

Tumours of the Central Nervous System Molecular Information Reporting Guide

Family/Last name Date of birth Given name(s) Patient identifiers Date of request Accession/Laboratory number Elements in **black text** are **CORE**. Elements in **grey text** are **NON-CORE**. indicates multi-select values indicates single select values

SCOPE OF THIS DATASET SECTION

REFER TO Tables 1-3 FOR CORE ELEMENTS REQUIRED FOR CENTRAL NERVOUS SYSTEM TUMOUR CLASSIFICATION (Elements 2-38 are only required for some tumours)

(Based on the World Health Organization Classification of Tumours of the Central Nervous System (2021))

ADEQUACY OF SPECIMEN FOR MOLECULAR ASSESSMENT (Note 1)

- Specimen is adequate for analysis
- Specimen is inadequate for analysis (select all that apply)

- Crush
- Autolysis
- Cautery
- Necrosis
- Decalcification
- Tumour cell quantity
- Fixation issues, *specify*

Other, *specify*

Representative blocks for ancillary studies, specify those blocks best representing tumour and/or normal tissue for further study

ALK/ROS1/MET/NTRK FAMILY ALTERATIONS^a (Note 2)

- Indeterminate
- Absent
- Present, *describe*

TESTING METHOD^b (select all that apply)

- Immunohistochemistry (IHC)
- In situ hybridisation (ISH)
- Next generation sequencing (NGS)
- Other, *specify*

^a Only core for some tumours - refer to [Tables 1-3](#).

^b Repeat for each alteration.

ATRX ALTERATIONS^a (Note 3)

- Indeterminate
- Absent
- Present, *describe*

TESTING METHOD (select all that apply)

- Sanger sequencing
- NGS
- PCR-based method
- IHC

- Indeterminate
- Intact nuclear expression
- Loss of nuclear expression

Other, *specify*

BCOR INTERNAL TANDEM DUPLICATION^a (Note 4)

- Indeterminate
- Absent
- Present, *describe*

TESTING METHOD (select all that apply)

- IHC
- ISH
- NGS
- Other, *specify*

BRAF ALTERATIONS^a (Note 5)

BRAF variant

- Indeterminate
- Absent
- BRAF p.V600E (c.1799T>A) variant present
- Other BRAF sequence variant present, *specify*

BRAF ALTERATIONS^a continued (Note 5)

VARIANTS ASSESSED (select all that apply)

- p.V600E
- Any variant in exon 15
- Other *BRAF* variant, *specify*

BRAF variant continued

TESTING METHOD (select all that apply)

- Sanger sequencing
- NGS
- PCR-based method
- IHC

BRAF p.V600E expression

- Indeterminate
- Negative
- Positive

Other, *specify*

BRAF rearrangement/duplication

- Indeterminate
- Absent
- Present, *describe*

VARIANTS ASSESSED (select all that apply)

- KIAA1549::BRAF* fusion
- BRAF::RAF1* fusion
- Other, *specify*

TESTING METHOD (select all that apply)

- ISH
- RT-PCR
- Array-based method
- RNA-sequencing
- Other, *specify*

C19MC ALTERATIONS^a (Note 6)

- Indeterminate
- Absent
- Present with low level gain
- Present, *describe including copy number*

TESTING METHOD (select all that apply)

- ISH
- Array-based method
- NGS
- Other, *specify*

LIN28A expression (IHC)^a

- Indeterminate
- Negative
- Positive

CDKN2A/B DELETION^a (Note 7)

- Indeterminate
- Absent
- Homozygous deletion
- Hemizygous/heterozygous deletion

TESTING METHOD (select all that apply)

- ISH
- Array-based method
- NGS
- Other, *specify*

CHROMOSOMAL ARM 1p/19q CODELETION^a (Note 8)

- Indeterminate
- None detected
- 1p/19q codeletion
- 1p only deletion
- 19q only deletion
- Polysomy, *specify*

TESTING METHOD (select all that apply)

- ISH
- Array-based method (including methylation arrays^c)
- PCR/Loss of heterozygosity assay
- NGS
- Other, *specify*

CHROMOSOME 7 GAIN (COMBINED WITH CHROMOSOME 10 LOSS)^a (Note 9)

- Indeterminate
- Absent
- Present, *describe*

TESTING METHOD (select all that apply)

- ISH
- Array-based method
- NGS
- Other, *specify*

CIC ALTERATIONS^a (Note 10)

- Indeterminate
- Absent
- Present, *describe*

TESTING METHOD (select all that apply)

- IHC
- ISH
- NGS
- Other, *specify*

^c Methylation array-based methods may provide strong but circumstantial evidence.

^a Only core for some tumours - refer to [Tables 1-3](#).

DICER1 ALTERATIONS^a (Note 11)

- Indeterminate
- Absent
- Present, *describe*

TESTING METHOD (select all that apply)

- IHC
- ISH
- NGS
- Other, *specify*

EGFR ALTERATIONS^a (Note 12)

EGFR amplification

- Indeterminate
- Absent
- Absent with low level gain
- Present, *describe including copy number*

TESTING METHOD (select all that apply)

- ISH
- Array-based method
- NGS
- Other, *specify*

EGFR variants (e.g., EGFRvIII or EGFR single nucleotide variants)

- Indeterminate
- Absent
- Present, *describe*

TESTING METHOD (select all that apply)

- NGS
- PCR-based method
- IHC
- Other, *specify*

EZH2 EXPRESSION (IHC)^a (Note 13)

- Indeterminate
- Negative
- Positive

FET ALTERATIONS^a (Note 14)

- Indeterminate
- Absent
- Present, *describe*

TESTING METHOD (select all that apply)

- IHC
- ISH
- NGS
- Other, *specify*

^a Only core for some tumours - refer to [Tables 1-3](#).

FGFR FAMILY ALTERATIONS^a (Note 15)

- Indeterminate
- Absent
- Present, *describe*

TESTING METHOD^b (select all that apply)

- IHC
- ISH
- NGS
- Other, *specify*

FOXR2 ALTERATIONS^a (Note 16)

- Indeterminate
- Absent
- Present, *describe*

TESTING METHOD (select all that apply)

- IHC
- ISH
- NGS
- Other, *specify*

HISTONE H3 VARIANTS AND LOSS OF H3 p.K28me3 (K27me3)^a (Note 17)

Histone H3 gene family variants

- Indeterminate
- Negative
- Positive for K27M
- Positive for G34R or G34V
- Positive, for other H3 variants, *specify*

TESTING METHOD (select all that apply)

- Sanger sequencing
- NGS
- PCR-based method
- IHC

Histone H3 K27M expression

- Indeterminate
- Negative
- Positive

Histone H3 G34R expression

- Indeterminate
- Negative
- Positive

Histone H3 K27me3 expression

- Indeterminate
- Intact expression
- Loss of expression

Other, *specify*

^b Repeat for each alteration.

IDH1/IDH2 ALTERATIONS^a (Note 18)

- Indeterminate
- Absent
- Present, *describe*

TESTING METHOD (select all that apply)

- Sanger sequencing
- NGS
- PCR-based method
- IHC

IDH1 R132H expression

- Indeterminate
- Negative
- Positive

Other, *specify*

MAPK PATHWAY ALTERATIONS^a (Note 19)

- Indeterminate
- Absent
- NF1 loss, *describe*

For *BRAF-KIAA1549* alterations refer to **BRAF ALTERATIONS** (Note 5)

For *FGRFR* alterations refer to **FGFR FAMILY ALTERATIONS** (Note 14)

Positive for other MAPK alteration, *describe*

TESTING METHOD^b (select all that apply)

- IHC
- ISH
- NGS
- Other, *specify*

METHYLOME PROFILING^a (Note 20)

Classifier (e.g., Heidelberg Brain Tumour Classifier)	Version (e.g., 12.5)	Methylation class	Score

MGMT promoter status

- Indeterminate
- Unmethylated
- Methylated

Most informative copy number variations, specify

^a Only core for some tumours - refer to [Tables 1-3](#).

^b Repeat for each alteration.

MN1 ALTERATIONS^a (Note 21)

- Indeterminate
- Absent
- Present, *describe*

TESTING METHOD (select all that apply)

- IHC
- ISH
- NGS
- Other, *specify*

MYB, MYBL1 ALTERATIONS^a (Note 22)

- Indeterminate
- Absent
- Present, *describe*

TESTING METHOD^b (select all that apply)

- IHC
- ISH
- NGS
- Other, *specify*

MYC GENE FAMILY AMPLIFICATION (MYC and/or MYCN)^a (Note 23)

- Indeterminate
- Absent
- Absent with low level gain
- Present, *describe including copy number*

TESTING METHOD^b (select all that apply)

- ISH
- Array-based method
- NGS
- Other, *specify*

PDGFRA ALTERATIONS^a (Note 24)

- Indeterminate
- Absent
- Present, *describe including copy number*

TESTING METHOD (select all that apply)

- IHC
- ISH
- NGS
- Other, *specify*

PITUITARY HORMONES AND TRANSCRIPTION FACTORS IMMUNOHISTOCHEMISTRY^a (Note 25)

Tumour cells are reactive for (select all that apply)

- Indeterminate
- Prolactin
- Human growth hormone
- β-TSH
- β-FSH
- β-LH
- Alpha subunit
- ACTH
- PIT1
- TPIT
- SF1
- Other, *specify*

PRC2 ALTERATION^a (Note 26)

- Indeterminate
- Absent
- Present, *describe*

TESTING METHOD (select all that apply)

- IHC
- ISH
- NGS
- Other, *specify*

PRKAR1A ALTERATION^a (Note 27)

- Indeterminate
- Absent
- Present, *describe*

TESTING METHOD (select all that apply)

- IHC
- ISH
- NGS
- Other, *specify*

PRKCA ALTERATION^a (Note 28)

- Indeterminate
- Absent
- Present, *describe*

TESTING METHOD (select all that apply)

- IHC
- ISH
- NGS
- Other, *specify*

^a Only core for some tumours - refer to [Tables 1-3](#).

SHH PATHWAY ALTERATIONS^a (Note 29)

- Indeterminate
- Absent
- Present, *describe*

TESTING METHOD^b (select all that apply)

- IHC
- ISH
- NGS
- Other, *specify*

SMARC FAMILY ALTERATIONS^a (Note 30)

SMARCA4/BRG1 alteration

- Indeterminate
- Absent
- Present, *describe sequence variant(s)*

TESTING METHOD (select all that apply)

- Sanger sequencing
- NGS
- PCR-based method
- Other, *specify*

BRG1 loss of expression (IHC)

- Indeterminate
- Intact nuclear expression
- Loss of nuclear expression

SMARCB1/INI1/SNF5 alteration

- Indeterminate
- Absent
- Present, *describe sequence variant(s)*

TESTING METHOD (select all that apply)

- Sanger sequencing
- NGS
- PCR-based method
- Other, *specify*

INI1 (BAF47) loss of expression (IHC)

- Indeterminate
- Intact nuclear expression
- Loss of nuclear expression

^b Repeat for each alteration.

STAT6 ALTERATIONS^a (Note 31)

STAT6 expression (IHC)

- Indeterminate
- Absence of nuclear expression
- Positive nuclear expression

STAT6 rearrangement

- Indeterminate
- Absent
- Present, *describe*

TESTING METHOD (select all that apply)

- ISH
- NGS
- Other, *specify*

TERT PROMOTER ALTERATIONS^a (Note 32)

- Indeterminate
- Absent
- Hotspot variant (C228T or C250T)
- Other sequence variant, *specify*

TESTING METHOD (select all that apply)

- Sanger sequencing
- NGS
- PCR-based method
- Other, *specify*

TP53 ALTERATIONS^a (Note 33)

TP53 variant

- Indeterminate
- Absent
- Present, *describe*

EXONS ANALYSED

- Exons 5-8
- All exons
- Other, *specify*

TESTING METHOD (select all that apply)

- Sanger sequencing
- NGS
- PCR-based method
- IHC

p53 expression

- Negative or rare, lightly positive cells
- Intermediate (intermediate numbers of predominantly lightly positive cells)
- Positive (diffuse and strong nuclear positivity)

Other, *specify*

^a Only core for some tumours - refer to [Tables 1-3](#).

TTF1 EXPRESSION (IHC)^a (Note 34)

- Indeterminate
- Negative
- Positive

WNT PATHWAY ALTERATIONS^a (Note 35)

- Indeterminate
- Absent
- Present, *describe*

TESTING METHOD^b (select all that apply)

- IHC
- ISH
- NGS
- Other, *specify*

YAP1 REARRANGEMENT^a (Note 36)

- Indeterminate
- Absent
- Present, *describe*

TESTING METHOD (select all that apply)

- ISH
- NGS
- Other, *specify*

ZFTA REARRANGEMENT^a (Note 37)

- Indeterminate
- Absent
- Present, *describe*

TESTING METHOD (select all that apply)

- IHC
- ISH
- NGS
- Other, *specify*

L1CAM expression (IHC)

- Indeterminate
- Negative
- Positive

RELA rearrangement

- Indeterminate
- Absent
- Present, *describe*

TESTING METHOD (select all that apply)

- ISH
- NGS
- Other, *specify*

^b Repeat for each alteration.

OTHER IMMUNOHISTOCHEMISTRY FINDINGS^a (Note 38)

- None identified
- Present, record test(s), methodology and results

^a Only core for some tumours - refer to [Tables 1-3](#).

OTHER MOLECULAR FINDINGS (Note 39)

- None identified
- Present, record test(s), methodology and results

Definitions

CORE elements

Core elements are those which are essential for the clinical management, staging or prognosis of the cancer. These elements will either have evidentiary support at Level III-2 or above (based on prognostic factors in the National Health and Medical Research Council levels of evidence¹). In rare circumstances, where level III-2 evidence is not available an element may be made a core element where there is unanimous agreement by the Dataset Authoring Committee (DAC).

The summation of all core elements is considered to be the minimum reporting standard for a specific cancer.

Molecular and immunohistochemical testing is a growing feature of cancer reporting. However, in many parts of the world this type of testing is limited by the available resources. In order to encourage the global adoption of ancillary tests for patient benefit, International Collaboration on Cancer Reporting (ICCR) includes the most relevant ancillary testing in ICCR Datasets as core elements, especially when they are necessary for the diagnosis. Where the technical capability does not yet exist, laboratories may consider temporarily using these data elements as non-core items.

NON-CORE elements

Non-core elements are those which are unanimously agreed should be included in the dataset but are not supported by level III-2 evidence. These elements may be clinically important and recommended as good practice but are not yet validated or regularly used in patient management.

Key information other than that which is essential for clinical management, staging or prognosis of the cancer such as macroscopic observations and interpretation, which are fundamental to the histological diagnosis and conclusion e.g., macroscopic tumour details, may be included as either core or non-core elements by consensus of the DAC.

 [Back](#)

Scope

This dataset section has been developed for the molecular assessment of primary central nervous system (CNS) tumours, whether that molecular assessment is nucleic acid or protein based. This section is to be used for those tumours in which molecular information is captured for diagnostic purposes. However, as this dataset section applies to a growing subset of CNS tumours, it is anticipated that its use will increase over time.

This dataset section has been developed for the molecular assessment of benign and malignant primary tumours of the central nervous system (CNS) and its coverings, as well as tumours from those structures of the peripheral nervous system immediately adjacent to the CNS. This dataset applies to both biopsy and resection specimens of adult and paediatric CNS tumours. Haematological lesions involving the CNS and germ cell tumours are not covered in detail as these are not the primary focus of the CNS dataset. Most sarcomas are not included and are covered by separate ICCR datasets.^{2,3} Secondary tumours of the CNS (for example, metastatic tumours from carcinomas, sarcomas or melanomas in other organs) are not covered in this dataset. Tumours of the pituitary gland are included as the majority of these tumours are reported by neuropathologists worldwide.

This dataset section on molecular assessment should be used in conjunction with the dataset sections on [Histological assessment](#) and the [Integrated final diagnosis](#).

The 2nd edition of this dataset incorporates the World Health Organization (WHO) Classification of Tumours of the CNS, 5th edition (CNS5), 2021.⁴ The ICCR dataset includes 5th edition Corrigenda, July 2024.⁵ A complete diagnosis of CNS tumours should ideally conform to the final integrated diagnoses in the 2021 WHO CNS5 Tumour Classification, which for most tumour types now require integration of elements from histological and ancillary analyses.

A list of changes in this dataset edition can be accessed [here](#).

The authors of this dataset can be accessed [here](#).

[↑ Back](#)

Overview of selected molecular (including protein) diagnostic markers for CNS tumours

Tables 1-3 describe the molecular and immunohistochemistry (IHC) markers listed as essential or desirable criteria for tumours in the WHO CNS5 Tumour Classification.⁴ The tables should be used as a reference to determine which markers are core (in bold) or non-core (non-bold) for each tumour entity. Molecular and IHC alterations which are core versus non-core correspond to WHO essential and desirable diagnostic criteria, respectively.

While these elements are deemed core, in some jurisdictions, consideration should be given to temporarily downgrading them to a non-core element until resources allow. Practical and economical guidelines, which include a comprehensive list of IHC markers, for diagnosing CNS tumours in resource-restrained jurisdictions are being developed by the Asian Oceanian Society of Neuropathology for Adapting Diagnostic Approaches for Practical Taxonomy in Resource-Restrained Regions (AOSNP-ADAPTR).⁶

The list of alterations is not exhaustive and other markers or assays may be helpful in some diagnostic circumstances. In addition, the tests listed are mostly related to 'ruling in' the corresponding diagnoses. However, it should be realised that the assays may also be used in particular diagnostic situations to 'rule out' other diagnoses. An example of this would be ATRX IHC showing a loss of nuclear expression, which is commonly used to support a diagnosis of IDH-mutant astrocytoma, but which is also used to rule out a possible diagnosis of oligodendroglioma, IDH-mutant and 1p/19q-codeleted.

