Supplemental Material 6 (SM6) Full BrainClassifier reports

Methylation profiling report

Supplier information

Sample identifier:	207166150179_R07C01
Sentrix ID:	207166150179_R07C01
Material type:	NA
Gender:	NA
Supplier diagnosis:	MEN-27(1)-T.ny

Automatic prediction		
Array type:	EPIC	
Material type:	DNA-FFPE	✗
Gender:	female	!

Legend: ✓ Ok ! Supplier information or prediction not available ✗ Warning, missmatch of prediction and supplier information

Brain tumor classifier results (12.5)

Methylation classes (Highest level >= 0.3, lower levels >= 0.1, all of lowest level)	Calibrated score	Interpretation	
Meningioma	0.99	match	✓
Meningioma	0.99	match	✓
Meningioma, Benign	0.99	match	✓
Mc Meningioma, Subtype Benign, Subclass 2 (novel)	0.76	no match	✗
Mc Meningioma, Subtype Benign, Subclass 3 (novel)	0.21	no match	✗
Mc Meningioma, Subtype Benign, Subclass 1 (novel)	0.00	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

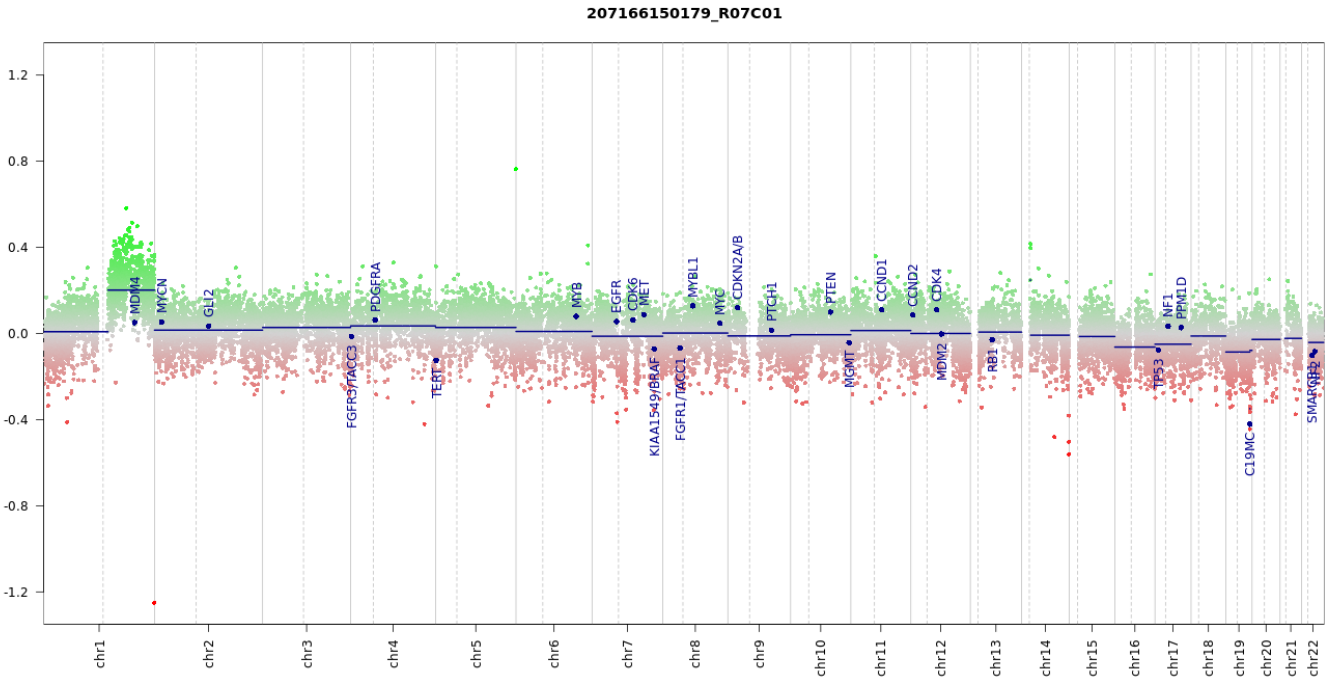
MC Meningioma, subtype benign, subclass 2 (novel): The "mc Meningioma benign" comprises meningiomas epigenetically in one of the groups benign-1, 2 or 3. Subclass benign-1 cases typically show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively fibroblastic, psammomatous or transitional. Subclass benign-2 cases typically show AKT1/TRAF7, KLF4/TRAF7 or SMO mutations and rarely other mutations or CNVs. Histology is mostly meningothelial (then typically AKT1 mutant) or secretory (KLF4 mutant). Subclass benign-3 cases typically show trisomy 5, other trisomies, and can show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively angiomatous, metaplastic, or microcytic. Prognosis in this mc is typically favourable, similar to WHO grade 1. Integration of meningioma subclasses into the brain tumor classifier is under development, thus, the specific meningioma classifier should be consulted in parallel. Integration of histology, methylation and CNVs can further increase prognostic accuracy.

MC Meningioma, subtype benign, subclass 3 (novel): The "mc Meningioma benign" comprises meningiomas epigenetically in one of the groups benign-1, 2 or 3. Subclass benign-1 cases typically show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively fibroblastic, psammomatous or transitional. Subclass benign-2 cases typically show AKT1/TRAF7, KLF4/TRAF7 or SMO mutations and rarely other mutations or CNVs. Histology is mostly meningothelial (then typically AKT1 mutant) or secretory (KLF4 mutant). Subclass benign-3 cases typically show trisomy 5, other trisomies, and can show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively angiomatous, metaplastic, or microcytic. Prognosis in this mc is typically favourable, similar to WHO grade 1. Integration of meningioma subclasses into the brain tumor classifier is under development, thus, the specific meningioma classifier should be consulted in parallel. Integration of histology, methylation and CNVs can further increase prognostic accuracy.

