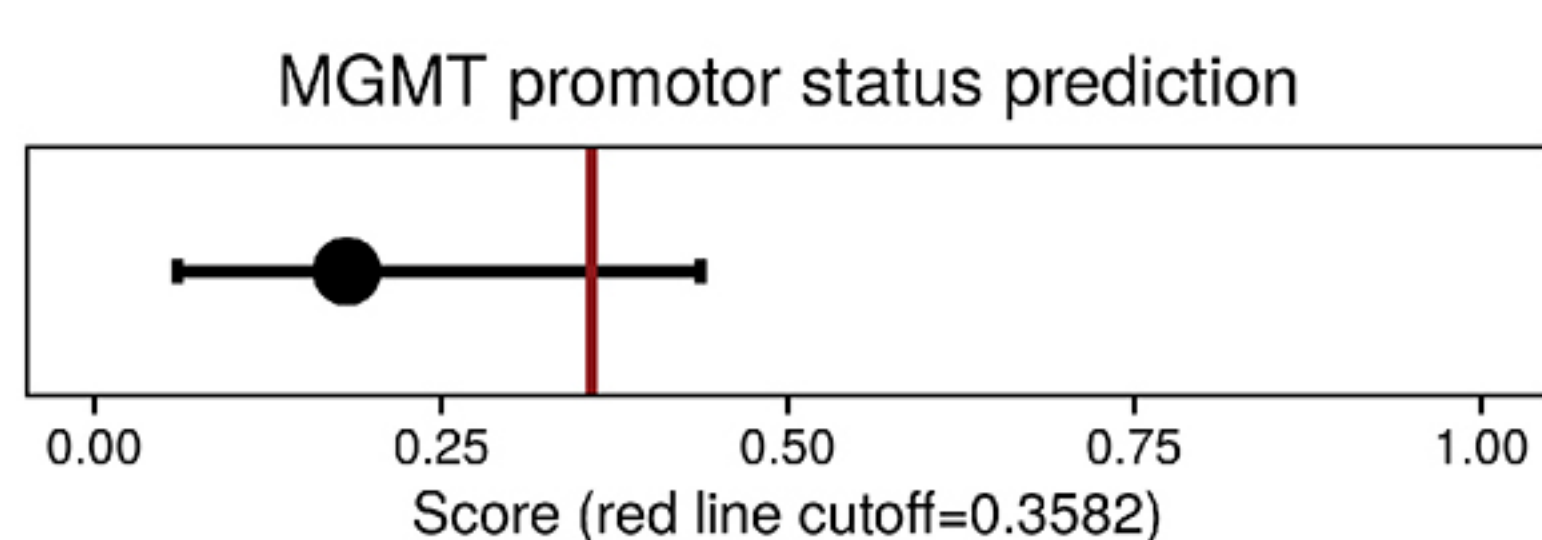
Methylation class glioblastoma, IDH wildtype, subtype RTK I: The methylation class "glioblastoma, IDH wildtype, subtype RTK I" is comprised of tumors with a histological diagnosis of glioblastoma, IDH wildtype. The tumors are located in the cerebral hemispheres. Median age is 64 years (range 29 to 84). 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.

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
not determinable	0.18188	0.05985	0.43705

(see Bady et al, J Mol Diagn 2016; 18(3):350-61)

Disclaimer

Classification using methylation profiling is a research tool under development, 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.