Some specific alterations recommended in the commentaries below represent one of several validated and equivalent approaches to the evaluation of the described molecular variable. For those alterations that have multiple testing modalities (e.g., sequencing for *BRAF* p.V600E and IHC for the mutant protein), it is assumed that only one of these testing modalities would be used per case unless one test yields equivocal results (e.g., a result of weak IHC positivity versus nonspecific background staining should be followed by gene sequencing). For some tests, relevance may be related to the age of the patient (e.g., *IDH1/IDH2* gene testing of a diffuse glioma that is negative for the IDH1 R132H variant protein in elderly versus young adult patients). The reader is referred to the commentaries under each molecular parameter for further information.

In many instances in this dataset, the term 'variant' or 'sequence alteration' is used in place of the term 'mutation', based on the consensus recommendations of the American College of Medical Genetics and

Genomics, the Association for Molecular Pathology, the Clinical Genome Resource, Cancer Genomics Consortium and the Variant Interpretation for Cancer Consortium.^{7,8}

The use of published algorithms may be helpful in some situations, such as for [molecular biomarker testing for the diagnosis of diffuse gliomas](#).⁹ Diagnostic algorithms can be beneficial to assist with stepwise decisions, especially when resources are limited. However, diagnostic algorithms can be overly rigid and have the potential to skew usage towards select molecular assays in place of acceptable alternative surrogate markers.

In many jurisdictions, it is a requirement to maintain records associated with molecular diagnostic marker testing, which can include the molecular platform used, the antibody clone, controls, validation, and specific methodology deployed etc. Documentation of these details should be considered according to local requirements and best practice procedures.

In addition to reporting the significant alterations found in multi-gene molecular tests, consideration should be given to reporting 'negative' or non-significant findings in summary format, for example, that 'no other relevant gene alterations were observed'.¹⁰ Documentation of the method and full gene list will allow for future retrieval and review if required.

Table 4 describes genetic CNS tumour syndromes summarised from the WHO CNS5 Tumour Classification.⁴

Table 1. Molecular and immunohistochemical alterations listed as essential or desirable diagnostic criteria for gliomas, glioneuronal and neuronal tumours in the 2021 World Health Organization Classification of Tumours of the Central Nervous System.^{4#}

Note: Alterations in **bold** correspond to core ICCR/essential WHO criteria; non-bold alterations correspond to non-core ICCR/desirable WHO criteria. Alterations in [brackets] are not derived from the tables of essential or desirable WHO CNS5 Tumour Classification criteria but are considered important predictive or prognostic markers by the ICCR CNS DAC. Refer to the hyperlinked specific notes for further details on core criteria. Refer to the 2021 WHO CNS5 Tumour Classification for full diagnostic criteria.⁴

TUMOUR FAMILY/tumour type	Alterations
ADULT-TYPE DIFFUSE GLIOMAS	
Astrocytoma, IDH-mutant	IDH1 p.R132^a or IDH2 p.R172^a ; ATRX^{b,c} or exclusion of chr 1p/19q^d ; [CDKN2A/B^e]; TP53^{c,f} ; MP
Oligodendroglioma, IDH-mutant and 1p/19q-codeleted	IDH1 p.R132^a or IDH2 p.R172^a ; chr 1p/19q^d ; MP, ATRX^f , TERT promoter^c
Glioblastoma, IDH-wildtype	IDH^{wt}/H3^{wt} ; TERT promoter^c or EGFR^g or chr +7/-10^h ; MP; [MGMT promoter methylation]
PAEDIATRIC-TYPE DIFFUSE LOW GRADE GLIOMAS	
Diffuse astrocytoma, <i>MYB</i> - or <i>MYBL1</i> -altered	IDH^{wt}/H3^{wt} ; MYBⁱ/MYBL1ⁱ or MP ; absence of OLIG2^f and MAP2^f
Angiocentric glioma	MYBⁱ ; MP
Polymorphous low grade neuroepithelial tumour of the young (PLNTY)	CD34^f ; IDH^{wt} ; BRAF p.V600^{f,j} or FGFR2^k/FGFR3^k or other MAPK pathway alteration ; absence of 1p/19q ^d ; [MP]
Diffuse low grade glioma, MAPK pathway-altered	MAPK pathway alteration ; IDH^{wt} ; H3^{wt} ; absence of CDKN2A^e ; MP
PAEDIATRIC-TYPE DIFFUSE HIGH GRADE GLIOMAS	
Diffuse midline glioma, H3K27-altered	H3 p.K28me3 (K27me3^b) ; H3 p.K28M (K27M^c) /pK28I (K27I ^c) or EGFR^{c,g} or EZH1^l or MP ; discrimination of H3.1 or H3.2 versus H3.3 p.K28 (K27)-mutant subtypes
Diffuse hemispheric glioma, H3G34-mutant	H3F3A p.G35 (G34Rⁱ or G34Vⁱ) ; (for unresolved lesions) MP ; ATRX^b , diffuse p53^f ; OLIG2^f ;
Diffuse paediatric-type high grade glioma, H3- and IDH-wildtype	IDH^{wt} ; H3^{wt} ; MP or PDGFRA^{c,g}/EGFR^{c,g}/MYCN^g ; H3 p.K28me3 (K27me3) retained
Infant-type hemispheric glioma	RTK family member abnormality e.g., NTRK family gene , ROS1^k , MET^k , ALK^k or MP
CIRCUMSCRIBED ASTROCYTIC GLIOMAS	
Pilocytic astrocytoma	MAPK pathway alteration , such as BRAF^{c,j,k} most frequent KIAA1549::BRAF ; [NF1^j , FGFR1^{j,k} ; NTRK1/2/3^k ; MP]

High grade astrocytoma with piloid features	MP ; MAPK pathway alteration e.g., <i>NF1</i> ^{b,c} , <i>BRAF</i> ^k esp. <i>KIAA1549::BRAF</i> , <i>FGFR1</i> ^c ; <i>CDKN2A/B</i> ^{c,e} or <i>CDK4</i> ^b ; <i>ATRX</i> ^{b,c}
Pleomorphic xanthoastrocytoma	MAPK pathway alteration (e.g., <i>BRAF</i> p.V600 ^j , <i>BRAF</i> ^{c,k} , <i>NTRK1/2/3</i> , <i>RAF1</i> , <i>NF1</i>), combined with <i>CDKN2A/B</i> ^e ; MP
Subependymal giant cell astrocytoma	GFAP ^f ; S100 ^f ; variable neuronal markers ^f e.g., class III β-tubulin ^f , neurofilament ^f , synaptophysin ^f , NeuN ^f ; TTF1 ^f , tuberin ^b , harmarin ^b , phosphorylated S6 ^f , <i>TSC1</i> ^c or <i>TSC2</i> ^c ; MP
Chordoid glioma	TTF1 ^f , <i>PRKCA</i> p.D463H ^c or MP
Astroblastoma, <i>MN1</i> -altered	MN1 ^h ; (for unresolved lesions) MP ; GFAP ^f , EMA ^f , [<i>BEND2</i> ^k]
GLIONEURONAL AND NEURONAL TUMOURS	
Ganglioglioma	BRAF ^{c,j,k} or other MAPK pathway alteration e.g., <i>RAF1</i> ^k , <i>KRAS</i> ^l , <i>NF1</i> ^{b,j} or (for unresolved lesions) MP ; absence of IDH ^c
Gangliocytoma	-
Desmoplastic infantile ganglioglioma/astrocytoma	MP or <i>RAF</i> ^{c,k} or <i>RAF1</i> ^{c,k} in the absence of <i>CDKN2A/B</i> ^e
Dysembryoplastic neuroepithelial tumour	FGFR1 ^{a,k,m} or (for unresolved lesions) MP
Diffuse glioneuronal tumour with oligodendroglioma-like features and nuclear clusters*†	MP ; OLIG2 ^f ; synaptophysin ^f ; GFAP ^b ; chr 14 ⁿ
Papillary glioneuronal tumour	<i>PRKCA</i> ^k (mostly <i>SLC44A1::PRKCA</i>); (for unresolved lesions) MP
Rosette-forming glioneuronal tumour	(for unresolved lesions) MP ; <i>FGFR1</i> ^c with <i>PIK3CA</i> ^c and/or <i>NF1</i> ^c
Myxoid glioneuronal tumour	<i>PDGFRA</i> p.K385 ⁱ ; <i>PDGFRA</i> ^c ; MP
Diffuse leptomeningeal glioneuronal tumour‡	OLIG2 ^f ; synaptophysin ^f ; chr 1p ^d ; MAPK alteration , mostly <i>BRAF</i> ^k such as <i>KIAA1549::BRAF</i> ; (for unresolved lesions) MP
Multinodular and vacuolating neuronal tumour	Synaptophysin ^f , HuC/HuD ^f or non-phosphorylated 200kDa NFP ^f ; OLIG2 ^f ; internexin A ^f , NeuN ^b or chromogranin ^b , MAPK alteration esp. <i>MAP2K1</i> ^c ; <i>FGFR2</i> ^k ; <i>BRAF</i> ^c
Dysplastic cerebellar gangliocytoma (Lhermitte-Duclos disease)	<i>PTEN</i> ^{b,c}
Central neurocytoma	Synaptophysin ^f ; (for unresolved lesions) MP
Extraventricular neurocytoma	Absence of IDH ^h ; Synaptophysin ^f ; (for unresolved lesions) MP ; <i>FGFR1</i> alteration, mostly <i>FGFR1::TACC1</i> , [<i>FGFR3</i> ^k]
Cerebellar liponeurocytoma	Synaptophysin ^f ; (for unresolved lesions) MP ; focal GFAP ^f

EPENDYMAL TUMOURS	
Supratentorial ependymoma, <i>ZFTA</i> fusion-positive	IHC features of ependymoma; <i>ZFTA</i> (<i>C11orf95</i>^k) mostly <i>ZFTA::RELA</i> ; MP, p65 (<i>RELA</i> ^f) or L1CAM ^f
Supratentorial ependymoma, <i>YAP1</i> fusion-positive	IHC features of ependymoma; <i>YAP1</i>^k ; MP, negative for p65 (<i>RELA</i>) ^f or L1CAM ^f
Posterior fossa ependymoma, group A (PFA)	IHC features of ependymoma; MP or global reduction of H3 p.K28me3 (K27me3^f) in tumour cell nuclei ; stable genome on genome-wide copy-number analysis
Posterior fossa ependymoma, group B (PFB)	IHC features of ependymoma; MP ; chromosomal instability and aneuploidy on genome-wide copy-number analysis, retained H3 p.K28me3 (K27me3 ^f) in tumour cell nuclei
Spinal ependymoma	IHC features of ependymoma ; MP, 22q ^d , absence of <i>MYCN</i> ^g
Spinal ependymoma, <i>MYCN</i> -amplified	IHC features of ependymoma; <i>MYCN</i>^g ; MP
Myxopapillary ependymoma	GFAP^f ; (for unresolved lesions) MP
Subependymoma	(for unresolved lesions) MP

MP – Methylome profiling; IHC – immunohistochemistry; MAPK – Mitogen-activated protein kinase; ^{wt} wildtype; ^a missense mutation/variant; ^b loss/absence of expression; ^c mutation/variant; ^d combined whole-arm deletion; ^e homozygous deletion; ^f expression; ^g gene amplification; ^h copy number alteration; ⁱ structural variant; ^j hotspot mutation/variant; ^k gene fusion; ^l overexpression; ^m internal tandem duplication; ⁿ monosomy. * Provisional tumour type; † Methylation profiling is so far the only method to clearly identify diffuse glioneuronal tumour with oligodendroglioma-like features and nuclear clusters, but if not available, morphological features may provide an approximation; ‡ This tumour type shows molecular overlap with pilocytic astrocytoma (*KIAA1549::BRAF* fusion) and oligodendroglioma (1p/19q codeletion). All diffuse leptomeningeal glioneuronal tumours are wildtype in *IDH1* and *IDH2*.

Of note, this list of alterations is not exhaustive, and some of the alterations are generally mutually exclusive (e.g., *IDH1* versus *IDH2* variant), while others can occur in combination in the same tumour (e.g., *TERT* promoter variant, *EGFR* amplification, and +7/-10). Furthermore, while this table lists the alterations, demonstration of lack of particular alteration(s) can also be essential to establish the correct diagnosis (e.g., absence of complete 1p/19q codeletion in IDH-mutant astrocytomas).

Modified from Table 1 in Sahm et al. Molecular diagnostic tools for the World Health Organization (WHO) 2021 classification of gliomas, glioneuronal and neuronal tumours; an EANO guideline (licenced under [CC-BY-NC 4.0](https://creativecommons.org/licenses/by-nc/4.0/)).¹⁰ This table does not represent a diagnostic algorithm and one should refer to the WHO CNS5 Tumour Classification on how to use this information.⁴

Table 2. Molecular and immunohistochemical alterations listed as essential and desirable diagnostic criteria for embryonal tumours in the 2021 World Health Organization Classification of Tumours of the Central Nervous System.⁴

Note: Alterations in **bold** correspond to core/essential WHO criteria; non-bold alterations correspond to non-core/desirable WHO criteria. Refer to the hyperlinked specific notes for further details on core criteria. Refer to the 2021 WHO CNS5 Tumour Classification for full diagnostic criteria.⁴

TUMOUR FAMILY/tumour type	Alterations
MEDULLOBLASTOMA, MOLECULARLY DEFINED	
Medulloblastoma, WNT-activated	WNT pathway activation or MP
Medulloblastoma, SHH-activated and <i>TP53</i> -wildtype	SHH pathway activation or MP ; <i>TP53</i> ^{wt}
Medulloblastoma, SHH-activated and <i>TP53</i> -mutant	SHH pathway activation or MP ; <i>TP53</i> ^a
Medulloblastoma, non-WNT/non-SHH	No WNT or SHH pathway activation or MP
OTHER CNS EMBRYONAL TUMOURS	
Atypical teratoid/rhabdoid tumour	SMARCB1/SMARCA4 ^b or (for unresolved lesions) MP ; <i>SMARCB1</i> ^c ; <i>SMARCA4</i> ^c
Cribriform neuroepithelial tumour*	SMARCB1 ^b ; EMA ^d
Embryonal tumour with multilayered rosettes (ETMR)	IHC features of ETMR ; C19MC ^c or DICER1 ^a ; (for unresolved lesions) MP
CNS neuroblastoma, <i>FOXR2</i> -activated	FOXR2 ^{e,f} or (for unresolved lesions) MP
CNS tumour with <i>BCOR</i> internal tandem duplication	BCOR exon 15 ^g ; (for unresolved lesions) MP
CNS embryonal tumour, NEC/NOS	Neuronal markers ^d ; absence of glial markers ^d

MP – Methylome profiling; IHC – immunohistochemistry; ETMR – embryonal tumour with multilayered rosettes; ^{wt} wildtype; ^a mutation/variant; ^b loss/absence of expression; ^c alteration; ^d expression; ^e structural variant; ^f gene fusion; ^g internal tandem duplication.

* Provisional tumour type.