MC Meningioma, subtype benign, subclass 1 (novel): The "mc Meningioma benign" comprises meningiomas epigenetically in one of the groups benign-1, 2 or 3. Subclass benign-1 cases typically show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively fibroblastic, psammomatous or transitional. Subclass benign-2 cases typically show AKT1/TRAF7, KLF4/TRAF7 or SMO mutations and rarely other mutations or CNVs. Histology is mostly meningothelial (then typically AKT1 mutant) or secretory (KLF4 mutant). Subclass benign-3 cases typically show trisomy 5, other trisomies, and can show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively angiomatous, metaplastic, or microcytic. Prognosis in this mc is typically favourable, similar to WHO grade 1. Integration of meningioma subclasses into the brain tumor classifier is under development, thus, the specific meningioma classifier should be consulted in parallel.

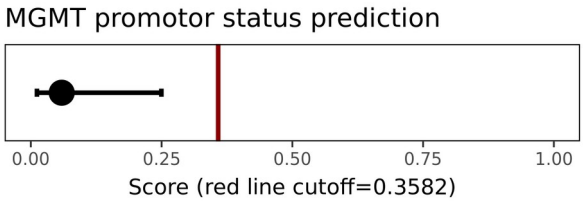
Integration of histology, methylation and CNVs can further increase prognostic accuracy.

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	0.05905	0.01170	0.24963

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

Disclaimer

Classification using methylation profiling is a tool for research use only, it is not verified and has not been clinically validated and, therefore, must not be used for diagnostic purposes. This tool is not HIPAA compliant.

Run information

Report: report_website_mnp_brain_v12.5_sample (Version 1.0)

Task version:

Task	Version
idat_preprocess	2.0.1
idat_qc	2.0.1
idat_predictBrain	2.0.1
idat_rs_gender	2.0.1
idat_cnvp	3.0.1
idat_mgmt	2.0.1
report_website_mnp_brain_v11b4_research	2.1
report_website_mnp_brain_v11b4_sample	2.1
idat_predictBrain	12.5
report_website_mnp_brain_v12.5_sample	1.0

Methylation profiling report

Supplier information

Sample identifier:	207166150179_R08C01
Sentrix ID:	207166150179_R08C01
Material type:	NA
Gender:	NA
Supplier diagnosis:	MEN-27(1)-X

Automatic prediction		
Array type:	EPIC	
Material type:	DNA-FFPE	✗
Gender:	female	!

Legend: ✓ Ok ! Supplier information or prediction not available ✗ Warning, missmatch of prediction and supplier information

Brain tumor classifier results (12.5)

Methylation classes (Highest level >= 0.3, lower levels >= 0.1, all of lowest level)	Calibrated score	Interpretation	
Meningioma	0.98	match	✓
Meningioma	0.98	match	✓
Meningioma, Benign	0.96	match	✓
Mc Meningioma, Subtype Benign, Subclass 3 (novel)	0.92	match	✓
Mc Meningioma, Subtype Benign, Subclass 2 (novel)	0.04	no match	✗
Mc Meningioma, Subtype Benign, Subclass 1 (novel)	0.00	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

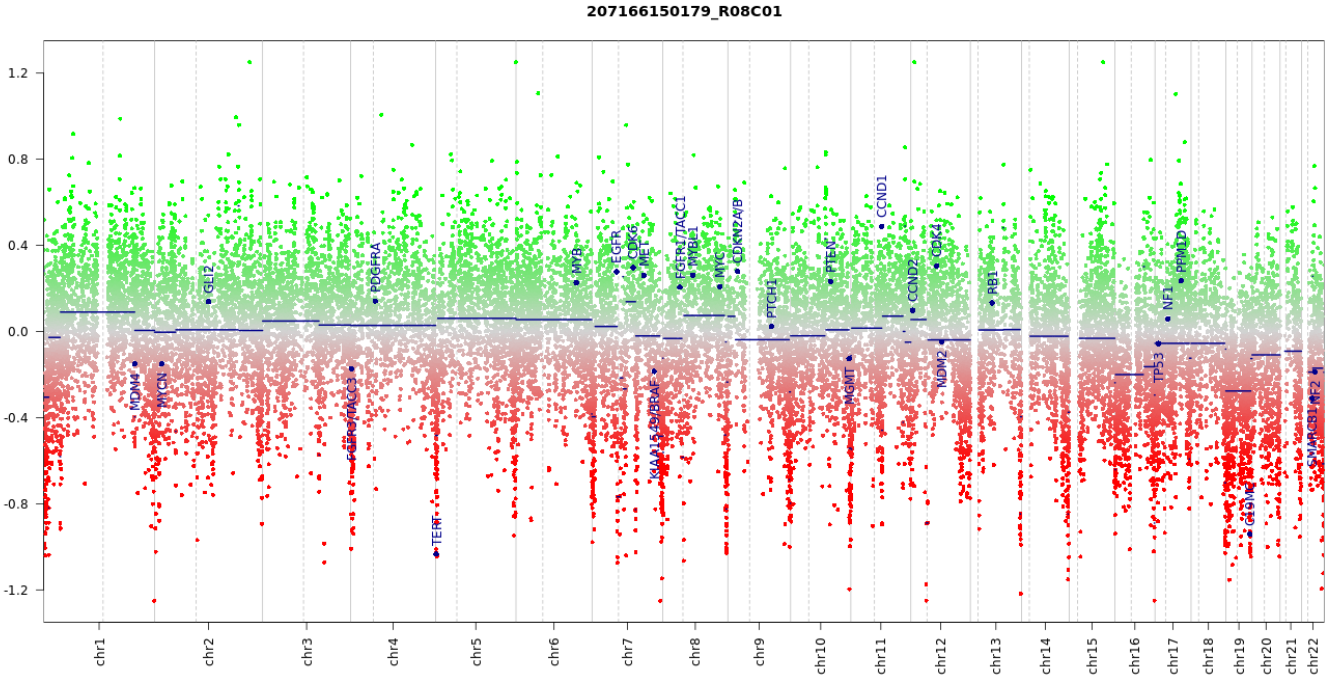
MC Meningioma, subtype benign, subclass 3 (novel): The "mc Meningioma benign" comprises meningiomas epigenetically in one of the groups benign-1, 2 or 3. Subclass benign-1 cases typically show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively fibroblastic, psammomatous or transitional. Subclass benign-2 cases typically show AKT1/TRAF7, KLF4/TRAF7 or SMO mutations and rarely other mutations or CNVs. Histology is mostly meningothelial (then typically AKT1 mutant) or secretory (KLF4 mutant). Subclass benign-3 cases typically show trisomy 5, other trisomies, and can show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively angiomatous, metaplastic, or microcytic. Prognosis in this mc is typically favourable, similar to WHO grade 1. Integration of meningioma subclasses into the brain tumor classifier is under development, thus, the specific meningioma classifier should be consulted in parallel. Integration of histology, methylation and CNVs can further increase prognostic accuracy.

MC Meningioma, subtype benign, subclass 2 (novel): The "mc Meningioma benign" comprises meningiomas epigenetically in one of the groups benign-1, 2 or 3. Subclass benign-1 cases typically show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively fibroblastic, psammomatous or transitional. Subclass benign-2 cases typically show AKT1/TRAF7, KLF4/TRAF7 or SMO mutations and rarely other mutations or CNVs. Histology is mostly meningothelial (then typically AKT1 mutant) or secretory (KLF4 mutant). Subclass benign-3 cases typically show trisomy 5, other trisomies, and can show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively angiomatous, metaplastic, or microcytic. Prognosis in this mc is typically favourable, similar to WHO grade 1. Integration of meningioma subclasses into the brain tumor classifier is under development, thus, the specific meningioma classifier should be consulted in parallel. Integration of histology, methylation and CNVs can further increase prognostic accuracy.

MC Meningioma, subtype benign, subclass 1 (novel): The "mc Meningioma benign" comprises meningiomas epigenetically in one of the groups benign-1, 2 or 3. Subclass benign-1 cases typically show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively fibroblastic, psammomatous or transitional. Subclass benign-2 cases typically show AKT1/TRAF7, KLF4/TRAF7 or SMO mutations and rarely other mutations or CNVs. Histology is mostly meningothelial (then typically AKT1 mutant) or secretory (KLF4 mutant). Subclass benign-3 cases typically show trisomy 5, other trisomies, and can show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively angiomatous, metaplastic, or microcytic. Prognosis in this mc is typically favourable, similar to WHO grade 1. Integration of meningioma subclasses into the brain tumor classifier is under development, thus, the specific meningioma classifier should be consulted in parallel.

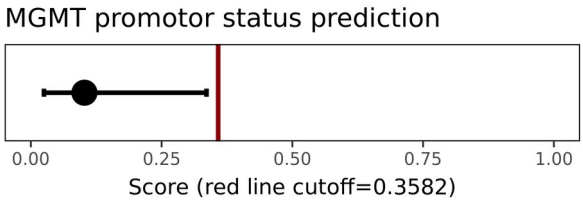
Integration of histology, methylation and CNVs can further increase prognostic accuracy.

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	0.10250	0.02513	0.33594

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

Disclaimer

Classification using methylation profiling is a tool for research use only, it is not verified and has not been clinically validated and, therefore, must not be used for diagnostic purposes. This tool is not HIPAA compliant.

Run information

Report: report_website_mnp_brain_v12.5_sample (Version 1.0)

Task version:

Task	Version
idat_preprocess	2.0.1
idat_qc	2.0.1
idat_predictBrain	2.0.1
idat_rs_gender	2.0.1
idat_cnvp	3.0.1
idat_mgmt	2.0.1
report_website_mnp_brain_v11b4_research	2.1
report_website_mnp_brain_v11b4_sample	2.1
idat_predictBrain	12.5
report_website_mnp_brain_v12.5_sample	1.0

Methylation profiling report

Supplier information

Sample identifier:	207166150179_R05C01
Sentrix ID:	207166150179_R05C01
Material type:	NA
Gender:	NA
Supplier diagnosis:	MEN-25(1)-T

Automatic prediction		
Array type:	EPIC	
Material type:	DNA-FFPE	✗
Gender:	female	!

Legend: ✓ Ok ! Supplier information or prediction not available ✗ Warning, missmatch of prediction and supplier information

Brain tumor classifier results (12.5)

Methylation classes (Highest level >= 0.3, lower levels >= 0.1, all of lowest level)	Calibrated score	Interpretation	
Meningioma	0.99	match	✓
Meningioma	0.99	match	✓
Meningioma, Benign	0.99	match	✓
Mc Meningioma, Subtype Benign, Subclass 1 (novel)	0.99	match	✓
Mc Meningioma, Subtype Benign, Subclass 3 (novel)	0.00	no match	✗
Mc Meningioma, Subtype Benign, Subclass 2 (novel)	0.00	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