Table 3. Molecular and immunohistochemical alterations listed as essential or desirable diagnostic criteria for other central nervous system tumours in the 2021 World Health Organization Classification of Tumours of the Central Nervous System.⁴

Note: Alterations in **bold** correspond to WHO essential criteria; non-bold alterations correspond to WHO desirable criteria. Alterations in [brackets] are not derived from the tables of essential or desirable WHO CNS5 Tumour Classification criteria but are considered important predictive or prognostic markers by the ICCR CNS DAC. Refer to the hyperlinked specific notes for further details on core criteria. Refer to the 2021 WHO CNS5 Tumour Classification for full diagnostic criteria.⁴

TUMOUR FAMILY/tumour type	Alterations
CHOROID PLEXUS TUMOURS	
Choroid plexus papilloma	IHC features of choroid plexus differentiation
Atypical choroid plexus papilloma	IHC features of choroid plexus differentiation ; in select cases: hyperploidy by genome-wide chromosomal copy-number analysis
Choroid plexus carcinoma	IHC features of choroid plexus differentiation ; <i>TP53</i> ^a ; MP; in select cases: demonstration of hypoploidy by genome-wide chromosomal copy-number analysis
CRANIAL & SPINAL NERVE TUMOURS	
Schwannoma	S100 ^b or SOX10 ^b ; absence of lattice-like CD34 ^b ; SMARCB1 ^c (INI1) in epithelioid schwannoma or mosaic pattern of SMARCB1 ^b (INI1) in syndrome associated schwannoma
Neurofibroma	S100 ^b ; lattice-like CD34 ^b ; p16 ^c in particular in the NF1 related subgroup
Perineurioma	EMA ^b or claudin-1 ^b or GLUT1 ^b ; absence of S100 ^b
Hybrid nerve sheath tumours	IHC for intermingled features of two types of benign nerve sheath tumours
Malignant melanotic nerve sheath tumour	S100/SOX10 ^b ; melanocytic markers ^b (e.g., HMB45 , melan-A) or PRKAR1A2 ^{a,c} ; (for unresolved lesions) MP
Malignant peripheral nerve sheath tumour	No more than focal/patchy S100/SOX10 ^b ; absence of SS18::SSX1/SSX2/SSX3 ^{d#} or PRC2 inactivation (molecularly or via H3 p.K28me3 ^c) or (for unresolved lesions) MP ; absence of H3 p.K28me3 ^{b,c} ; neurofibromin ^c
Cauda equina neuroendocrine tumour (previously paraganglioma)	Synaptophysin ^b or chromogranin ^b in chief cells; (for unresolved lesions) MP ; S100 ^b in sustentacular cells; cytokeratin ^b in chief cells, reticulin silver stain
GERM CELL TUMOURS	
Mature teratoma	-
Immature teratoma	-
Teratoma with somatic-type malignancy	-

Germinoma	Nuclear OCT4^b ; widespread membranous KIT^b or podoplanin^b (D2-40) or absence of 5-methylcytosine^b ; absence of CD30^b ; absence of AFP^b ; hCG^b
Embryonal carcinoma	CD30^b ; nuclear OCT4^b ; absent or focal KIT^b ; absence of hCG^b ; absence of AFP^b ; cytokeratin ^b
Yolk sac tumour	AFP^b ; absent or focal non-membranous KIT^b ; absent or focal CD30^b ; absence of β-hCG^b
Choriocarcinoma	β-hCG^c ; absence of KIT^b or absence of podoplanin^b (D2-40) ; absence of AFP^b ; absence of OCT4^b
Mixed germ cell tumour	-
MELANOCYTIC TUMOURS	
Meningeal melanocytosis/meningeal melanomatosis	In children often NRAS^a ; rarely BRAF^a
Meningeal melanocytoma/meningeal melanoma	GNAQ^a ; GNA11^a ; PLCB4^a or CYSLTR2^a (for corroborating CNS origin of the neoplasm); SF3B1^a , EIFAX^a , BAP1^a , chr 3 ^e , complex copy-number variations (as an indicator of aggressive behaviour)
MENINGIOMAS	
Meningioma	[TERT promoter^a ; CDKN2A/B^c features of CNS WHO grade 3 meningioma]; MP ; demonstration of biallelic inactivation of NF2 or alterations in other drivers of conventional meningioma (TRAF7 , AKT1 , KLF4 , SMO , PIK3CA , SMARCE1 in clear cell meningioma, BAP1 in rhabdoid meningioma); EMA^b ; SSTR2A^b ; chr. 22/22q in lower grade meningioma ^f ; loss of chr. 1p; chr. 6; chr. 10q; chr. 14q; chr. 18 in higher grade meningioma
MESENCHYMAL, NON-MENINGOTHELIAL TUMOURS	
Solitary fibrous tumour	STAT6^b ; NAB2::STAT6^d
Haemangiomas and vascular malformations	-
Hemangioblastoma	Inhibin^b ; loss or inactivation of VHL^{a,c,#} ; absence of IHC staining for markers of renal cell carcinoma
Intracranial mesenchymal tumour, FET::CREB fusion-positive	FET::CREB^d ; CD99^b ; EMA^b ; desmin^b
CIC-rearranged sarcoma	CIC^d ; CD99^b ; ETV4^b ; WT1^b ; MP
Primary intracranial sarcoma, DICER1-mutant	DICER1^a ; (for unresolved lesions) MP
Ewing sarcoma	Diffuse and membranous CD99^b ; FET::ETS^d ; NKX2-2^b ; PAX7^b
Chordoma	Brachyury^b ; in poorly differentiated chordoma SMARCB1^c (INI1)

PINEAL TUMOURS	
Pineocytoma	IHC for pineal parenchymal differentiation e.g., synaptophysin ^b
Pineal parenchymal tumour of intermediate differentiation	IHC for pineal parenchymal differentiation e.g., synaptophysin ^b ; (for unresolved lesions) MP ; KBTBD4 ^g
Pineoblastoma	SMARCB1 ^b (INI1); MP
Papillary tumour of the pineal region	Characteristic IHC e.g., cytokeratins ^b , SPDEF ^b , CD56 ^b ; MP
Desmoplastic myxoid tumour of the pineal region, <i>SMARCB1</i> -mutant*	SMARCB1 ^c ; (for unresolved lesions) MP
TUMOURS OF THE SELLAR REGION	
Adamantinomatous craniopharyngioma	Nuclear β -catenin ^b ; CTNNB1 ^a ; absence of BRAF p.V600E ^a
Papillary craniopharyngioma	BRAF p.V600E ^{a, b} ; absence of nuclear β -catenin ^b ; absence of CTNNB1 ^a
Pituicytoma	TTF1 ^b ; absence of pituitary hormone ^b and hormone transcription factor ^b ; absence of neuronal and neuroendocrine marker ^b
Granular cell tumour of the sellar region	TTF1 ^b ; absence of pituitary hormone ^b and hormone transcription factor ^b ; absence of neuronal and neuroendocrine marker ^b ; CD68 ^b or α 1-antitrypsin ^b
Spindle cell oncocytoma	TTF1 ^b ; absence of pituitary hormone ^b and hormone transcription factor ^b ; absence of neuronal and neuroendocrine marker ^b ; antimitochondrial antigen ^b
Pituitary adenoma/Pituitary neuroendocrine tumour	IHC for pituitary hormones and/or lineage-specific transcription factors ; Ki-67 ^b (MIB1), [cytokeratins]
Pituitary blastoma	DICER1 ^h

MP – Methylome profiling; IHC – immunohistochemistry; ^a mutation/variant; ^b expression; ^c loss/absence of expression; ^d gene fusion; ^e monosomy; ^f copy number alteration; ^g insertion; ^h alteration.

* Provisional tumour type, [#] [VHL](#) and absence of [SS18::SSX1/SSX2/SSX3](#) have been designated non-core alterations by the ICCR CNS DAC.

Mesenchymal chondrosarcoma and chondrosarcoma are not included as they are covered in the ICCR Soft tissue sarcoma datasets.^{2,3}

Table 4. Genetic central nervous system (CNS) tumour syndromes and alterations from the 2021 World Health Organization Classification of Tumours of the CNS.⁴

Genetic tumour syndromes	Genes involved (chromosomal location)	Tumours of the nervous system
Neurofibromatosis type 1	<i>NF1</i> (17q11.2) ^a	Neurofibroma; ANNUBP; hybrid neurofibroma/schwannoma; MPNST; pilocytic astrocytoma; other gliomas
Neurofibromatosis type 2	<i>NF2</i> (22q12.2) ^a	(Bilateral) schwannoma; meningioma; spinal ependymoma; hybrid neurofibroma/schwannoma
Schwannomatosis	<i>SMARCB1</i> (22q11.23) ^a or <i>LZTR1</i> (22q11.21) ^a ; and <i>NF2</i> (22q12.2) ^a ('four-hit, three-step mechanism')	Schwannoma; meningioma; hybrid neurofibroma/schwannoma; MPNST
Von Hippel-Lindau syndrome	<i>VHL</i> (3p25.3) ^a	Hemangioblastoma
Tuberous sclerosis	<i>TSC1</i> (9q34.13) ^a or <i>TSC2</i> (16p13.3) ^a	Subependymal giant cell astrocytoma
Li-Fraumeni syndrome	<i>TP53</i> (17p13.1) ^{a,d,e}	Choroid plexus carcinoma; IDH-wildtype glioblastoma; IDH-mutant astrocytoma, medulloblastoma
Cowden syndrome	<i>PTEN</i> (10q23.31) ^a	Dysplastic cerebellar gangliocytoma (Lhermitte-Duclos disease)
CMMRD syndrome, Lynch syndrome	<i>PMS2</i> (7p22.1) ^{a,e} or <i>MSH12</i> (2p21) ^{a,e} ; or <i>MSH6</i> (2p16.3) ^{a,e} or <i>MLH1</i> (3p22.2) ^{a,e} ; genomic profiling of MMRD; absence of MMR ^f , <i>POLE</i> ^a etc.	IDH-wildtype high grade glioma; IDH-mutant astrocytoma; medulloblastoma
Familial adenomatous polyposis 1	<i>APC</i> (5q22.2) ^a	Medulloblastoma, WNT-activated
Nevoid basal cell carcinoma syndrome	<i>PTCH1</i> (9q22.32) ^a , [<i>PTCH2</i> (1p34.1) ^a] or <i>SUFU</i> (10q24.32) ^a	Medulloblastoma, SHH-activated
Rhabdoid tumour predisposition syndrome	<i>SMARCB1</i> (22q11.23)/ <i>SMARCA4</i> (19p13.2) ^a	Atypical teratoid/rhabdoid tumour
Carney complex	Inactivating <i>PRKAR1A</i> (17q24.2) ^a	Malignant melanotic nerve sheath tumour
DICER1 syndrome	<i>DICER1</i> (14q32.13) ^a ; <i>DICER1</i> ^{a,c} involving remaining allele	Pituitary blastoma; pineoblastoma; ciliary body medulloepithelioma; DICER1-associated CNS sarcoma; ETMR-like infantile cerebellar embryonal tumour
Familial paraganglioma syndrome	Germline susceptibility gene variant; <i>SDHB</i> (1p36.13) ^g (high predictive value for <i>SDHB/C/D</i> ^a)	Paraganglioma
Melanoma-astrocytoma syndrome	<i>CDKN2A/2B</i> (9p21.3) ^a	Pleomorphic xanthoastrocytoma, low grade diffuse astrocytoma; IDH—wildtype glioblastoma; schwannoma; neurofibroma

Use of this dataset is only permitted subject to the details described at: [Disclaimer - International Collaboration on Cancer Reporting \(iccr-cancer.org\)](https://www.iccr-cancer.org/)

Familial retinoblastoma	<i>RB1</i> (13q14.2) ^h	Retinoblastoma; pineoblastoma
BAP1 tumour predisposition syndrome	<i>BAP1</i> (3p21.1) ^a	Meningioma, rhabdoid or papillary
Fanconi anaemia	Positive chr breakage analysis (diepoxybutane test); <i>FANC</i> ^a	Medulloblastoma
ELP1-medulloblastoma syndrome	<i>ELP1</i> (9q31.3) ^h	Medulloblastoma, SHH-activated

ANNUBP – Atypical neurofibromatosis neoplasm with uncertain biologic potential; MPNST – Malignant peripheral nerve sheath tumour; CMMRD – Constitutional mismatch repair deficiency; MP – Methylome profiling; ^{wt} wildtype; ^a mutation/variant; ^b combined whole-arm deletion; ^c loss of heterozygosity; ^d structural variant; ^e partial/complete deletion; ^f expression; ^g loss/absence of expression; ^h alteration.

For more information refer to the 2021 WHO CNS5 Tumour Classification.⁴

Note 1 – Adequacy of specimen for molecular assessment (Non-core)

The 2021 WHO CNS5 Tumour Classification uses histology, IHC and molecular parameters to define many tumour entities.⁴ Procuring viable and adequate tumour tissue allows appropriate histological and molecular assessment. However, the requirements for an adequate specimen for molecular assessment are not always the same as those for histological assessment. For example, ischemic times are critical for the quality of nucleic acid in general; the sooner samples can be frozen or fixed, the better. If immediate freezing or immediate appropriate fixation is not possible, placement in a refrigerator may reduce the degradation of nucleic acids.

Crush or freezing artefacts may affect adequacy for histopathology, including IHC or in situ hybridisation (ISH) testing, but do not often affect adequacy for molecular assays. Samples embedded in optimal cutting temperature (OCT) compound for cryostat sectioning can be a good source, and an advantage of using such samples is that one can evaluate tumour cell quantity as well as quality by checking histological sections of each sample.

Formalin-fixed, paraffin-embedded (FFPE) tissue samples also often provide a valuable source of information for molecular assessment. FFPE samples, however, can sometimes be more difficult for molecular biology assays because of fixation issues (such as overfixation and decalcification) that often cause nucleic acid degradation, resulting in fragmented DNA and RNA transcripts. Nonetheless, many laboratories have optimised molecular assays for FFPE tissue, given its commonplace nature.

Histological examination of tissue specimens used for nucleic acid extraction and subsequent molecular testing is essential to assure that vital tumour tissue with sufficient neoplastic cell content is being analysed. In certain cases, microdissection of cellular tumour areas may be required to ensure sensitivity of molecular analysis.

↑ Back

Note 2 – *ALK/ROS1/MET/NTRK* family alterations (Core)*

***ALK* fusion or rearrangement**

The *ALK* (Anaplastic Lymphoma Kinase) gene (2p23) belongs to the insulin receptor superfamily of receptor tyrosine kinases (RTKs) and activates multiple downstream signal transduction pathways, including MAPK/PI3K/AKT/mTOR and JAK/STAT pathways.¹¹ In cancer, *ALK* can be activated by gene fusions or point mutations/variants. Among gliomas, *ALK* fusions are mostly restricted to Infant-type hemispheric glioma (IHG) that are characterised by RTK gene fusions involving *ALK*, *ROS1*, *NTRK* or *MET*.^{12,13}

ALK fusions have been reported in about a third (39/130) of IHGs.¹² Thirteen different fusion partners have been observed.¹² All *ALK* fusions contain the complete *ALK* kinase domain at the C-terminal end, while the N-terminal partners retain variable domains in the chimeric protein, although most N-terminal partners have a coiled-coil or dimerisation domain.¹⁴

ALK fusions can be detected by ISH using dual-label break apart probes, next generation sequencing (NGS)-based gene fusion panel sequencing or whole transcriptome sequencing. Fusions lead to increased *ALK* protein expression that can be detected by IHC, a common method used to identify *ALK*-activated tumours. In a number of jurisdictions, IHC assays have been approved as companion diagnostics to aid in the identification of patients eligible for treatment with *ALK* inhibitors like crizotinib.^{15,16}

The most common indications for *ALK* fusion testing in CNS tumour diagnostics include intracerebral metastases of NSCLC (non-small cell lung carcinoma) in adults and a differential diagnosis of IHG in children.¹⁷ Among non-glioma tumours that occasionally involve the CNS, *ALK*-positive anaplastic large cell

lymphomas are characterised by oncogenic *ALK* fusions. *ALK* fusions have also been noted in *ALK*-positive histiocytosis, which is a novel type of systemic histiocytic proliferative disorder occurring predominantly in young children, rarely showing exclusive involvement of the CNS.^{18,19}

In addition to being a diagnostic marker for IHGs, *ALK* fusions also appear to be prognostic in this tumour type, although additional investigation is needed. One study observed a higher 5-year overall survival rate in patients with *ALK* rearranged tumours (53.8%), as compared to *ROS* and *NTRK* altered tumours.¹³ *ALK* rearranged tumours with low grade histology were diagnosed at an older age and had better survival rates, as compared to those of patients with *ALK* altered high grade gliomas.

The presence of *ALK* fusions also provides opportunity for targeted therapy using *ALK* inhibitors, and early experience has demonstrated responses.^{17,20} Interestingly, different *ALK* fusion-positive tumours have varying sensitivity to *ALK* inhibitors.¹⁴

Investigation of *ALK* alteration is a core element for infant-type hemispheric glioma.

***ROS1* fusion or rearrangement**

The *ROS1* (ROS proto-oncogene 1) gene (6q22.1) closely resembles *ALK* both in sequence and structure. Both receptors signal via the RAS/MAPK as well as the JAK/STAT and PI3K/AKT/mTOR pathways.¹⁷ *ROS1* fusions arise through intrachromosomal 6q micro-deletions in IDH-wildtype glioblastomas, although they are very rare as indicated by only 3 of 520 tumours in the Cancer Genome Atlas cohort.¹⁷ *ROS1* fusions are also reported in IHG.^{12,13} In a series of 118 infants with IHG, 7 (4%) were diagnosed with a *ROS1* fusion.¹³ Clark et al¹² (2020) showed *ROS1* fusion as a driving alteration in 9 out of 130 cases.

Immunohistochemistry (IHC), ISH (break apart probes), and DNA- or RNA-based NGS (custom panels or commercially available panels) can be used to detect *ROS1* fusion. However, each of these methods has limitations. IHC can be used as a screening method, yet it may identify tumours with increased protein expression in the absence of a fusion. Therefore, in case of a positive *ROS1* immunostaining, confirmation with either ISH or NGS should be performed.²¹

ROS1 fusions, though rare, are a diagnostic marker for IHGs in the appropriate clinical and radiological setting and also provide options for targeted therapy. Furthermore, one study reported that patients with tumours that harboured *ROS1* alterations had a lower 5-year overall survival rate, as compared to those with *ALK* alterations (25% versus 53.8%).¹³

Reports on successful targeted treatment of CNS tumours in children with *ROS1*-positive fusions such as IHG are anecdotal, but responses have been reported.^{22,23}

Investigation of *ROS1* alteration is a core element for infant-type hemispheric glioma.

***NTRK* family alterations**

The neurotrophic tyrosine receptor kinase (*NTRK*) genes include *NTRK1* (1q23.1), *NTRK2* (9p21.33), and *NTRK3* (15q25.3) and encode tropomyosin receptor kinases (TRKs), a family of RTKs involved in the development and maturation of the central and peripheral nervous system.

Although oncogenic variants and alternative splicing occur, fusions are the most common alterations of *NTRK* in tumours. The most common alteration is a fusion between an *NTRK* gene and another N-terminal partner. All these aberrations result in the constitutive activation of the kinase due to loss of the extracellular domain.¹⁴

NTRK fusions are reported in about 4% of paediatric gliomas and most of these are high grade. They are most prevalent in IHG.^{12,13,24} Clark et al¹² (2020) reported that the most commonly targeted genes in their series were

in *NTRK1/2/3*. *NTRK2* was found with numerous novel partners but was largely seen in other glioma subtypes (e.g., H3K27M in midline regions), suggesting an important difference in *NTRK2* compared to *NTRK1/3* fusion-positive cases.