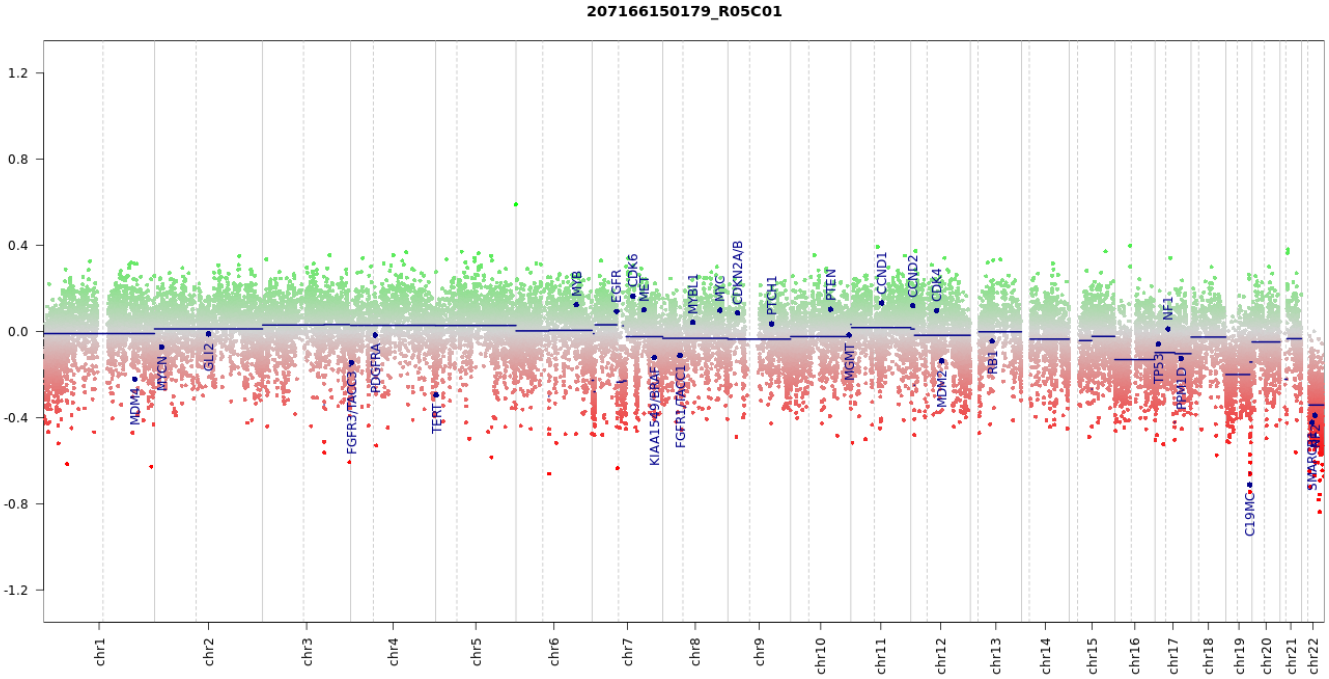
MC Meningioma, subtype benign, subclass 1 (novel): The "mc Meningioma benign" comprises meningiomas epigenetically in one of the groups benign-1, 2 or 3. Subclass benign-1 cases typically show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively fibroblastic, psammomatous or transitional. Subclass benign-2 cases typically show AKT1/TRAF7, KLF4/TRAF7 or SMO mutations and rarely other mutations or CNVs. Histology is mostly meningothelial (then typically AKT1 mutant) or secretory (KLF4 mutant). Subclass benign-3 cases typically show trisomy 5, other trisomies, and can show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively angiomatous, metaplastic, or microcytic. Prognosis in this mc is typically favourable, similar to WHO grade 1. Integration of meningioma subclasses into the brain tumor classifier is under development, thus, the specific meningioma classifier should be consulted in parallel. Integration of histology, methylation and CNVs can further increase prognostic accuracy.

MC Meningioma, subtype benign, subclass 3 (novel): The "mc Meningioma benign" comprises meningiomas epigenetically in one of the groups benign-1, 2 or 3. Subclass benign-1 cases typically show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively fibroblastic, psammomatous or transitional. Subclass benign-2 cases typically show AKT1/TRAF7, KLF4/TRAF7 or SMO mutations and rarely other mutations or CNVs. Histology is mostly meningothelial (then typically AKT1 mutant) or secretory (KLF4 mutant). Subclass benign-3 cases typically show trisomy 5, other trisomies, and can show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively angiomatous, metaplastic, or microcytic. Prognosis in this mc is typically favourable, similar to WHO grade 1. Integration of meningioma subclasses into the brain tumor classifier is under development, thus, the specific meningioma classifier should be consulted in parallel. Integration of histology, methylation and CNVs can further increase prognostic accuracy.

MC Meningioma, subtype benign, subclass 2 (novel): The "mc Meningioma benign" comprises meningiomas epigenetically in one of the groups benign-1, 2 or 3. Subclass benign-1 cases typically show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively fibroblastic, psammomatous or transitional. Subclass benign-2 cases typically show AKT1/TRAF7, KLF4/TRAF7 or SMO mutations and rarely other mutations or CNVs. Histology is mostly meningothelial (then typically AKT1 mutant) or secretory (KLF4 mutant). Subclass benign-3 cases typically show trisomy 5, other trisomies, and can show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively angiomatous, metaplastic, or microcytic. Prognosis in this mc is typically favourable, similar to WHO grade 1. Integration of meningioma subclasses into the brain tumor classifier is under development, thus, the specific meningioma classifier should be consulted in parallel.

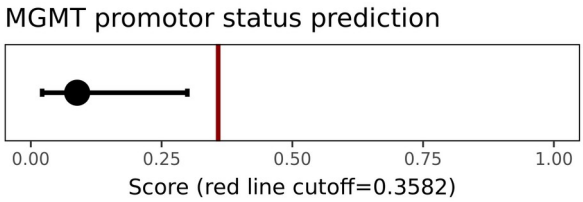
Integration of histology, methylation and CNVs can further increase prognostic accuracy.

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	0.08858	0.02165	0.29919

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

Disclaimer

Classification using methylation profiling is a tool for research use only, it is not verified and has not been clinically validated and, therefore, must not be used for diagnostic purposes. This tool is not HIPAA compliant.

Run information

Report: report_website_mnp_brain_v12.5_sample (Version 1.0)

Task version:

Task	Version
idat_preprocess	2.0.1
idat_qc	2.0.1
idat_predictBrain	2.0.1
idat_rs_gender	2.0.1
idat_cnvp	3.0.1
idat_mgmt	2.0.1
report_website_mnp_brain_v11b4_research	2.1
report_website_mnp_brain_v11b4_sample	2.1
idat_predictBrain	12.5
report_website_mnp_brain_v12.5_sample	1.0

Methylation profiling report

Supplier information

Sample identifier:	207166150179_R06C01
Sentrix ID:	207166150179_R06C01
Material type:	NA
Gender:	NA
Supplier diagnosis:	MEN-25(1)-X

Automatic prediction		
Array type:	EPIC	
Material type:	DNA-FFPE	✗
Gender:	male	!

Legend: ✓ Ok ! Supplier information or prediction not available ✗ Warning, missmatch of prediction and supplier information

Brain tumor classifier results (12.5)

Methylation classes (Highest level >= 0.3, lower levels >= 0.1, all of lowest level)	Calibrated score	Interpretation	
Meningioma	0.67	no match	✗
Meningioma	0.67	no match	✗
Meningioma, Benign	0.54	no match	✗
Mc Meningioma, Subtype Benign, Subclass 3 (novel)	0.50	no match	✗
Mc Meningioma, Subtype Benign, Subclass 1 (novel)	0.02	no match	✗
Mc Meningioma, Subtype Benign, Subclass 2 (novel)	0.00	no match	✗
Meningioma, Malignant	0.11	no match	✗
Mc Meningioma, Subtype Malignant (novel)	0.11	no match	✗

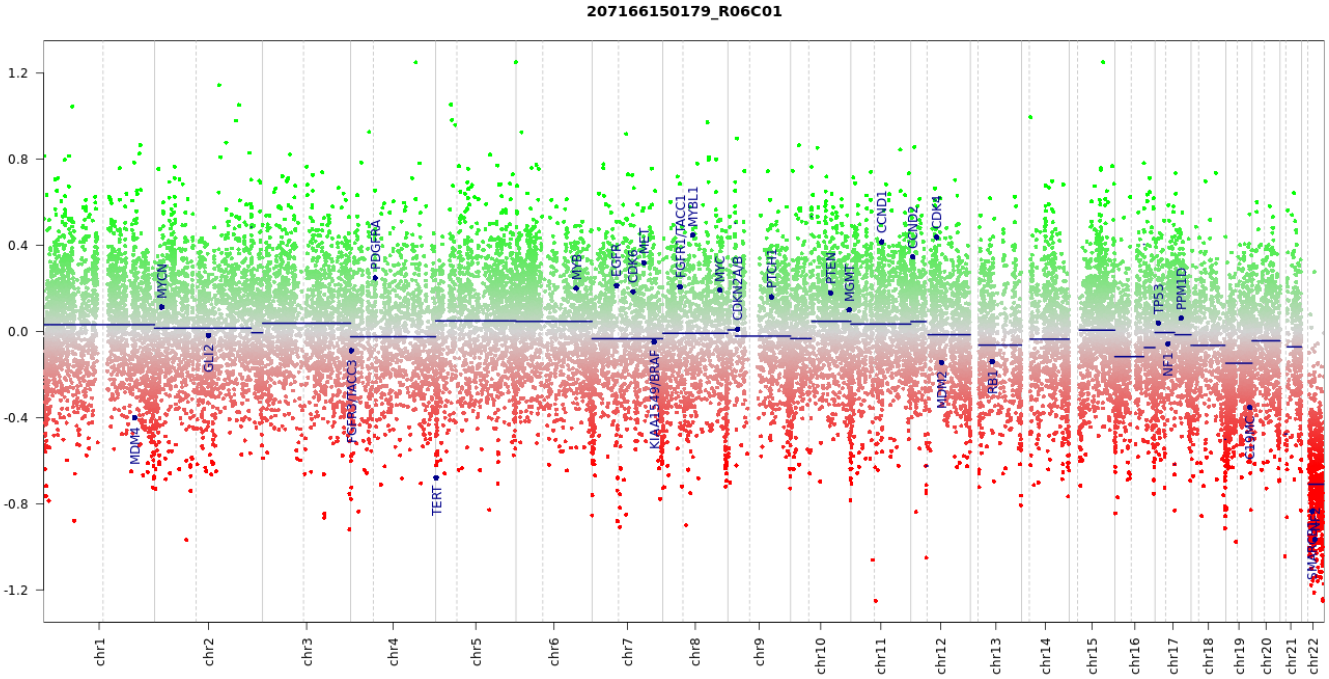
Legend: ✓ Match (score >= 0.9) ✗ No match (score < 0.9): possibly still relevant for low tumor content and low DNA quality cases. ● Match to MC family member (score >= 0.5)

Class descriptions

MC Meningioma, subtype benign, subclass 3 (novel): The "mc Meningioma benign" comprises meningiomas epigenetically in one of the groups benign-1, 2 or 3. Subclass benign-1 cases typically show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively fibroblastic, psammomatous or transitional. Subclass benign-2 cases typically show AKT1/TRAF7, KLF4/TRAF7 or SMO mutations and rarely other mutations or CNVs. Histology is mostly meningothelial (then typically AKT1 mutant) or secretory (KLF4 mutant). Subclass benign-3 cases typically show trisomy 5, other trisomies, and can show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively angiomatous, metaplastic, or microcytic. Prognosis in this mc is typically favourable, similar to WHO grade 1. Integration of meningioma subclasses into the brain tumor classifier is under development, thus, the specific meningioma classifier should be consulted in parallel. Integration of histology, methylation and CNVs can further increase prognostic accuracy.
MC Meningioma, subtype benign, subclass 1 (novel): The "mc Meningioma benign" comprises meningiomas epigenetically in one of the groups benign-1, 2 or 3. Subclass benign-1 cases typically show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively fibroblastic, psammomatous or transitional. Subclass benign-2 cases typically show AKT1/TRAF7, KLF4/TRAF7 or SMO mutations and rarely other mutations or CNVs. Histology is mostly meningothelial (then typically AKT1 mutant) or secretory (KLF4 mutant). Subclass benign-3 cases typically show trisomy 5, other trisomies, and can show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively angiomatous, metaplastic, or microcytic. Prognosis in this mc is typically favourable, similar to WHO grade 1. Integration of meningioma subclasses into the brain tumor classifier is under development, thus, the specific meningioma classifier should be consulted in parallel. Integration of histology, methylation and CNVs can further increase prognostic accuracy.
MC Meningioma, subtype benign, subclass 2 (novel): The "mc Meningioma benign" comprises meningiomas epigenetically in one of the groups benign-1, 2 or 3. Subclass