Among adult CNS tumours, NTRK fusions have been reported at a frequency of 1-2% in glioblastoma, IDH-wildtype.²⁵ They have also been described in approximately 2% of pilocytic astrocytomas (PAs)²⁶, and rarely in diffuse low grade gliomas, MAPK pathway-altered.²⁷

NTRK fusion genes in CNS tumours can be assessed by ISH, reverse transcriptase-polymerase chain reaction (RT-PCR) or RNA-based sequencing (either panel based or whole transcriptome). Endogenous and physiological NTRK expression renders assessment by IHC in the nervous system challenging and thus molecular techniques are recommended.²⁸

NTRK fusions are diagnostic markers of IHGs and also appear to carry prognostic significance. In one study,¹³ it was reported that NTRK fusion-positive tumours had an intermediate prognosis, as compared to *ALK*- and *ROS*-altered tumours in that the 5-year overall survival rate was 42.9%.

NTRK fusion provides an opportunity for targeted therapy with specific small molecule inhibitors. Larotrectinib and entrectinib have been conditionally approved by both the European Medicines Agency and the United States Food and Drug Administration (FDA) for NTRK fusion-positive cancers. Additional data regarding the efficacy of NTRK inhibitors in adult and paediatric CNS tumour patients are needed.^{14,17}

Investigation of NTRK alteration is a core element for infant-type hemispheric glioma.

***MET* alterations**

The *MET* oncogene (7q31.2) encodes hepatocyte growth factor/HGF, an RTK that plays a pivotal role in differentiation, cell proliferation, angiogenesis, migration, invasion, genomic stability and resistance to therapy.¹⁷ Dysregulation of *MET* signalling and activation of downstream pathways (RAS/MAPK, PI3K/AKT, and STAT pathways) can be caused by various mechanisms, including *MET* amplification, point mutation, fusion and *MET* exon skipping alteration.^{17,29,30}

Amplifications of *MET* have been reported in 0.7-6.2 % of IDH-wildtype glioblastomas and 5.2-17 % of IDH-mutant astrocytomas. They have also been identified in 20% of diffuse midline gliomas H3 K27-altered, in 10% of diffuse hemispheric gliomas H3 G34-mutant, and in gliomas arising after irradiation.^{31,32}

A variety of *MET* fusions have been detected in CNS tumours. *MET* fusions with variable N-terminal fusion partners have been described mainly in diffuse paediatric-type high grade gliomas, H3-wildtype and IDH-wildtype, IHG and in 3% of IDH-wildtype glioblastoma.^{12-14,17,33} Rarely, *MET* alterations have been reported in diffuse low grade gliomas, MAPK pathway-altered.²⁷

MET fusions in adult patients have been reported in a small subset of IDH-mutant astrocytomas (mainly in high grade and recurrent tumours) and in IDH-wildtype glioblastomas.^{14,34,35}

Exon skipping alterations of *MET* exon 14 and exon 7-8 have not been analysed to any significant extent in CNS tumours. However, few studies have reported these alterations in 6%-8% of high grade gliomas.^{17,35} Similarly, the frequency of *MET* sequence variants in CNS tumours has not been precisely defined.¹⁷

There is no established and validated diagnostic test to assess *MET* alterations in CNS tumours by IHC. Specific *MET* protein antibodies have been tested to detect *MET* amplifications in gliomas, but standardised methods do not exist. Furthermore, the usefulness of *MET* IHC to detect *MET* fusions and exon skipping alterations is unclear. Hence, the preferred method is molecular detection of *MET* alterations.

Due to the frequent occurrence of multiple *MET* alterations simultaneously (e.g., amplifications, fusions with various breakpoints, exon skipping etc.), a hybrid capture based (targeted) DNA/RNA sequencing approach is recommended.^{17,30}

The detection of a *MET* fusion can aid in establishing the diagnosis of IHGs and also provides options for targeted therapy. The effectiveness of *MET* inhibitors in CNS tumours have been investigated in several phase I and II studies, but the effectiveness in biomarker-stratified cohorts with *MET* alterations has largely not been assessed.³⁶

Investigation of *MET* alteration is a core element for infant-type hemispheric glioma.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 3 – *ATRX* alterations (Core)*

The diagnosis of an IDH-mutant astrocytoma (CNS WHO grade 2, 3 or 4) is supported by the presence of *TP53* expression or alteration (mutation or deletion), in addition to loss of expression or alteration of the *ATRX* (α -thalassaemia/mental retardation syndrome X-linked) gene (Xq21.1).^{37,38} Evaluation for *ATRX* alteration is also commonly used to rule out the possibility of an oligodendroglioma, IDH-mutant and 1p/19q-codeleted.

Determination of *ATRX* loss of nuclear expression/mutations can be achieved in a number of ways, with a practical and cost-effective manner being IHC. The loss of nuclear *ATRX* immunostaining in neoplastic cells, with its maintained expression in non-neoplastic cells, such as endothelial cells or non-neoplastic glia, is strongly associated with *ATRX* genetic alterations and can be reliably used as a surrogate marker.³⁹ Mosaic staining patterns have also been reported, but these are not always associated with *ATRX* sequence alterations.⁴⁰ In combination with IHC for IDH1 R132H mutant protein and p53, *ATRX* IHC provides definitive results in the majority of cases, with the added benefit of preserving cytoarchitecture for microscopic examination.

Investigation of *ATRX* alteration is a core element for astrocytoma, IDH-mutant.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 4 – *BCOR* internal tandem duplication (Core)*

Demonstration of a *BCOR* (BCL-6 Corepressor) internal tandem duplication (ITD) is required for the diagnosis of CNS tumour with *BCOR* ITD, introduced as a new embryonal tumour type in the WHO CNS5 Tumour Classification.⁴

This alteration consists of a solitary heterozygous *BCOR* ITD in exon 15 of the *BCOR* gene (Xp11.4). As its name implies, *BCOR* acts as an interacting corepressor of BCL-6, with an epigenetic regulator function, taking part in the polycomb repressive complex 1 (PRC1).⁴¹ This alteration is also found in various other neoplasms, such as small round cell sarcomas of soft tissues, clear cell sarcomas of the kidney and primitive myxoid mesenchymal tumour of infancy.⁴²

In routine neuropathological practice, RT-PCR or RNA sequencing by NGS could be used to detect *BCOR* ITDs, but strong and diffuse nuclear immunoexpression of *BCOR* has been reported as a practical surrogate for the presence of this alteration.⁴³ Furthermore, DNA methylation profiling can be used to classify CNS tumours with *BCOR* ITD as such, based on their methylation ‘fingerprint’.⁴⁴

In similarity with soft tissue tumours, rare CNS tumours sharing the same DNA-methylation cluster as CNS tumours with *BCOR* ITD, present with an alternative *BCOR* alteration, such as deletion of *BCOR*, sequence variation of the *BCOR* gene or an *EP300::BCOR(L1)* fusion.⁴⁴ These tumours show magnetic resonance imaging homologies with CNS-*BCOR* ITD, but are significantly distinct from their *BCOR* ITD counterparts in terms of age, location, progression-free survival, tumour growth pattern, and also immunopositivity for the *BCOR* protein.^{45,46} Indeed, such CNS *BCOR* tumours with alternative alterations express variable *BCOR* by IHC with a high proportion of cases being immunonegative.^{43,47,48}

Immunohistochemistry (IHC) for *SATB2* has been reported as a sensitive but non-specific immunohistochemical marker for tumours with *BCOR* ITD and for alternative *BCOR* alterations.⁴³

Investigation of *BCOR* alteration is a core element for CNS tumours with *BCOR* internal tandem duplication.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 5 – *BRAF* alterations (Core)*

***BRAF* genetic alterations**

The *BRAF* (V-Raf Murine Sarcoma Viral Oncogene Homolog B protooncogene; 7q34) p.V600E sequence variant in exon 15, which is the most common *BRAF* alteration, affects a large variety of CNS tumours. It has been reported in 96% of papillary craniopharyngiomas, 65-75% of pleomorphic xanthoastrocytomas with and without anaplasia, 25-60% of gangliogliomas, 20-25% of dysembryoplastic neuroepithelial tumours, and 7% of PAs.^{49,50} *BRAF* variants have also been detected in about one-half of epithelioid glioblastomas and in up to 25% of diffuse astrocytic gliomas in children and young adults.⁵¹ The detection of a *BRAF* sequence variant has diagnostic implications in specific tumours, such as pleomorphic xanthoastrocytomas, ganglioglioma, dysembryoplastic neuroepithelial tumour, or epithelioid glioblastoma. Moreover, the detection of the variant can help to distinguish a ganglioglioma from the cortical infiltration of a diffuse glioma.

Besides its diagnostic value, *BRAF* sequence variants may allow for targeted therapy against mutant *BRAF* p.V600 protein. In paediatric low grade gliomas, the *BRAF* p.V600E sequence variant has been linked to poor response to conventional cytotoxic therapy and poor prognosis.⁵² In routine settings, *BRAF* p.V600E can be identified by IHC or by molecular approaches, such as high-resolution melting analysis, pyrosequencing, allele-specific quantitative polymerase chain reaction (ASQ-PCR), droplet-based digital PCR (ddPCR), NGS and Sanger sequencing.⁵³ Although Sanger sequencing is a well-established tool to detect *BRAF* p.V600E and other rarer *BRAF* variants, it has a detection threshold of 20% (of mutant alleles). In samples that contain a minority of mutant cells, molecular methods with much lower thresholds, such as ASQ-PCR, ddPCR, or NGS, are more sensitive.

***BRAF* p.V600E immunohistochemistry**

Immunohistochemistry (IHC) is a commonly used method to detect *BRAF* p.V600E mutant protein in FFPE tissue of CNS tumours. Monoclonal antibodies (such as clone VE1 and clone V600E) against *BRAF* p.V600E are commercially available. Clone VE1 is the most widely used and is sensitive and specific.⁵⁴ The concordance

between IHC and detection of the BRAF p.V600E variant by molecular genetic techniques demonstrates variability between studies in different types of neoplasms, but the overall concordance is strong.⁵⁴ IHC plays a key role when FFPE material available is not sufficient for molecular genetic analysis and when low tumour cell content may lead to false-negative results.

BRAF rearrangement/duplication

Circumscribed duplication of the *BRAF* locus is a common copy number variation (CNV) that occurs in PAs of the cerebellum, hypothalamus, or optic chiasm, but may occur in PAs from other sites as well.

The mitogen-activated protein kinase (MAPK) signalling pathway is a key signalling pathway in the development of PA. The major alterations leading to constitutive activation of MAPK in PAs are gene fusions and missense variants involving *BRAF*, in particular *BRAF* p.V600E.

Identification of the *KIAA1549::BRAF* fusion has been used as a diagnostic marker for PAs. It has also been observed in pilomyxoid astrocytoma, ganglioglioma and diffuse leptomeningeal glioneuronal tumour (DLGNT). *KIAA1549::BRAF* fusions, while all coding for a fusion protein that includes the activating *BRAF* kinase domain, can be derived from at least nine different fusion site combinations. This makes RT-PCR a difficult method to identify or exclude all variants of the fusion gene. ISH analysis or ddPCR, which demonstrates the tandem duplication at 7q34, is an indirect way to indicate the presence of a *KIAA1549::BRAF* fusion. However, *BRAF* copy number gains due to trisomy 7 or whole 7q gains are common in glioblastomas, IDH-wildtype, and should not be mistaken as circumscribed *BRAF* duplication or *BRAF* fusion.

RNA sequencing can identify all types of *BRAF* and *RAF1* fusion variants in a single experiment. Also, because of its association with a tandem duplication, the presence of a *KIAA1549::BRAF* fusion can often be inferred from the CNV plot as obtained by methylation profiling.⁵⁵

Investigation of *BRAF* alteration is a core element for polymorphous low grade neuroepithelial tumour of the young and ganglioglioma; also, *BRAF* alteration is a frequent cause MAPK pathway activation which is a core element for PA.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 6 – C19MC alterations (Core)*

Demonstration of C19MC (C19MC microRNA cluster) alteration is required for the diagnosis of the most frequent molecular subtype of embryonal tumour with multilayered rosettes (ETMR).⁵⁶ This alteration consists of C19MC amplification or fusion, typically a focal high-level amplicon of chromosome 19q13.42 covering a large, poorly characterised microRNA cluster and the miR-371-373 locus, which map about 100 kb apart. The width and the level of gains at this locus, as assessed by array-comparative genomic hybridisation (array-CGH), are variable but always encompass the same microRNA (miRNA) cluster.

Even in the absence of multilayered rosettes, a CNS embryonal tumour with C19MC alteration is diagnosed as ETMR, C19MC-altered.⁴ In routine neuropathological practice, FISH or chromogenic ISH, or high-resolution cytogenetic techniques (e.g., array-CGH, single nucleotide polymorphism (SNP) arrays, methylation arrays) can be used to detect amplification of the C19MC region.

A small subset of ETMRs carry *DICER1* sequence variants. ETMRs lacking C19MC and *DICER1* alterations are designated as ETMR, NEC (not elsewhere classified), and those that are not tested for these alterations or in which the test results are inconclusive as ETMR, NOS (not otherwise specified).⁴

Investigation of C19MC alteration is a core element for embryonal tumour with multilayered rosettes.

* Only core for some tumours – refer to [Tables 1-3](#).

 **Back**

Note 7 – *CDKN2A/B* deletion (Core)*

Homozygous deletion of the *CDKN2A/B* (cyclin-dependent kinase inhibitor 2A/B; 9p21.3) genes are associated with higher grade diffuse gliomas and have been introduced in the WHO CNS5 Tumour Classification as a marker for CNS WHO grade 4 IDH-mutant astrocytomas.⁴

In addition, *CDKN2A/B* homozygous deletions have been shown to be a characteristic genetic feature in pleomorphic xanthoastrocytomas, occurring in up to 87% of cases in one series. In this situation, along with *BRAF* p.V600E variant, the *CDKN2A/B* homozygous deletions do not connote more aggressive behaviour.⁵⁷

In meningiomas, homozygous deletion of *CDKN2A/B* is associated with aggressive clinical behaviour and has been introduced as a genetic marker for CNS WHO grade 3 in the WHO CNS5 Tumour Classification.

In neuropathological practice, high-resolution cytogenetic and molecular techniques (e.g., array-CGH, SNP arrays, methylation arrays, NGS arrays with copy number plots, ddPCR) can be used to detect homozygous *CDKN2A/B* deletions.

The *CDKN2A* gene encodes the p16 protein, which can be detected using IHC. However, loss of p16 nuclear staining cannot be recommended as a substitute for assessing homozygous *CDKN2A* deletion. In contrast, in one study IHC for MTAP (S-methyl-50-thioadenosinephosphorylase, a product of the *MTAP* gene which is located on chromosome 9p21 in close proximity to the *CDKN2A* and *CDKN2B* loci) was found to show an excellent correlation with *CDKN2A/B* status.⁵⁸

Investigation of *CDKN2A/B* alteration is a core element for astrocytoma, IDH-mutant; diffuse low grade glioma, MAPK pathway-altered; desmoplastic infantile ganglioglioma; and meningioma.

* Only core for some tumours – refer to [Tables 1-3](#).

 **Back**

Note 8 – Chromosomal arm 1p/19q codeletion (Core)*

Whole-arm deletions of chromosome arms 1p and 19q together with *IDH1* (isocitrate dehydrogenase (NADP(+)) 1) or *IDH2* missense variants constitute the diagnostic criteria for oligodendroglioma, IDH-mutant and 1p/19q-codeleted, CNS WHO grades 2 or 3.⁴

Of note, only whole-arm 1p/19q codeletion combined with an IDH missense variant is diagnostically relevant. Partial deletions on either chromosome arm may be found in other types of diffuse gliomas, including IDH-

wildtype glioblastomas, and are neither diagnostic for IDH-mutant and 1p/19q-codeleted oligodendroglial tumours⁴ nor associated with favourable patient outcome.⁵⁹ Moreover, detection of 1p/19q codeletion in the absence of IDH mutation is suspicious of partial deletions which can be encountered in IDH-wildtype glioblastoma.

Various techniques are being used for the diagnostic assessment of 1p/19q codeletion. Commonly used methods include microsatellite analysis for loss of heterozygosity (LOH), FISH or chromogenic ISH (CISH), and multiplex ligation-dependent probe amplification (MLPA), and methylation arrays.

Fluorescence or chromogenic ISH can be applied to routine FFPE sections. However, analysis is often restricted to single loci on each chromosome arm, which may not reliably distinguish whole-arm losses from partial deletions. In addition, polysomies of chromosomes 1 or 19 may complicate diagnostic assessment and have been associated with less favourable outcomes.⁶⁰

Loss of heterozygosity (LOH) analysis and MLPA assess multiple loci along each chromosome arm and thereby reduce the risk of false-positive findings due to partial deletions. However, extraction of tumour DNA (and for LOH ideally also of non-tumour DNA extracted from a blood or buccal swab sample) is required for these techniques.

Microarray-based approaches may also be used for diagnostic purposes, including DNA methylation bead arrays that allow for simultaneous detection of 1p/19q codeletion, *MGMT* promoter methylation, and glioma CpG island methylator phenotype (G-CIMP) status indicative of IDH mutation.⁶¹

Panel-based NGS approaches have been used for 1p/19q detection and simultaneous sequence alteration analyses of *IDH1* and *IDH2*, as well as other alterations commonly associated with 1p/19q codeletion, such as *TERT* promoter and *CIC* variants. In addition, ddPCR approaches based on SNPs on 1p and 19q may be used.

The use of an antibody panel including H3K28me3 (H3K27me3), H3 p.K28M (H3 p.K27M) mutant protein, IDH1 p.R132H,⁶² vimentin, and ATRX,⁶³ has been reported as greatly facilitating recognition of oligodendrogliomas, IDH-mutant and 1p/19q-codeleted. However, these immunohistochemical approaches are not sufficient to substitute for 1p/19q codeletion testing and hence establishing the diagnosis of IDH-mutant and 1p/19q-codeleted oligodendroglioma.

Investigation of 1p/19q alteration is a core element for oligodendroglioma, IDH-mutant and 1p/19q-codeleted as was for astrocytoma, IDH-mutant; investigation of 1p copy number loss is a core element for diffuse leptomeningeal glioneuronal tumour.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 9 – Chromosome 7 gain (combined with chromosome 10 loss) (Core)*

Based on robust evidence in the literature, the Consortium to Inform Molecular and Practical Approaches to CNS Tumour Taxonomy – Not Official WHO (cIMPACT-NOW) update 3 recommended in 2018 the use of combined whole arm chromosome 7 gain and whole arm chromosome 10 loss (+ 7/- 10) as a molecular criterion sufficient for identifying a histologically lower grade appearing (grade 2 or 3) IDH-wildtype diffuse astrocytic glioma, as glioblastoma IDH-wildtype (CNS WHO grade 4), especially in the elderly.⁶⁴ This recommendation has been adopted by the WHO CNS5 Tumour Classification.⁴

Partial gains on chromosome 7 and partial losses on chromosome 10 exhibited a diagnostic and prognostic value similar to that of complete +7 (trisomy 7) or complete -10 (monosomy 10).⁶⁵ Methods to detect the +7/-10 marker include ISH, ddPCR, MLPA, NGS, and array-based techniques including those used for methylome profiling.

Investigation of chromosome 7 gain combined with chromosome 10 loss (+7/-10) is a core element for glioblastoma, IDH-wildtype.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 10 – *CIC* alterations (Core)*

The *CIC* (capicua transcriptional repressor) gene (19q13.2), or rarely *ATNX1/ATNXL1* (ataxin-1; 6p22.3) gene fusion, is currently considered a requirement for the diagnosis of *CIC*-rearranged sarcoma, regardless of whether it arises within the CNS, soft tissue, bone, or viscera. Although originally considered ‘Ewing-like’ or part of the ‘Ewing sarcoma family’ of related undifferentiated round cell sarcomas, it has since been distinguished as a unique tumour type with a significantly worse prognosis than that of Ewing sarcoma.⁶⁶

Potentially useful surrogate immunostains include CD99 (less extensive than Ewing sarcoma), WT1, ETV4, calretinin, MYC, NUT (for *CIC::NUTM1* fusion cases), and DUX4 (for *CIC::DUX4* fusion cases).⁶⁷⁻⁷² However, a definitive diagnosis requires molecular confirmation to detect gene fusions via different techniques, such as ISH, RT-PCR, NGS (RNA or DNA), or anchored multiplex PCR. Methylation profiling may also be diagnostically useful, given that these tumours have a unique cluster that is distinct from other tumour types in the differential diagnosis.

CIC-rearranged and *ATNX1*-rearranged sarcomas of the CNS cluster together with their soft tissue counterparts, suggesting that they are likely the same tumour type despite the differing frequencies of fusion partners.^{71,73} Nevertheless, additional cases need to be studied to confirm this initial impression.

CIC gene alterations are also common in IDH-mutant and 1p/19q-codeleted oligodendrogliomas, although they typically consist in sequence variants in that tumour type.⁷⁴⁻⁷⁶

Investigation of *CIC* alteration is a core element for *CIC*-rearranged sarcoma.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 11 – *DICER1* alterations (Core)*

The *DICER1* (dicer 1, ribonuclease III; 14q32.13) gene encodes the Dicer protein - a ribonuclease (RNase) III endoribonuclease that assists in producing microRNA, which regulates gene expression at the posttranscriptional level. Most sequence variants in this gene lead to an abnormally short DICER protein, which is likely unable to produce miRNA. Without regulation by miRNA, genes may be expressed abnormally, causing cells to grow and divide uncontrollably, leading to tumour formation.

A heterozygous *DICER1* germline variant with low penetrance causes *DICER1* syndrome, a rare autosomal dominant genetic tumour syndrome.⁴ Individuals with such a variant have an increased risk of developing many types of tumours due to the acquisition of a secondary somatic missense variant in *DICER1* in one of the five hotspot codons in the RNase IIIb domain.⁴

Primary intracranial *DICER1*-altered lesions include pineoblastoma, pituitary blastoma, primary intracranial sarcoma, and ETMRs lacking C19MC alteration. These tumours can have overlapping histological features, with primitive mesenchymal differentiation, rhabdomyoblastic and chondroid features, as well as spindle cell patterns.

Identification of a somatic *DICER1* pathogenic variant in tumour tissue may suggest the presence of a germline *DICER1* pathogenic variant.⁴ Identifying a heterozygous germline pathogenic variant in *DICER1* establishes the diagnosis of *DICER1* syndrome. Molecular genetic testing approaches include gene-targeted and more comprehensive genomic testing, such as exome and genome sequencing.

Investigation of *DICER1* alteration is a core element for embryonal tumour with multilayered rosettes; primary intracranial sarcoma, *DICER*-mutant; and pituitary blastoma.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 12 – *EGFR* alterations (Core)*

The *EGFR* (epidermal growth factor receptor; 7p12) gene is the most commonly amplified proto-oncogene in gliomas.⁷⁷ *EGFR* amplification is detectable in approximately 40% of IDH-wildtype glioblastomas (CNS WHO grade 4) and is particularly common in tumours from adult patients with the classic or RTK2 molecular subtype of glioblastoma.^{31,78} Other CNS tumours that may carry *EGFR* amplifications include subsets of paediatric-type high grade glioma, IDH-wildtype and H3-wildtype, and rare instances of diffuse midline glioma, H3 K27-altered.

EGFR amplification is commonly associated with missense variants and genetic rearrangements, the most common of which, *EGFRvIII*, being detectable in about 50% of *EGFR*-amplified glioblastomas.^{79,80} *EGFRvIII* carries a unique peptide encoded by the fusion site of exons 1 and 8 that has served as a tumour-specific epitope for anti-*EGFRvIII* immunotherapy.⁸¹

In adult-type diffuse gliomas, *EGFR* amplification (+/- *EGFRvIII*) is virtually restricted to glioblastoma, IDH-wildtype. The cIMPACT-NOW update 3 recommended in 2018 the use of *EGFR* amplification as a molecular criterion sufficient for identifying a histologically lower grade appearing (grade 2 or 3) IDH-wildtype diffuse astrocytic glioma as glioblastoma, IDH-wildtype (CNS WHO grade 4).⁶⁴ This recommendation has been adopted by the WHO CNS5 Tumour Classification.

Detection of *EGFR* amplification or *EGFRvIII* positivity also may be clinically relevant as a predictive marker of response to molecularly-guided therapies targeting *EGFR* and/or *EGFRvIII*.^{82,83}

EGFR amplification is usually seen in the majority of neoplastic cells in a given tumour and can be readily detected by ISH on routine FFPE tissue sections, although amplification levels may be heterogeneous from cell to cell. Targeted molecular techniques based on extracted tumour DNA, such as RT-PCR and MLPA, are also suitable for diagnostic detection of *EGFR* amplification. Microarray-based genomic or epigenetic analyses, as well as NGS approaches, are increasingly being used.⁸⁴

Gene amplification (defined by a circumscribed high-level copy number gain of the *EGFR* gene at 7p12) needs to be distinguished from low-level copy number gains of chromosome 7 caused by numerical chromosomal abnormalities, in particular trisomy 7, which is a frequent alteration in IDH-wildtype glioblastomas³⁸ (see also **Note 9 – CHROMOSOME 7 GAIN (COMBINED WITH CHROMOSOME 10 LOSS)**). To date, there is no evidence that different levels of *EGFR* gene amplification (e.g., increases in copy number of 10-fold versus 100-fold) have distinct diagnostic or prognostic impact.

Detection of *EGFRvIII* in *EGFR*-amplified glioblastomas can also be performed at the DNA level, e.g., by MLPA, microarray-based techniques and NGS. However, detection at the mRNA or protein level using RT-PCR or IHC with *EGFRvIII*-specific antibodies appears to be more sensitive.⁷⁹ This is due to the fact that *EGFRvIII* positivity usually shows regional heterogeneity and sometimes affects only a minor subset of the tumour cells.⁷⁹ Thus, representative sampling of tumour tissue is an important issue to avoid false-negative testing for *EGFRvIII*. Unfortunately, precise cut-off values for the distinction between high- and low-level copy number gains have not been defined and may need to be adjusted for each testing method.

Investigation of *EGFR* alteration is a core element for glioblastoma, IDH-wildtype; diffuse midline glioma, H3K27-altered; and diffuse paediatric-type high grade glioma, H3- and IDH-wildtype.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 13 – EZHIP expression (IHC) (Core)*

Nuclear overexpression of EZHIP protein (enhancer of zest homologs inhibitory protein; *EZHIP* gene located on Xp11.22) protein results in loss of nuclear H3 p.K28me3 (K27me3) expression in posterior fossa group A (PFA) ependymomas and in a subset of diffuse midline gliomas, H3 K27-altered. In these tumours, the EZHIP protein conformationally mimics the structure of oncogenic H3 p.K28M variants and disrupts the activity of the PRC2 complex.^{85,86} EZHIP overexpression can be demonstrated by antibodies for the EZHIP protein^{87,88} or by RNA expression analysis.

Investigation of EZHIP expression is a core element for diffuse midline glioma, H3K27-altered.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 14 – FET alterations (Core)*

Fusions between members of the FET (nearly always *EWSR1*, but rarely *FUS*) and CREB (*CREB1*, *CREM* or *ATF1*) gene families help define a novel CNS tumour type referred to as intracranial mesenchymal tumour, FET::CREB fusion-positive.^{89,90} Given the histopathologic and genetic overlap with another rare soft tissue tumour type, prior cases have often been diagnosed as angiomatoid fibrous histiocytoma;⁹¹ however, recent methylation profiling studies suggest that these are likely two different entities.⁹⁰

An immunohistochemical profile with combined EMA, CD99, and desmin should raise suspicion for this tumour type, but is not entirely specific.^{89,91} As such, confirmation of a FET::CREB fusion should be attained using various methodologies, including ISH, RT-PCR, NGS (RNA or DNA), and anchored multiplex PCR. Methylation

profiling studies suggest that there may be two distinct epigenetic subtypes with differing clinicopathologic and prognostic associations.⁹⁰ However, further studies are needed to confirm these findings in larger cohorts.

Investigation of FET alteration is a core element for intracranial mesenchymal tumour, FET::CREB fusion-positive; and Ewing sarcoma.

* Only core for some tumours – refer to [Tables 1-3](#).

 **Back**

Note 15 – FGFR family alterations (Core)*

The FGFR (fibroblast growth factor receptor) family comprises four highly conserved transmembrane tyrosine kinase receptors, encoded by *FGFR1* (8p11.23), *FGFR2* (10q26.13), *FGFR3* (4p16.3) and *FGFR4* (5q35.2), and one kinase-lacking core receptor (FGFR5; gene location 4p16.3). These growth factor receptors trigger downstream signalling pathways implicated in tumourigenesis, including the mitogen activated protein kinase (MAPK) pathway and the phosphoinositide-3-kinase (PI3K)/Akt pathways. FGFR plays key roles in CNS development, and in the context of neoplastic transformation it modulates tumour cell migration, differentiation, proliferation, and survival as well as angiogenesis.

FGFR gene alterations involve a broad spectrum of mutational types, such as hotspot point variants, fusions, internal domain duplication (ITD).⁹² They are most commonly found in low grade glial or glioneuronal tumours, and less frequently in high grade gliomas. *FGFR1* hotspot variants are found across multiple tumour types, such as in PA, rosette forming glioneuronal tumour, dysembryoplastic neuroepithelial tumour, occasionally ganglioglioma and the rare diffuse low grade glioma, MAPK pathway-altered.⁹² These hotspot variants have also been described in H3 K27M-altered diffuse midline gliomas and in diffuse gliomas in children and adults.

FGFR1::TACC1 fusions are common in extraventricular neurocytoma. *FGFR2::CTNNA3* fusions are characteristic of polymorphous low grade neuroepithelial tumour of the young.⁹² In IDH-wildtype glioblastomas, *FGFR3::TACC3* fusions are rare events but are associated with distinct morphologic features (e.g., calcification, ‘chicken-wire’ capillaries, and bland oligodendrocyte-like cytology) and a better prognosis;⁹³ they are also mutually exclusive with *EGFR* amplifications.⁹²

Histologically, many tumours with FGFR alterations show neurocytic or oligodendroglioma-like histological features.⁹²

There are no single useful histological or immunohistochemical surrogate markers to detect FGFR alterations. Therefore, the diagnostic approach usually requires a combination of methylome profiling, to narrow down or determine the tumour type (methylation class), and NGS to confirm DNA sequence variants or fusions (e.g., by DNA or RNA NGS, respectively).

FGFR alterations are clinically relevant, not only because of their diagnostic implications, but also because they may represent targets for cancer therapies,^{94,95} although evidence of efficacy in CNS tumours needs further evaluation.¹⁷

Investigation of FGFR alteration is a core element for polymorphous low grade neuroepithelial tumour of the young; and dysembryoplastic neuroepithelial tumour.

* Only core for some tumours – refer to [Tables 1-3](#).

 **Back**

Note 16 – *FOXR2* alterations (Core)*

Fusions accompanied by high levels of expression of the *FOXR2* (forkhead box R2; Xp11.21) gene in a CNS neoplasm with primitive neuroectodermal morphologic features are diagnostic of CNS neuroblastoma, *FOXR2*-activated.

FOXR2 fusions and resulting overexpression are best demonstrated using RNA sequencing techniques. The alterations are most commonly intragenic duplication events involving the *FOXR2* gene, or less commonly, intergenic translocations with non-recurrent partner genes.⁹⁶ Where RNA sequencing is not available, methylome profiling may be used to classify CNS neuroblastoma, *FOXR2*-activated. Surrogate immunohistochemical profiles combined with copy number alterations have also been proposed as sensitive and specific surrogate markers for CNS neuroblastoma, *FOXR2*-activated, namely: OLIG2, synaptophysin and SOX10 immunopositivity; vimentin negativity; and 1q gain.⁹⁷

Investigation of *FOXR2* alteration is a core element for CNS neuroblastoma, *FOXR2*-activated.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 17 – Histone H3 variants and loss of H3 p.K28me3 (K27me3) (Core)*

Various molecular methods can be used to detect the H3 p.K28M (K27M) variant, including pyrosequencing, TaqMan PCR, ddPCR, Sanger sequencing, and NGS. A similar array of methods can be used for H3.3 p.G35 (G34) variants; however, due to the GC rich nature of this region, targeted methods can be more difficult to design. For detection of both variants using targeted methods (and alignment of non-targeted methods), consideration needs to be given to the high degree of homology among the H3 genes (human H3 variants include H3.3, H3.1, H3.2, CENP-A, H3t, H3.X and H3.Y) and the number of genes encoding each protein (H3.3 is encoded by two genes, *H3F3A* and *H3F3B*, while H3.1 and H3.2 are each encoded by multiple genes found within gene clusters). The exact gene being tested, and the method used should be provided in the report. In addition, variant-specific antibodies are available that can reliably be used on FFPE tissue to detect H3 p.K28M (K27M), H3 p.G35R (G34R) and H3 p.G35V (G34V) variants. Of note, according to the recently revised nomenclature of (human) histone genes *H3F3A* (1q42.12) is now *H3-3A*, and *H3F3B* (17q25.1) is now *H3-3B*.⁹⁸

Histone H3 p.K28M (K27M) variant (sequencing) and expression (immunohistochemistry)

Recurrent sequence variants in *H3-3A* (H3.3) or *H3C2/3/11* (H3.1) are characteristic of diffuse midline gliomas, H3K27-altered. Very rarely *H3C14* (H3.2), with lysine 28 (27) substituted for methionine (H3 p.K28M (K27M)) or isoleucine (H2 p.K27I) also indicate diffuse midline glioma, H3 K27-altered.

These tumours can arise across a broad spectrum of ages and midline locations, including older adults, but are most frequently encountered in the paediatric age group in the pons. In teenagers and young adults, non-pontine locations are more frequent, including the spinal cord, thalamus and cerebellum.⁹⁹ These tumours overall have a poor prognosis (median survival approximately 12 months) with older age at presentation and receipt of radiotherapy associated with modestly better survival.

The H3 p.K27M variant can also be found in diffuse astrocytomas without classic high grade features that generally behave more aggressively than their wild type counterparts. In occasional cases, this variant has been found in other tumour types, including ganglioglioma, PA and ependymoma. The outcome for patients with

circumscribed low grade gliomas with H3 p.K27M variants is worse than their wildtype counterparts. Data on a small number of cases shows no outcome difference between PFA ependymomas with and without the H3 K27M variant, however.¹⁰⁰⁻¹⁰²

Testing for this alteration should be considered, in patients with midline diffuse gliomas. These alterations can be identified by sequencing or a variant-specific antibody. Detection of the variant by either IHC or sequencing is required for the diagnosis of the H3 p.K27M mutant subtypes of diffuse midline glioma, H3 K27-altered. Lack of H3 K27me3 is not a specific marker for H3 p.K27M.