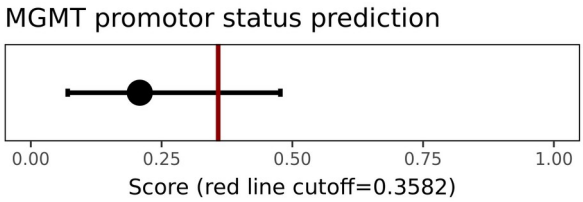
benign-1 cases typically show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively fibroblastic, psammomatous or transitional. Subclass benign-2 cases typically show AKT1/TRAF7, KLF4/TRAF7 or SMO mutations and rarely other mutations or CNVs. Histology is mostly meningothelial (then typically AKT1 mutant) or secretory (KLF4 mutant). Subclass benign-3 cases typically show trisomy 5, other trisomies, and can show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively angiomatous, metaplastic, or microcytic. Prognosis in this mc is typically favourable, similar to WHO grade 1. Integration of meningioma subclasses into the brain tumor classifier is under development, thus, the specific meningioma classifier should be consulted in parallel. Integration of histology, methylation and CNVs can further increase prognostic accuracy.

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	0.20833	0.07053	0.47714

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

Disclaimer

Classification using methylation profiling is a tool for research use only, it is not verified and has not been clinically validated and, therefore, must not be used for diagnostic purposes. This tool is not HIPAA compliant.

Run information

Report: report_website_mnp_brain_v12.5_sample (Version 1.0)

Task version:

Task	Version
idat_preprocess	2.0.1
idat_qc	2.0.1
idat_predictBrain	2.0.1
idat_rs_gender	2.0.1
idat_cnvp	3.0.1
idat_mgmt	2.0.1
report_website_mnp_brain_v11b4_research	2.1
report_website_mnp_brain_v11b4_sample	2.1
idat_predictBrain	12.5
report_website_mnp_brain_v12.5_sample	1.0

Methylation profiling report

Supplier information

Sample identifier:	207166150100_R07C01
Sentrix ID:	207166150100_R07C01
Material type:	NA
Gender:	male
Supplier diagnosis:	MEN-4-T

Automatic prediction		
Array type:	EPIC	
Material type:	DNA-FFPE	✗
Gender:	female	✗

Legend: ✓ Ok ! Supplier information or prediction not available ✗ Warning, missmatch of prediction and supplier information

Brain tumor classifier results (12.5)

Methylation classes (Highest level >= 0.3, lower levels >= 0.1, all of lowest level)	Calibrated score	Interpretation	
Meningioma	0.99	match	✓
Meningioma	0.99	match	✓
Meningioma, Benign	0.99	match	✓
Mc Meningioma, Subtype Benign, Subclass 3 (novel)	0.96	match	✓
Mc Meningioma, Subtype Benign, Subclass 2 (novel)	0.01	no match	✗
Mc Meningioma, Subtype Benign, Subclass 1 (novel)	0.01	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

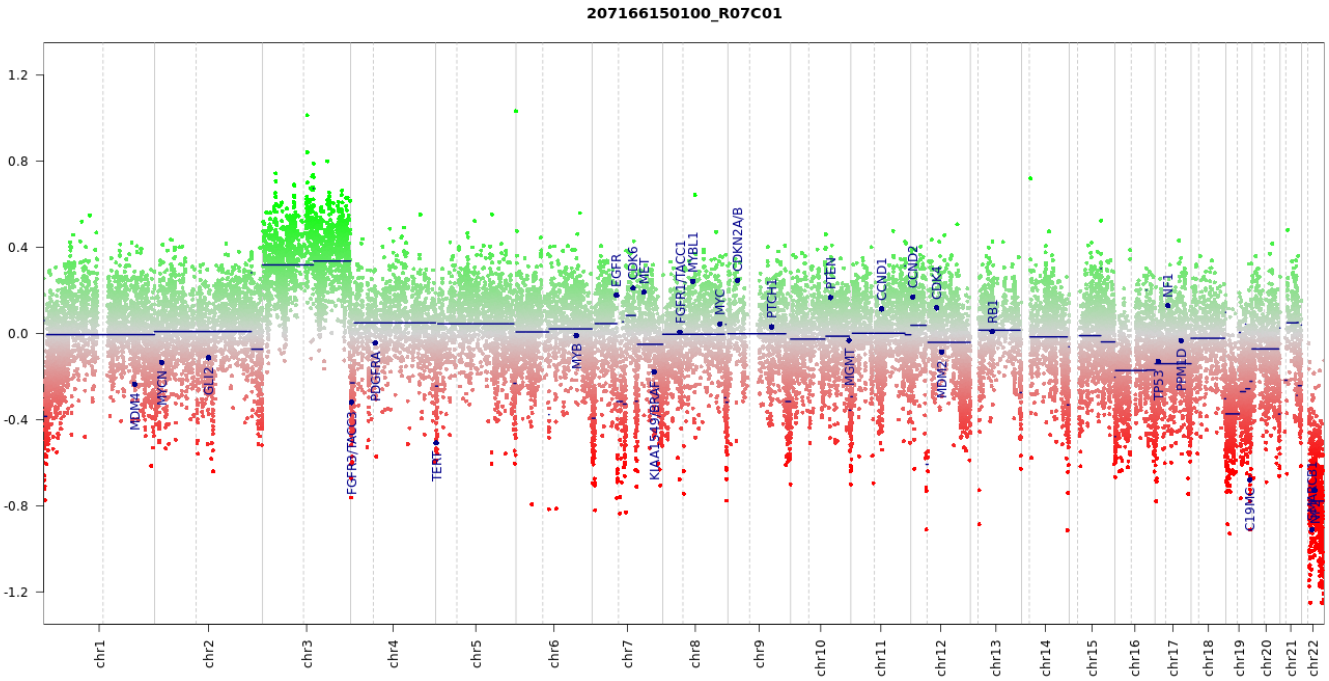
MC Meningioma, subtype benign, subclass 3 (novel): The "mc Meningioma benign" comprises meningiomas epigenetically in one of the groups benign-1, 2 or 3. Subclass benign-1 cases typically show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively fibroblastic, psammomatous or transitional. Subclass benign-2 cases typically show AKT1/TRAF7, KLF4/TRAF7 or SMO mutations and rarely other mutations or CNVs. Histology is mostly meningothelial (then typically AKT1 mutant) or secretory (KLF4 mutant). Subclass benign-3 cases typically show trisomy 5, other trisomies, and can show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively angiomatous, metaplastic, or microcytic. Prognosis in this mc is typically favourable, similar to WHO grade 1. Integration of meningioma subclasses into the brain tumor classifier is under development, thus, the specific meningioma classifier should be consulted in parallel. Integration of histology, methylation and CNVs can further increase prognostic accuracy.

MC Meningioma, subtype benign, subclass 2 (novel): The "mc Meningioma benign" comprises meningiomas epigenetically in one of the groups benign-1, 2 or 3. Subclass benign-1 cases typically show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively fibroblastic, psammomatous or transitional. Subclass benign-2 cases typically show AKT1/TRAF7, KLF4/TRAF7 or SMO mutations and rarely other mutations or CNVs. Histology is mostly meningothelial (then typically AKT1 mutant) or secretory (KLF4 mutant). Subclass benign-3 cases typically show trisomy 5, other trisomies, and can show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively angiomatous, metaplastic, or microcytic. Prognosis in this mc is typically favourable, similar to WHO grade 1. Integration of meningioma subclasses into the brain tumor classifier is under development, thus, the specific meningioma classifier should be consulted in parallel. Integration of histology, methylation and CNVs can further increase prognostic accuracy.

MC Meningioma, subtype benign, subclass 1 (novel): The "mc Meningioma benign" comprises meningiomas epigenetically in one of the groups benign-1, 2 or 3. Subclass benign-1 cases typically show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively fibroblastic, psammomatous or transitional. Subclass benign-2 cases typically show AKT1/TRAF7, KLF4/TRAF7 or SMO mutations and rarely other mutations or CNVs. Histology is mostly meningothelial (then typically AKT1 mutant) or secretory (KLF4 mutant). Subclass benign-3 cases typically show trisomy 5, other trisomies, and can show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively angiomatous, metaplastic, or microcytic. Prognosis in this mc is typically favourable, similar to WHO grade 1. Integration of meningioma subclasses into the brain tumor classifier is under development, thus, the specific meningioma classifier should be consulted in parallel.

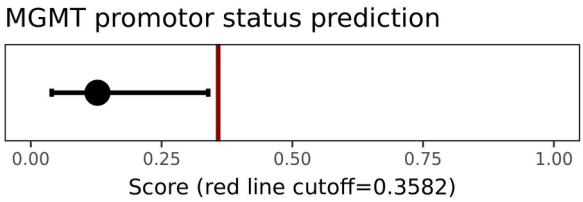
Integration of histology, methylation and CNVs can further increase prognostic accuracy.

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	0.12743	0.03991	0.33911

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

Disclaimer

Classification using methylation profiling is a tool for research use only, it is not verified and has not been clinically validated and, therefore, must not be used for diagnostic purposes. This tool is not HIPAA compliant.

Run information

Report: report_website_mnp_brain_v12.5_sample (Version 1.0)

Task version:

Task	Version
idat_preprocess	2.0.1
idat_qc	2.0.1
idat_predictBrain	2.0.1
idat_rs_gender	2.0.1
idat_cnvp	3.0.1
idat_mgmt	2.0.1
report_website_mnp_brain_v11b4_research	2.1
report_website_mnp_brain_v11b4_sample	2.1
idat_predictBrain	12.5
report_website_mnp_brain_v12.5_sample	1.0

Methylation profiling report

Supplier information

Sample identifier:	207166150100_R08C01
Sentrix ID:	207166150100_R08C01
Material type:	NA
Gender:	male
Supplier diagnosis:	MEN-4-X

Automatic prediction		
Array type:	EPIC	
Material type:	DNA-FFPE	✗
Gender:	female	✗

Legend: ✓ Ok ! Supplier information or prediction not available ✗ Warning, missmatch of prediction and supplier information

Brain tumor classifier results (12.5)

Methylation classes (Highest level >= 0.3, lower levels >= 0.1, all of lowest level)	Calibrated score	Interpretation	
Meningioma	0.86	no match	✗
Meningioma	0.86	no match	✗
Meningioma, Benign	0.84	no match	✗
Mc Meningioma, Subtype Benign, Subclass 1 (novel)	0.61	no match	✗
Mc Meningioma, Subtype Benign, Subclass 3 (novel)	0.17	no match	✗
Mc Meningioma, Subtype Benign, Subclass 2 (novel)	0.05	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