Immunohistochemistry (IHC) with an antibody against the N-terminus of the mutant protein is highly sensitive and specific for detection of the H3 p.K28M (K27M) protein from either H3.3 or H3.1. In practice, the antibody can produce a fair amount of background cytoplasmic staining in non-tumour cells and only diffuse strong nuclear staining in most (or all) tumour cells should be considered positive. Further, poorly fixed tissue or tissue from post-mortem or older blocks may be false negative. If equivocal, a molecular method should be considered as the standard of care.

Histone H3 p.G35R (G34R) or p.G35V (G34V) variants (sequencing) and expression (immunohistochemistry)

Recurrent variants in *H3-3A* (H3.3) with glycine 35 substituted for arginine (H3 p.G35R) or infrequently valine (H3 p.G35V) are found most commonly in diffuse hemispheric high grade gliomas of the adolescent and young adult population.⁴ The H3 p.G35R variant is found in approximately 15-20% of hemispheric high grade glioma cases in the paediatric age group.¹⁰³ Testing for this alteration should be considered, in hemispheric, IDH-wildtype, high grade gliomas, particularly if *ATRX* is lost and *p53* is diffusely immunopositive. These alterations can be identified by sequencing, PCR or variant-specific antibodies against H3.3 p.G35R or H3.3 p.G35V.

In practice, the antibody works well for IHC on FFPE tissue with specific nuclear staining but does not stain all tumour cells; as a result, sensitivity may be an issue. If IHC results are equivocal or if suspicion for an H3 p.G35R/V variant is high, a molecular method should be considered as the standard of care.

Loss of H3 p.K28me3 (H3 K27me3) expression (immunohistochemistry)

The presence of the H3 p.K28M (K27M) mutant protein is associated with a fairly widespread (and thus detectable on Western blot or IHC) loss of the repressive trimethyl (me3) mark on H3 lysine 28 (H3 p.K28me3), often written as H3K27me3 when referring to the protein or antibody. Tumour cells harbouring the H3 p.K28M variant (either H3.1 or H3.3 p.K28M) will typically show loss of nuclear expression of H3K27me3 on IHC with retention of staining in entrapped non-neoplastic cells, e.g., endothelial cells (similar to the pattern seen with *ATRX* or *INI1*). However, it should be noted that while loss of H3K27me3 is sensitive for detection of H3 p.K27M variant tumours, it is not specific.

Other tumours, notably malignant peripheral nerve sheath tumours and PFA ependymomas,¹⁰⁴ will also show loss of H3 K27me3. In fact, this lack of nuclear H3 K27me3 immunoreactivity is considered an essential diagnostic criterion for PFA ependymomas.^{88,104,105}

Similarly, in some H3-wildtype cases, partial loss may be seen. Thus, while helpful for confirmation when combined with an H3 p.K27M stain, loss of H3K27me3 staining by itself should be considered a non-specific surrogate marker for identifying H3 p.K27M-mutant diffuse midline gliomas.

In non-H3 p.K27M-mutant subtypes of diffuse midline glioma, H3K27me3 is typically lost in combination with either *EZH1* overexpression or an *EGFR* gene alteration.

Investigation of histone H3 variants and/or of H3 p.K28me3 alteration is a core element for glioblastoma, IDH-wildtype; diffuse astrocytoma, *MYB*- or *MYBL1*-altered; diffuse low grade glioma, MAPK pathway-altered;

diffuse midline glioma, H3K27-altered; diffuse hemispheric glioma, H3G34-mutant; diffuse paediatric-type high grade glioma, H3- and IDH-wildtype; and posterior fossa ependymoma, group A.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 18 – *IDH1/IDH2* alterations (Core)*

IDH (isocitrate dehydrogenase) is an enzyme that exists in five isoforms, each of which catalyses the reaction of isocitrate to α -ketoglutarate. Hotspot missense variants in *IDH1* (2q34) or *IDH2* (15q26.1) diagnostic markers for astrocytomas, IDH-mutant, CNS WHO grades 2-4 and oligodendroglioma, IDH-mutant and 1p/19q-codeleted, CNS WHO grade 2 or 3.⁴

The mutant IDH1 and IDH2 proteins lead to the production of the oncometabolite 2-hydroxyglutarate, which inhibits the function of numerous α -ketoglutarate-dependent enzymes. Inhibition of the family of histone demethylases and the ten-eleven translocation (TET) family of 5-methylcytosine hydroxylases has profound effects on the epigenetic status of mutated cells and leads to G-CIMP.

IDH2 variants are much less frequent than *IDH1* variants in diffuse gliomas, but are enriched in IDH-mutant and 1p/19q-codeleted oligodendrogliomas and in infratentorial IDH-mutant astrocytomas.¹⁰⁶

A monoclonal antibody has been developed to the IDH1 p.R132H protein that allows for the detection of the most common type of IDH variant by IHC. The ability of the antibody to detect individual IDH R132H-mutant cells within a normal background (e.g., in the infiltration zone of an IDH-mutant diffuse glioma), makes this method more sensitive than Sanger sequencing for identifying p.R132H-mutant gliomas.¹⁰⁷ However, *IDH2* variants and other less common *IDH1* variants cannot be detected using IHC with this antibody, and in the appropriate clinical setting, it may be necessary to test for other *IDH1* and *IDH2* variants by sequencing analysis. The WHO CNS5 Classification recommends that sequencing may not be warranted in the setting of a negative p.R132H immunostain in glioblastomas arising in patients older than 55 years due to the rarity of non-R132H *IDH1* and *IDH2* variants in patients in this age group.¹⁰⁸ By contrast, all diffusely infiltrating gliomas with CNS WHO grade 2 and 3 histology that lack IDH1 p.R132H positivity by IHC should be assessed for less common *IDH1* or *IDH2* variants by sequencing or other appropriate methods. Methylome profiling does not detect an *IDH1* or *IDH2* oncogenic variant as such, but the DNA methylome ‘fingerprint’ is a very reliable surrogate marker for IDH-mutant status of diffuse gliomas.¹⁰

Investigation of IDH alteration is a core element for astrocytoma, IDH-mutant; oligodendroglioma, IDH-mutant and 1p/19q-co-deleted; glioblastoma, IDH-wildtype; diffuse astrocytoma, *MYB*- or *MYBL1*-altered; polymorphous low grade neuroepithelial tumour of the young; diffuse low grade glioma, MAPK pathway-altered; diffuse paediatric-type high grade glioma, H3- and IDH-wildtype; and extraventricular neurocytoma.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 19 – MAPK pathway alterations (Core)*

The MAPK (mitogen-activated protein kinase) signalling pathway is a complex cellular signalling system involved in regulating a wide variety of cellular processes, including cell growth, differentiation, apoptosis, and response to stress. The pathway translates a diverse range of extracellular stimuli - including growth factors, cytokines, and environmental stressors - into cellular responses.

Different mechanisms can lead to dysregulation of the MAPK pathway in cancer. One common mechanism is the activation of growth factor receptors, which can stimulate MAPK pathway activation through various downstream signalling molecules. Genetic alterations in the MAPK pathway genes, such as *BRAF*, *NRAS*, *KRAS* and *NF1*, can also lead to hyperactivation and contribute to cancer development.

The MAPK pathway is frequently dysregulated in gliomas,⁴ and this dysregulation is associated with increased proliferation and reduced apoptosis, leading to tumour growth and progression. The activation of the MAPK pathway is often driven by alterations in genes encoding the BRAF protein or the NF1 protein.

The importance of the MAPK pathway in cancer has led to the development of targeted therapies that inhibit its activity. Drugs inhibiting BRAF and/or MEK signalling, two critical components of the pathway, have been approved for treating melanoma and other cancers, including gliomas. However, resistance to these drugs can develop, highlighting the need for continued research into the complex mechanisms that regulate MAPK pathway activity in CNS tumours.

Investigation of MAPK pathway alteration is a core element for polymorphous low grade neuroepithelial tumour of the young; diffuse low grade glioma, MAPK pathway-altered; PA; ganglioglioma; and diffuse leptomeningeal glioneuronal tumour.

* Only core for some tumours – refer to [Tables 1-3](#).

↑ [Back](#)

Note 20 – Methylome profiling (Core)*

The categorisation of CNS tumours based on their genome-wide methylome profiles greatly aids their precise classification,¹⁰⁹ often in combination with the DNA copy number profile derived from the same array.¹¹⁰

Methylome profiling can:

1. establish a methylation class (often a surrogate for a diagnosis) for most CNS tumour types including histologically ambiguous CNS tumours of both adult and paediatric patients;
2. provide a detailed whole genome CNV profile;
3. subclassify or risk stratify established tumour types, such as ependymomas, medulloblastomas, or meningiomas based on their methylation fingerprint +/- CNV alterations; and
4. provide information on *MGMT* promoter methylation status.

Methylome profiling can also be useful as a diagnostic tool for very small biopsies. CNS tumours classified on the basis of their methylome profile generally behave clinically more homogeneously than those classified by histology alone.

The determination to perform methylation profiling depends on (i) local availability or access to supra-regional centres, (ii) availability of funding in the respective healthcare system, (iii) ability/knowledge to integrate data

by a neuropathologist, as well as (iv) clinical need and relevance to therapy (e.g., risk prognostication of meningiomas).

The technology used for methylome-based tumour classification is currently mainly based on hybridisation of bead chip arrays from a single supplier. However, other approaches, such as long-read sequencing have been established.¹¹¹ The processing of the methylation data requires a classification tool, and currently the gold standard for the diagnostic implementation is the DKFZ/Heidelberg classifier for CNS tumours (www.moleculareuropathology.org),¹⁰⁹ although alternatives based on the same principle have been established to address accreditation issues or to refine classification.¹¹²

The implementation and acceptance of this technology has substantially empowered the neuropathology community by enabling more accurate, reliable, and reproducible diagnoses. Thus, DNA methylome-based classification has been widely introduced as a diagnostic tool in the WHO CNS5 Tumour Classification.¹¹³ In fact, unequivocal classification of certain tumour types, such as high grade astrocytoma with piloid features and paediatric-type high grade diffuse gliomas IDH-wildtype and H3-wildtype, require the demonstration of a tumour type-specific methylome profile.¹¹³

The use of the DNA methylome classifier requires caution and awareness of potential pitfalls.¹¹² Technical and operational risks include recognition of sample mix-up, low DNA amount and poor quality DNA. It is recommended to process reasonably distinct tumour entities on each chip (currently eight samples per chip), and results that cannot be reconciled with patient sex, histology, location, or clinical presentation may require repeat investigation. Interpretational pitfalls arise from incorrect classification results, due to low tumour content, e.g., admixture of CNS tissue, inflammatory cells, tumour recurrences/post-radiotherapy, and tumours arising in genetic tumour syndromes.

Generally, low grade glial and glioneuronal tumours can be difficult to classify with the current algorithms.²⁷ The DKFZ/Heidelberg classifier uses calibrated classifier scores to indicate likelihood of the assignment of a tumour to a distinct methylation class,¹⁰⁹ with classifier scores >0.9 indicating a significant match. Lower calibrated classifier scores need to be interpreted with caution and may not be reliable indicators of a certain diagnosis but can still provide useful guidance when integrated with results from orthogonal tests.^{109,112}

Copy number variations (CNV) are returned as part of the readout from the methylation array (or from long-read whole genome sequencing), and can complement the diagnosis, provide additional confidence in establishing a diagnosis when the methylome profile is returned with a low calibrated score,¹¹⁰ or form part of a prognostication algorithm, such as in meningiomas.¹¹⁴ Therefore, CNVs (including specific gene deletions or amplifications) should also be included in the report if diagnostically relevant. Gene duplication and/or gene fusions can sometimes also be inferred from the plot but may need confirmation by other methods. Low amplitudes of CNVs may indicate low tumour cell content or clonal heterogeneity in the investigated tissue sample.

No specific formal recommendations exist currently for how methylome data should be reported. It has been suggested that pathology reports should contain information on:

1. estimated tumour cell content of the extracted DNA;
2. amount of DNA input;
3. estimated tumour cell fraction;
4. quality of bisulphite conversion;
5. CNS tumour classifier version(s) used;
6. highest scoring methylation category with the respective calibrated score(s); and
7. sub-classification with score(s), if applicable.¹⁰

In addition to the DNA copy number profile and assignment to distinct methylation families, classes and subclasses - the DKFZ/Heidelberg classifier provides the *MGMT* promoter methylation status based on a specific algorithm.¹¹⁵ Generally, there is good concordance with other methods of targeted assessment of *MGMT* promoter methylation.^{116,117} However, there is currently no consensus as to which testing method best predicts response to alkylating agent chemotherapy.¹¹⁸

Methylome profiling (MP) is a core element (especially for unresolved lesions) for diffuse astrocytoma, *MYB*- or *MYBL1*-altered; diffuse midline glioma, H3K27-altered; diffuse hemispheric glioma, H3G34-mutant; diffuse paediatric-type high grade glioma, H3- and IDH-wildtype; infant-type hemispheric glioma; high grade astrocytoma with piloid features; astroblastoma, *MN1*-altered; ganglioglioma; desmoplastic infantile ganglioglioma; dysembryoplastic neuroepithelial tumour; diffuse glioneuronal tumour with oligodendroglioma-like features and nuclear clusters; papillary glioneuronal tumour; rosette-forming glioneuronal tumour; diffuse leptomeningeal glioneuronal tumour; central neurocytoma; extraventricular neurocytoma; cerebellar liponeurocytoma; posterior fossa ependymoma, group A; posterior fossa ependymoma, group B; myxopapillary ependymoma; subependymoma; medulloblastoma, WNT-activated; medulloblastoma, SHH-activated and *TP53*-wildtype; medulloblastoma, SHH-activated and *TP53*-mutant; medulloblastoma, non-WNT/non-SHH; atypical teratoid/rhabdoid tumour; embryonal tumour with multilayered rosettes; CNS neuroblastoma, *FOXR2*-activated; CNS tumour with *BCOR* internal tandem duplication; malignant melanotic nerve sheath tumour; malignant peripheral nerve sheath tumour; cauda equina neuroendocrine tumour; meningioma; pineal parenchymal tumour of intermediate differentiation; papillary tumour of the pineal region; and desmoplastic myxoid tumour of the pineal region, *SMARCB1*-mutant.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 21 – *MN1* alterations (Core)*

According to the WHO CNS5 Tumour Classification, demonstration of an *MN1* (meningioma 1; 22q12.1) gene alteration is required for the diagnosis of astroblastoma, *MN1*-altered.⁴ These rare glial neoplasms have a strong female predominance and are characterised by relatively compact growth, predominantly perivascular tumour cell arrangement (astroblastic rosette) and perivascular fibrous stroma.

Fusions between *MN1* (22q12.1) and BEN domain containing 2 (*BEND2*; Xp22.13) or more rarely with *CXXC5* (*CXXC*-type zinc finger protein 5) are characteristic. *MN1* is a transcriptional coregulator important in development and is implicated in the pathogenesis of meningioma and acute myeloid leukemia.^{119,120}

Astroblastomas, *MN1*-altered display a distinct DNA methylome profile. Tumours with astroblastoma-like histology and DNA methylome profile, often located in the spinal cord, have been identified which lack *MN1* fusions but feature *BEND2* fusions, in particular *EWSR1::BEND2* or *MAMLD1::BEND2*. These tumours likely represent a molecular subtype of astroblastoma, however, have not yet been considered in the WHO CNS5 classification.

Molecular studies are necessary to evaluate for characteristic *MN1* or *BEND2* fusions by break apart ISH, PCR, RNA or DNA sequencing.

Nuclear *MN1* immunoreactivity has been described in *MN1::BEND2* tumours but not in non-*MN1::BEND2* astroblastomas.¹²¹ However, the specificity and sensitivity of this biomarker remains to be evaluated.

Investigation of *MN1* alteration is a core element for astroblastoma, *MN1*-altered.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 22 – *MYB*, *MYBL1* alterations (Core)*

MYB (v-myb avian myeloblastosis viral oncogene homolog; 6q23.3) and *MYBL1* (8q13.1) rearrangements, most commonly gene fusions of *MYB* or *MYBL1* with various partner genes, are diagnostic alterations in diffuse astrocytoma, *MYB/MYBL1*-altered and in angiocentric glioma, with the latter typically featuring *QKI::MYB* fusions.^{113,122} *MYB* gene amplification is rare.^{123,124}

Diagnostic detection of *MYB* or *MYBL1* fusions can be performed by targeted next generation fusion panel sequencing or by whole transcriptome sequencing. Alternatively, *MYB/MYBL1* alterations can be detected by using interphase ISH. DNA methylome analysis also identifies gliomas with *MYB* or *MYBL1* alterations but cannot distinguish between diffuse astrocytoma, *MYB/MYBL1*-altered versus angiocentric glioma.^{123,125}

Investigation of *MYB* or *MYBL1* alteration is a core element for diffuse astrocytoma, *MYB*- or *MYBL1*-altered.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 23 – *MYC* gene family amplification (*MYC* and/or *MYCN*) (Core)*

The *MYC* (v-myc avian myelocytomatosis viral oncogene homolog; 8q24.21) protein has a fundamental role in cell proliferation, cell size, differentiation, stem cell self-renewal, and apoptosis. Its deregulation occurs in many cancers including a range of CNS tumours. The *MYC* transcription factor family also includes its paralogues *MYCN* and *MYCL*.¹²⁶

MYC, *MYCN*, and *MYCL* amplifications are prognostically relevant in medulloblastomas.¹²⁷ *MYC* and *MYCN* gene amplification and fusions are seen in SHH-activated and in non-WNT/non-SHH medulloblastomas, but almost never in the WNT-activated type.^{127,128} Furthermore, *MYCN*-amplification is listed in the WHO CNS5 Tumour Classification as an essential diagnostic criterion for spinal ependymoma, *MYCN*-amplified.⁴ Rarely, such aggressive spinal ependymomas may show amplification of *MYC*.¹²⁹

A commonly used laboratory method to detect *MYC* gene family amplifications is FISH or CISH. Other approaches include RT-PCR, ddPCR, NGS, MLPA, or array technologies.

Investigation of *MYC* or *MYCN* alteration is a core element for diffuse paediatric-type high grade glioma, H3- and IDH-wildtype; and spinal ependymoma, *MYCN*-amplified.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 24 – *PDGFRA* alterations (Core)*

PDGFRA (platelet-derived growth factor receptor, alpha polypeptide; 4q12) gene alterations have been described in several CNS tumour types, including low grade and high grade gliomas as well as glioneuronal tumours. These alterations include gains/amplifications and/or DNA sequence variants of *PDGFRA*.

PDGFRA amplifications and/or sequence alterations are found in variable frequency in both paediatric-type and adult-type high grade gliomas, including:

- diffuse paediatric-type high grade gliomas, H3-wildtype and IDH-wildtype;¹³⁰
- diffuse midline gliomas, H3 K27-altered;¹³¹
- diffuse hemispheric gliomas, H3 G34-mutant;¹³²
- glioblastomas, IDH-wildtype;¹³³ and
- astrocytomas, IDH-mutant (roughly a third of the CNS WHO grade 4 tumours);¹³⁴ and
- myxoid glioneuronal tumour, (within the right context) dinucleotide mutation in *PDGFRA* resulting in p.K385L (or p.K385I) being diagnostic for this diagnosis.¹³⁵⁻¹³⁷

Investigation of *PDGFRA* alteration is a core element for diffuse paediatric-type high grade glioma, H3- and IDH-wildtype.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 25 – Pituitary hormones and transcription factors immunohistochemistry (Core)*

Standard IHC evaluation of pituitary neuroendocrine tumours/pituitary adenomas can include immunostaining for specific anterior pituitary hormones (prolactin, growth hormone, follicle stimulating hormone, luteinising hormone, thyroid stimulating hormone, alpha-subunit of glycoproteins, adrenocorticotrophic hormone (PRL, GH, FSH, LH, TSH, ASU, ACTH, respectively) and pituitary transcription factors (PIT1, TPIT, SF1).^{138,139} Other transcriptions factors, including GATA3 and ER α , may be useful in certain instances.¹³⁸ Practical suggestions for evidence-based IHC workup have been published by McDonald (2024).¹⁴⁰

Immunohistochemistry (IHC) for these proteins, coupled with cytokeratin (AE1/AE3 or CAM5.2) staining, for presence or absence of rounded cytoplasmic inclusions known as fibrous bodies, allows classification of pituitary tumours/pituitary adenomas for prognosis and medical treatment purposes.

For diagnostic purposes, some advocate first screening with three antibodies (PIT1, SF1, and TPIT) and then using the other anterior pituitary hormone assays based on initial results.¹⁴¹⁻¹⁴³ Others utilise the full panel initially and may variably supplement the panel.¹⁴⁴ The proliferation-associated marker Ki-67 (MIB1) is used for evaluation of the proliferative potential of tumours.^{138,144} There appears to be little utility for p53 IHC, with rare exceptions, such as corticotroph tumours/adenomas.^{138,145,146}

The WHO 5th edition CNS⁴ and Endocrine¹⁴⁷ Classification systems note that: “Special tumour/adenoma subtypes that commonly show aggressive behaviour...include sparsely granulated somatotroph tumour/adenoma, lactotroph tumours/adenomas in men, Crooke cell tumour/adenoma and silent corticotroph tumour/adenoma, and immature PIT1-lineage adenoma (previously called ‘silent subtype 3 adenoma’).”

For tumours of the posterior pituitary gland (granular cell tumour of the sellar region, pituicytoma, spindle cell oncocytoma), nuclear staining for the transcription factor TTF1 is used as a diagnostic marker.¹⁴⁸

Investigation of pituitary hormones and transcription factors by IHC is a core element for pituicytoma; granular cell tumour of the sellar region; spindle cell oncocytoma; and pituitary adenoma/pituitary neuroendocrine tumour.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 26 – PRC2 alteration (Core)*

PRC2 (polycomb Repressive Complex 2) is an epigenetic regulator that is frequently inactivated in malignant peripheral nerve sheath tumours (MPNSTs).

In MPNSTs, loss-of-function genetic alterations or epigenetic silencing of PRC2 components, such as EZH2 (Enhancer of Zeste Homolog 2) or SUZ12 (Suppressor of Zeste 12), results in reduced H3K27me3 levels at target gene promoters. Consequently, this dysregulation leads to the activation of genes promoting tumour progression.

H3K27me3 loss has been shown to be a relatively specific marker for MPNSTs and may be helpful in the differential diagnosis to distinguish MPNSTs from histologic mimics, especially when supportive Schwann cell markers are absent.¹⁴⁹

Components of the PRC2 complex, such as EZH2, represent therapeutic targets undergoing clinical trials and further research.

Investigation of PRC2 alteration is a core element for malignant peripheral nerve sheath tumour.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 27 – PRKAR1A alteration (Core)*

PRKAR1A (protein kinase, cAMP-dependent, regulatory, type I, alpha; 17q24.2) encodes the regulatory subunit of cyclic AMP-dependent protein kinase A (PKA) and is associated with Carney complex, a syndrome characterised by an increased risk of several types of tumours, including malignant melanotic nerve sheath tumours. These nerve sheath tumours demonstrate frequent loss of function alterations in *PRKAR1A*.¹⁵⁰ *PRKAR1A* alterations can be in the form of single base pair substitutions, deletions and insertions, or rearrangements.

Loss of PRKAR1A expression can also be detected using IHC.

Investigation of *PRKAR1A* alteration is a core element for malignant melanotic nerve sheath tumour.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 28 – PRKCA alteration (Core)*

PRKCA (protein kinase C alpha; 17q24.2) encodes a protein kinase involved in cellular signalling pathways related to proliferation and differentiation. *PRKCA* alterations, including gene rearrangements, are diagnostic for papillary glioneuronal tumours,¹⁵¹ which can be challenging to classify and thus are an essential WHO criterium for these tumours.⁴

In addition, the hotspot *PRKCA* missense variant p.D463H is highly specific for chordoid gliomas and is considered a desirable diagnostic WHO criterium for these tumours.⁴

Investigation of *PRKCA* alteration is a core element for papillary glioneuronal tumour.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 29 – SHH pathway alterations (Core)*

About 30% of all medulloblastomas are characterised by SHH (sonic hedgehog) pathway activation, caused by genetic alterations in *PTCH1*, *SUFU*, *SMO*, or other genes encoding components of the SHH signalling pathway.

In SHH-activated medulloblastomas, the *TP53* status needs to be assessed for a precise diagnosis as this group encompasses two very different disease entities. *TP53*-wildtype SHH-activated medulloblastomas occur mostly in adolescents/adults and young children and are associated with a favourable prognosis if adequately treated. In contrast, *TP53*-mutant SHH-activated medulloblastomas typically occur in older children and have a dismal prognosis.

A substantial subset of the SHH-activated medulloblastomas has the desmoplastic/nodular (D/N) phenotype and a small minority concerns medulloblastomas with extensive nodularity. The large cell/anaplastic (LC/A) phenotype is relatively frequent in the group of *TP53*-mutant SHH-activated medulloblastomas.

SHH activation can reliably be assessed by immunohistochemical cytoplasmatic staining for the SHH target proteins GAB1 and p75NGFR. Furthermore, these medulloblastomas share expression of nuclear YAP1 with WNT-activated medulloblastomas but lack OTX2 expression as well as nuclear accumulation of β -catenin protein. DNA methylation and mRNA expression profiles can be used for detecting SHH-activated medulloblastomas as well. As germline alterations are relatively frequent in patients with SHH-activated medulloblastoma, patients with this tumour requires genetic counselling.

The canonical inherited syndrome associated with *TP53*-wildtype SHH-activated medulloblastoma is naevoid basal cell carcinoma (Gorlin) syndrome, which is mostly due to inactivating germline alterations in *PTCH1* (9q22.32; encoding the receptor for the SHH protein), and more rarely due to a *SUFU* (10q24.32) or *PTCH2* (1p34.1) mutation. Germline alterations in *ELP1* (9q31.3) and in *GPR161* (1q24.2) have also been reported in SHH-activated medulloblastomas. More than half of the patients with a SHH-activated and *TP53*-mutant medulloblastomas have germline rather than somatic *TP53* alterations (Li-Fraumeni syndrome).

Widespread and strong immunohistochemical staining for p53 in an SHH-activated medulloblastomas strongly indicates a *TP53*-mutant tumour. Most of these tumours show cytological anaplasia, at least focally. Ideally, because of the important consequences for treatment decisions and possible germ line alterations, SHH-activated tumours should be sequenced for presence/absence of *TP53* (17p13.1) alterations.^{4,152-155}

Non-WNT/non-SHH medulloblastomas express OTX2 but lack staining of tumour cells for YAP1, GAB1, p75NGFR and nuclear β -catenin. Also, non-WNT/non-SHH medulloblastomas are generally not associated with genetic tumour syndromes (only rare cases have been reported in individuals with a germline alteration in *CREBBP* (Rubinstein–Taybi syndrome) or in the DNA repair genes *PALB2* (16p12.2) or *BRCA2* (13q13.1)).¹⁵³

Investigation of SHH pathway alteration is a core element for medulloblastoma, SHH-activated and *TP53*-wildtype; medulloblastoma, SHH-activated and *TP53*-mutant; and medulloblastoma, non-WNT/non-SHH.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 30 – SMARC family alterations (Core)*

Atypical teratoid/rhabdoid tumour (AT/RT) is defined as a CNS embryonal tumour that frequently (but not invariably) contains rhabdoid cells and demonstrates inactivation of the SMARC (SWI/SNF related, matrix associated, actin dependent regulator of chromatin) genes *SMARCB1* (INI1) or *SMARCA4* (BRG1).

SMARCB1/INI1/SNF5 alterations

Inactivation of the *SMARCB1* (*INI1*, *BAF47*, *SNF5*) gene (22q11.23) is present in almost all cases of AT/RT, resulting in nuclear loss of SMARCB1 protein which can be evaluated by IHC. Genetic aberrations of the *SMARCB1* locus may include homozygous or heterozygous deletions and a variety of coding sequence variants, leading to inactivation of both alleles. However, genetic testing is usually not required for making the diagnosis of AT/RT because IHC is highly sensitive.

Since SMARCB1 is a constitutively expressed protein, IHC staining for SMARCB1 in the nuclei of non-neoplastic cells (such as vascular and inflammatory cells) serves as an internal positive control. Some AT/RTs with nuclear loss of SMARCB1 exhibit cytoplasmic staining, possibly representing dysfunctional truncated protein.

In tumours with histological features of AT/RTs but without demonstration of *SMARCB1* or *SMARCA4* alterations, a diagnosis of 'CNS embryonal tumour with rhabdoid features, NEC' can be made.

A variety of other tumour types that involve the nervous system may exhibit loss of nuclear SMARCB1, including cribriform neuroepithelial tumour, poorly differentiated chordoma, rhabdoid tumour of the sellar region, myxoid meningeal tumours, and sinonasal carcinoma.⁴ The molecular and nosologic relationship of these tumours to AT/RT is unclear. Furthermore, complete or incomplete (reduced, mosaic) loss of nuclear SMARCB1 protein expression has been found in some cases of choroid plexus carcinoma, synovial sarcoma, epithelioid schwannoma, and schwannoma associated with schwannomatosis.

SMARCA4/BRG1 alterations

The *SMARCA4* gene (19p13.2) encodes the transcription activator BRG1, also known as adenosine triphosphate (ATP)-dependent chromatin remodeller SMARCA4. AT/RTs with *SMARCA4* alterations are extremely rare. Loss of BRG1 expression (and retention of INI1 expression) in these tumours can be readily demonstrated by IHC. Associated genetic alterations of *SMARCA4*, whether copy number alterations or mutations, can be detected by a variety of array or sequencing methods.

Investigation of SMARC alteration is a core element for atypical teratoid/rhabdoid tumour; cribriform neuroepithelial tumour; poorly differentiated chordoma; and desmoplastic myxoid tumour of the pineal region, *SMARCB1*-mutant.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 31 – STAT6 alterations (Core)*

In-frame *NAB2::STAT6* gene fusions result from chromosome 12q13 inversions and represent highly sensitive and specific signature alterations of meningeal solitary fibrous tumours (SFT) of grade 1, 2, or 3. These fusions are also characteristic of the analogous soft tissue/extracranial counterparts.

STAT6 (signal transducer and activator of transcription 6) staining of tumour cell nuclei is a highly reliable and practical surrogate for detecting this signature alteration, with nearly 100% sensitivity and specificity regardless of the fusion variant,^{156,157} and is listed as essential diagnostic criterion for SFT in the WHO CNS5 Tumour Classification.⁴

***NAB2::STAT6* gene fusion**

NAB2::STAT6 gene fusions are detectable using RT-PCR, ISH or various sequencing techniques, including NGS if designed appropriately.^{156,158} Over 40 fusion variants have been detected to date, with the most common meningeal SFT-associated fusions bringing together exon 6 of *NAB2* (NGFI-A-binding protein 2; 2q13.3) with exons 16, 17, or 18 of *STAT6* (2q13.3) in approximately half of all cases.¹⁵⁸

STAT6 nuclear expression (immunohistochemistry)

The STAT6 protein is normally expressed in the cytoplasm of cells, whereas *NAB2* is expressed in nuclei; however, the *NAB2::STAT6* fusions cause the STAT6 protein to translocate to the nucleus. Nearly all meningeal and extracranial SFTs display strong and extensive/diffuse nuclear positivity, whereas other diagnostic considerations, such as meningiomas, nerve sheath tumours, and various sarcomas, either lack expression or show only cytoplasmic staining. As such, the pathologist is cautioned against rendering a diagnosis of SFT in the absence of nuclear STAT6 immunoreactivity.

Investigation of STAT6 alteration is a core element for solitary fibrous tumour.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 32 – *TERT* promoter alterations (Core)*

The *TERT* (telomerase reverse transcriptase; 5p15.33) gene encodes a major component of the protein complex telomerase and contributes to maintaining telomere length. Sequence variants in the *TERT* promoter create new binding sites for erythroblast transformation specific transcription factors and subsequently increase expression and activity of telomerase.

TERT promoter variants are detectable in the majority of glioblastomas, IDH-wildtype and of oligodendrogliomas, IDH-mutant and 1p/19q-codeleted, but are typically absent in astrocytomas, IDH-mutant.^{159,160}

In 2018, cIMPACT-NOW update 3 recommended the use of *TERT* promoter alteration as a molecular criterion for identifying a histologically lower grade appearing (grade 2 or 3) IDH-wildtype, adult-type diffuse astrocytic glioma as glioblastoma, IDH-wildtype (CNS WHO grade 4).⁶⁴ This recommendation has been adopted by the WHO CNS5 Tumour Classification.⁴ However, others have suggested using caution when assimilating IDH-wildtype, histologically grade 2 gliomas to ‘molecular glioblastomas’ in case of ‘isolated *TERT* promoter mutation’ (lacking *EGFR* amplification as well as combined gain of whole chromosome 7 and loss of whole chromosome 10).^{161,162} DNA methylome profiling and NGS may substantiate the diagnosis in such cases by demonstrating methylome profiles and additional genetic alterations of IDH-wildtype glioblastoma.

Approximately 20% of medulloblastomas carry *TERT* promoter alterations, and they are more common in adult patients and in the SHH-activated molecular type.¹⁵⁹ In meningiomas, *TERT* promoter alterations have been found in 6% of tumours where they represent a marker of poor prognosis and according to the WHO CNS5

Tumour Classification can be used to assign a CNS WHO grade 3.¹⁶³ Approximately 50% of SFTs carry a *TERT* promoter alteration while other tumours of the CNS only uncommonly exhibit these alterations.¹⁵⁹

Two hotspot missense variants (abbreviated as C228T and C250T) represent the vast majority of *TERT* promoter alterations in CNS tumours. Other variants have been rarely detected in CNS tumours, such as C228A and C249T in gliomas.¹⁵⁹ *TERT* promoter variants can be detected by various molecular techniques, with Sanger sequencing, NGS and RT-PCR being most commonly used.

Investigation of *TERT* promoter alteration is a core element for glioblastoma, IDH-wildtype; and meningioma.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 33 – *TP53* alterations (Core)*

Sequence variants in the *TP53* (tumour protein p53; 17p13.1) gene are found in a variety of cancers including >80% of IDH-mutant diffuse astrocytic gliomas.³⁷ *TP53* variants are less common in IDH-wildtype glioblastomas (23-28%) and are notably uncommon in oligodendrogliomas, IDH-mutant and 1p/19q-codeleted.