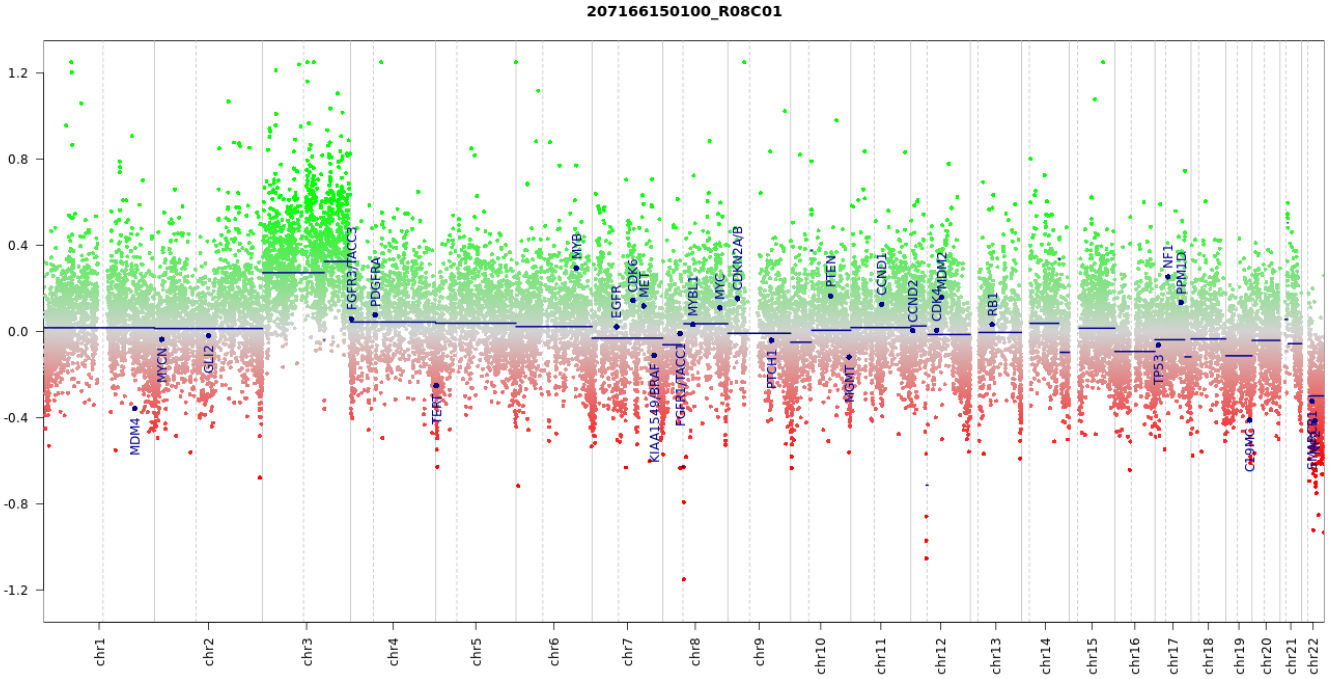
MC Meningioma, subtype benign, subclass 1 (novel): The "mc Meningioma benign" comprises meningiomas epigenetically in one of the groups benign-1, 2 or 3. Subclass benign-1 cases typically show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively fibroblastic, psammomatous or transitional. Subclass benign-2 cases typically show AKT1/TRAF7, KLF4/TRAF7 or SMO mutations and rarely other mutations or CNVs. Histology is mostly meningothelial (then typically AKT1 mutant) or secretory (KLF4 mutant). Subclass benign-3 cases typically show trisomy 5, other trisomies, and can show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively angiomatous, metaplastic, or microcytic. Prognosis in this mc is typically favourable, similar to WHO grade 1. Integration of meningioma subclasses into the brain tumor classifier is under development, thus, the specific meningioma classifier should be consulted in parallel. Integration of histology, methylation and CNVs can further increase prognostic accuracy.

MC Meningioma, subtype benign, subclass 3 (novel): The "mc Meningioma benign" comprises meningiomas epigenetically in one of the groups benign-1, 2 or 3. Subclass benign-1 cases typically show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively fibroblastic, psammomatous or transitional. Subclass benign-2 cases typically show AKT1/TRAF7, KLF4/TRAF7 or SMO mutations and rarely other mutations or CNVs. Histology is mostly meningothelial (then typically AKT1 mutant) or secretory (KLF4 mutant). Subclass benign-3 cases typically show trisomy 5, other trisomies, and can show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively angiomatous, metaplastic, or microcytic. Prognosis in this mc is typically favourable, similar to WHO grade 1. Integration of meningioma subclasses into the brain tumor classifier is under development, thus, the specific meningioma classifier should be consulted in parallel. Integration of histology, methylation and CNVs can further increase prognostic accuracy.

MC Meningioma, subtype benign, subclass 2 (novel): The "mc Meningioma benign" comprises meningiomas epigenetically in one of the groups benign-1, 2 or 3. Subclass benign-1 cases typically show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively fibroblastic, psammomatous or transitional. Subclass benign-2 cases typically show AKT1/TRAF7, KLF4/TRAF7 or SMO mutations and rarely other mutations or CNVs. Histology is mostly meningothelial (then typically AKT1 mutant) or secretory (KLF4 mutant). Subclass benign-3 cases typically show trisomy 5, other trisomies, and can show 22q deletions/NF2 mutations and rarely other mutations or CNVs. Histology is mostly but not exclusively angiomatous, metaplastic, or microcytic. Prognosis in this mc is typically favourable, similar to WHO grade 1. Integration of meningioma subclasses into the brain tumor classifier is under development, thus, the specific meningioma classifier should be consulted in parallel.

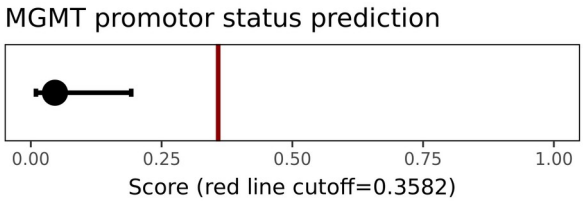
Integration of histology, methylation and CNVs can further increase prognostic accuracy.

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	0.04615	0.00976	0.19192

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

Disclaimer

Classification using methylation profiling is a tool for research use only, it is not verified and has not been clinically validated and, therefore, must not be used for diagnostic purposes. This tool is not HIPAA compliant.

Run information

Report: report_website_mnp_brain_v12.5_sample (Version 1.0)

Task version:

Task	Version
idat_preprocess	2.0.1
idat_qc	2.0.1
idat_predictBrain	2.0.1
idat_rs_gender	2.0.1
idat_cnvp	3.0.1
idat_mgmt	2.0.1
report_website_mnp_brain_v11b4_research	2.1
report_website_mnp_brain_v11b4_sample	2.1
idat_predictBrain	12.5
report_website_mnp_brain_v12.5_sample	1.0