Detection of a *TP53* variant may be used to support the diagnosis of IDH-mutant astrocytoma. However, exclusion of 1p/19q codeletion and ATRX loss of expression is not sufficient to establish this diagnosis, as rare cases of usually high grade and/or recurrent oligodendroglioma, IDH-mutant and 1p/19q-codeleted may also feature *TP53* variants. Furthermore, *TP53* variants are important for classifying medulloblastomas, SHH pathway-activated and *TP53*-mutant. *TP53* alterations are common in some other types of brain tumours but are not listed as essential or desirable diagnostic criterion for these latter tumours.

Different DNA sequencing techniques may be used for detecting *TP53* variants, with NGS covering the entire coding sequence being most reliable, as sequence alterations tend to cluster in exons 5 to 8 but may also affect other exons. The vast majority of alterations are missense variants.

Immunohistochemistry (IHC) is a useful screening tool, given that most *TP53* missense variants result in increased p53 protein half-life that produces strong immunoreactivity in the majority of tumour cell nuclei (rather than scattered positivity and/or light nuclear staining). Strong p53 positivity in >10% of the tumour cell nuclei has been found to have a sensitivity of 77.4-78.8% and a specificity of 78.6-96.7% when compared to sequencing.^{164,165} Positive nuclear p53 staining correlates well with missense sequence variants with a sensitivity of 92% and a specificity of 79.4%, whereas only 33% of tumours with truncating *TP53* alterations show p53 positivity,¹⁶⁵ with such alterations typically leading to negative staining.¹⁶⁶

Investigation of *TP53* alteration is a core element for medulloblastoma, SHH-activated and *TP53*-wildtype; and medulloblastoma, SHH-activated and *TP53*-mutant.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 34 – TTF1 expression (IHC) (Core)*

The TTF1 (thyroid transcription factor 1; 14q13.3) protein, encoded by the homeobox gene *NKX2-1* (14q13.3),¹⁶⁷ is essential for organogenesis of the lung and thyroid gland. Furthermore, in the human embryonic and adult brain nuclear TTF1 expression appears to be restricted to the ventral forebrain and diencephalic origin structures, including normal pituicytes of the neurohypophysis,¹⁶⁸ ependymal cells of the third ventricle and glial cells of the organum vasculosum of the lamina terminalis.¹⁶⁹

TTF1 nuclear expression in CNS tumours has been reported in posterior pituitary tumours including pituicytomas, spindle cell oncocytomas and granular cell tumours of the neurohypophysis, in ependymomas of the third ventricle, subependymal giant cell astrocytomas, and chordoid gliomas.¹⁶⁸⁻¹⁷⁵ In addition, glioblastomas with primitive neuronal components may express TTF1 in the embryonal, GFAP-negative tumour cell component depending which antibody clone is being utilised.¹⁷⁶

Investigation of TTF1 expression is a core element for pituicytoma; granular cell tumour of the sellar region; and spindle cell oncocytoma.

* Only core for some tumours – refer to [Tables 1-3](#).

↑ Back

Note 35 – WNT pathway alterations (Core)*

Approximately 10% of all medulloblastomas are characterised by WNT pathway activation by an activating variant in exon 3 of the *CTNNB1* gene (catenin (cadherin-associated protein), beta 1; 3p22.1), or rarely, sequence variants in *APC* (adenomatous polyposis coli; 5q22.2) or other genes encoding components of this pathway. These medulloblastomas cannot be identified as such based on haematoxylin-eosin stained sections alone. Most of them have classic morphology. The precise identification of these tumours is important because of their favourable prognosis in the paediatric age (<16 years) under current treatment regimens, and the evaluation of possible reduction of treatment intensity.

Immunohistochemically, WNT-activated medulloblastomas typically show YAP1 staining of tumour nuclei, nuclear expression of OTX2, and are negative for the SHH target proteins GAB1 and p75NGFR. Furthermore, in most WNT-activated medulloblastomas at least some tumour cell nuclei are positive for β -catenin protein, but discrimination from strong cytoplasmic staining of the tumour cells may be challenging. It has been recommended to use at least two of the following methods for reliable identification of WNT-activated medulloblastomas: IHC, sequencing of *CTNNB1* exon 3, methylome profiling and RNA profiling.

Rarely, WNT-activated medulloblastomas are diagnosed within the setting of constitutional mismatch repair deficiency syndrome or in individuals with germline *APC* alterations and a predisposition to colon cancer, but the vast majority of these medulloblastomas are sporadic.^{4,153,154,177}

Investigation of WNT pathway alteration is a core element for medulloblastoma, WNT-activated; and medulloblastoma, non-WNT/non-SHH.

* Only core for some tumours – refer to [Tables 1-3](#).

↑ Back

Note 36 – *YAP1* rearrangement (Core)*

In the WHO CNS5 Tumour Classification, supratentorial ependymoma, *YAP1* (yes-associated protein 1; 11q22.1) fusion-positive, has been introduced as a separate tumour type.⁴ Supratentorial ependymomas with *YAP1* fusion are rare and mostly restricted to young children.¹⁷⁸

Fusions involving the *YAP1* gene can be detected by a variety of methods; however, an IHC approach is currently not available. Transcriptome sequencing can detect *YAP1* fused to several gene partners, such as *MAMLD1* (Xq.28).¹⁷⁸ Methods using RT-PCR or interphase ISH are alternatives.¹⁷⁸

Investigation of *YAP1* rearrangement is a core element for supratentorial ependymoma, *YAP1* fusion-positive.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 37 – *ZFTA* rearrangement (Core)*

In the WHO CNS5 Tumour Classification, the supratentorial ependymomas formerly coined as *RELA* (v-rel avian reticuloendotheliosis viral oncogene homolog A; 11q13.1) fusion-positive are now listed as supratentorial ependymoma, *ZFTA* (zinc finger translocation associated; 11q13.1) fusion-positive (with *ZFTA* being the new designation for *C11orf95*).⁴ Approximately two-thirds of supratentorial ependymomas in children are *ZFTA* fusion-positive, with in the vast majority of these harbouring *RELA* as the fusion partner.^{4,178} Demonstration of a *ZFTA* fusion is required for their diagnosis in the WHO CNS5 Tumour Classification.⁴

These fusions can be identified by RNA sequencing, RT-PCR based techniques, or ISH; whole genome sequencing can also detect the fusion. Targeted RNA sequencing and RT-PCR design should take into consideration the complex nature of the fusion events generated by chromothripsis on chromosome 11.

In situ hybridisation (ISH) probes against either *ZFTA* or *RELA* may be used to detect chromosome 11 rearrangements.¹⁷⁹ *ZFTA* fusion-positive ependymomas with or without *RELA* represent the same tumour entity in the WHO CNS5 Tumour Classification. It is known that a broader spectrum of tumours than classic ependymomas exhibit *ZFTA* fusions without *RELA*.¹⁸⁰ Supratentorial ependymomas without *ZFTA* (and without *YAP1*) fusion also exist.¹⁸¹

L1CAM (cytoplasmic staining) and p65 (nuclear staining) in cases with *ZFTA::RELA* fusions, represent surrogate IHC markers for *ZFTA* fusion-positive tumours. Strong and diffuse L1CAM immunopositivity is a sensitive but not a specific surrogate marker as it can also be expressed by other tumour types. Nonetheless, L1CAM IHC is recommended for indicating that a supratentorial ependymoma likely belongs to the *ZFTA* fusion-positive category, when fusion testing is not possible or yields equivocal results.

Investigation of *ZFTA* rearrangement is a core element for supratentorial ependymoma, *ZFTA* fusion-positive.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 38 – Other immunohistochemistry findings (Core)*

A growing number of IHC tests represent core ICCR or essential WHO diagnostic criteria, including IHC for Brachyury, CD34, GFAP, S100, class III β -tubulin, neurofilament, synaptophysin, NeuN, OLIG2, HuC/HuD, non-phosphorylated 200kDa NFP, SOX10, EMA, claudin-1, GLUT1, OCT4, KIT, CD30 loss, AFP loss, hCG, cytokeratin, inhibin, CD99, ETV6, WT1, SPDEF, CD56, β -catenin and others.

Practical and economical guidelines, which include a comprehensive list of IHC markers, for diagnosing CNS tumours in resource-restrained jurisdictions are being developed by the Asian Oceanian Society of Neuropathology for Adapting Diagnostic Approaches for Practical Taxonomy in Resource-Restrained Regions (AOSNP-ADAPTR).⁶

To achieve ideal results, IHC should involve careful optimisation of antigen retrieval techniques and appropriate antibody selection. The inclusion of appropriate positive and negative controls, including on-slide controls, will ensure accurate and reliable results, enhance interpretation of staining patterns and minimise the risk of false-positive or false-negative findings.

Investigation of other IHC findings is a core element for supratentorial ependymoma, *ZFTA* fusion-positive; supratentorial ependymoma, *YAP1* fusion-positive; posterior fossa ependymoma, group A; posterior fossa ependymoma, group B; spinal ependymoma; spinal ependymoma, *MYCN*-amplified; embryonal tumour with multilayered rosettes; choroid plexus papilloma; atypical choroid plexus papilloma; choroid plexus carcinoma; hybrid nerve sheath tumours; pineocytoma; pineal parenchymal tumour of intermediate differentiation; papillary tumour of the pineal region; and pituitary adenoma/pituitary neuroendocrine tumour.

* Only core for some tumours – refer to [Tables 1-3](#).

 [Back](#)

Note 39 – Other molecular findings (Non-core)

These sections should be used for documenting findings for other genetic alterations and/or for other tumour types, such as metastases and haematological lesions.

 [Back](#)

References

- 1 Merlin T, Weston A and Tooher R (2009). Extending an evidence hierarchy to include topics other than treatment: revising the Australian 'levels of evidence'. *BMC Med Res Methodol* 9:34.
- 2 International Collaboration on Cancer Reporting (2021). *Soft Tissue Sarcoma Histopathology Reporting Guide – Biopsy Specimens. 1st edition*. Available from: <https://www.iccr-cancer.org/datasets/published-datasets/soft-tissue-bone/soft-tissue-sarcoma-biopsy-specimens/> (Accessed 1st March 2024).

- 3 International Collaboration on Cancer Reporting (2021). *Soft Tissue Sarcoma Histopathology Reporting Guide – Resection Specimens. 1st edition*. Available from: <https://www.iccr-cancer.org/datasets/published-datasets/soft-tissue-bone/soft-tissue-sarcoma-resection-specimens/> (Accessed 1st March 2024).
- 4 WHO Classification of Tumours Editorial Board (2021). *Central Nervous System Tumours, WHO Classification of Tumours, 5th Edition, Volume 6*. IARC Press, Lyon, France.
- 5 WHO Classification of Tumours Editorial Board (2024). *Central Nervous System Tumours, WHO Classification of Tumours, 5th Edition, Volume 6 - Corrigenda July 2024*. Available from: file:///C:/Users/tinas/Downloads/CNS5%20Corrigenda%20doc_2024-07-08-1.pdf (Accessed 1st August 2024).
- 6 Buckland ME, Sarkar C, Santosh V, Al-Hussaini M, Park SH, Tihan T, Ng HK and Komori T (2023). Announcing the Asian Oceanian Society of Neuropathology guidelines for Adapting Diagnostic Approaches for Practical Taxonomy in Resource-Restrained Regions (AOSNP-ADAPTR). *Brain Pathol*:e13201.
- 7 Horak P, Griffith M, Danos AM, Pitel BA, Madhavan S, Liu X, Chow C, Williams H, Carmody L, Barrow-Laing L, Rieke D, Kreutzfeldt S, Stenzinger A, Tamborero D, Benary M, Rajagopal PS, Ida CM, Lesmana H, Satgunaseelan L, Merker JD, Tolstorukov MY, Campregher PV, Warner JL, Rao S, Natesan M, Shen H, Venstrom J, Roy S, Tao K, Kanagal-Shamanna R, Xu X, Ritter DI, Pagel K, Krysiak K, Dubuc A, Akkari YM, Li XS, Lee J, King I, Raca G, Wagner AH, Li MM, Plon SE, Kulkarni S, Griffith OL, Chakravarty D and Sonkin D (2022). Standards for the classification of pathogenicity of somatic variants in cancer (oncogenicity): Joint recommendations of Clinical Genome Resource (ClinGen), Cancer Genomics Consortium (CGC), and Variant Interpretation for Cancer Consortium (VICC). *Genet Med* 24(5):986-998.
- 8 Richards S, Aziz N, Bale S, Bick D, Das S, Gastier-Foster J, Grody WW, Hegde M, Lyon E, Spector E, Voelkerding K and Rehm HL (2015). Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology. *Genet Med* 17(5):405-424.
- 9 Brat DJ, Aldape K, Bridge JA, Canoll P, Colman H, Hameed MR, Harris BT, Hattab EM, Huse JT, Jenkins RB, Lopez-Terrada DH, McDonald WC, Rodriguez FJ, Souter LH, Colasacco C, Thomas NE, Yount MH, van den Bent MJ and Perry A (2022). Molecular Biomarker Testing for the Diagnosis of Diffuse Gliomas. *Arch Pathol Lab Med* 146(5):547-574.
- 10 Sahm F, Brandner S, Bertero L, Capper D, French PJ, Figarella-Branger D, Giangaspero F, Haberler C, Hegi ME, Kristensen BW, Kurian KM, Preusser M, Tops BBJ, van den Bent M, Wick W, Reifenberger G and Wesseling P (2023). Molecular diagnostic tools for the World Health Organization (WHO) 2021 classification of gliomas, glioneuronal and neuronal tumors; an EANO guideline. *Neuro Oncol* 25(10):1731-1749.
- 11 Hallberg B and Palmer RH (2016). The role of the ALK receptor in cancer biology. *Ann Oncol* 27 Suppl 3:iii4-iii15.

- 12 Clarke M, Mackay A, Ismer B, Pickles JC, Tatevossian RG, Newman S, Bale TA, Stoler I, Izquierdo E, Temelso S, Carvalho DM, Molinari V, Burford A, Howell L, Virasami A, Fairchild AR, Avery A, Chalker J, Kristiansen M, Hauptfear K, Dalton JD, Orisme W, Wen J, Hubank M, Kurian KM, Rowe C, Maybury M, Crosier S, Knipstein J, Schüller U, Kordes U, Kram DE, Snuderl M, Bridges L, Martin AJ, Doey LJ, Al-Sarraj S, Chandler C, Zebian B, Cairns C, Natrajan R, Boulton JKR, Robinson SP, Sill M, Dunkel IJ, Gilheeny SW, Rosenblum MK, Hughes D, Proszek PZ, Macdonald TJ, Preusser M, Haberler C, Slavc I, Packer R, Ng HK, Caspi S, Popović M, Faganel Kotnik B, Wood MD, Baird L, Davare MA, Solomon DA, Olsen TK, Brandal P, Farrell M, Cryan JB, Capra M, Karremann M, Schittenhelm J, Schuhmann MU, Ebinger M, Dinjens WNM, Kerl K, Hettmer S, Pietsch T, Andreiuolo F, Driever PH, Korshunov A, Hiddingh L, Worst BC, Sturm D, Zuckermann M, Witt O, Bloom T, Mitchell C, Miele E, Colafati GS, Diomedi-Camassei F, Bailey S, Moore AS, Hassall TEG, Lowis SP, Tsoli M, Cowley MJ, Ziegler DS, Karajannis MA, Aquilina K, Hargrave DR, Carceller F, Marshall LV, von Deimling A, Kramm CM, Pfister SM, Sahm F, Baker SJ, Mastronuzzi A, Carai A, Vinci M, Capper D, Popov S, Ellison DW, Jacques TS, Jones DTW and Jones C (2020). Infant High-Grade Gliomas Comprise Multiple Subgroups Characterized by Novel Targetable Gene Fusions and Favorable Outcomes. *Cancer Discov* 10(7):942-963.
- 13 Guerreiro Stucklin AS, Ryall S, Fukuoka K, Zapotocky M, Lassaletta A, Li C, Bridge T, Kim B, Arnoldo A, Kowalski PE, Zhong Y, Johnson M, Li C, Ramani AK, Siddaway R, Nobre LF, de Antonellis P, Dunham C, Cheng S, Boué DR, Finlay JL, Coven SL, de Prada I, Perez-Somarriba M, Faria CC, Grotzer MA, Rushing E, Sumerauer D, Zamecnik J, Krskova L, Garcia Ariza M, Cruz O, Morales La Madrid A, Solano P, Terashima K, Nakano Y, Ichimura K, Nagane M, Sakamoto H, Gil-da-Costa MJ, Silva R, Johnston DL, Michaud J, Wilson B, van Landeghem FKH, Oviedo A, McNeely PD, Crooks B, Fried I, Zhukova N, Hansford JR, Nageswararao A, Garzia L, Shago M, Brudno M, Irwin MS, Bartels U, Ramaswamy V, Bouffet E, Taylor MD, Tabori U and Hawkins C (2019). Alterations in ALK/ROS1/NTRK/MET drive a group of infantile hemispheric gliomas. *Nat Commun* 10(1):4343.
- 14 Roosen M, Odé Z, Bunt J and Kool M (2022). The oncogenic fusion landscape in pediatric CNS neoplasms. *Acta Neuropathol* 143(4):427-451.
- 15 Department of Health and Human Services, Food and Drug Administration (2015). *Letter to Ventana Medical Systems on approval of premarket authorization application for the VENTANA ALK (D5F3) CDx Assay*. Available from: http://www.accessdata.fda.gov/cdrh_docs/pdf14/P140025a.pdf (Accessed 1st March 2024).
- 16 Marchetti A, Di Lorito A, Pace MV, Iezzi M, Felicioni L, D'Antuono T, Filice G, Guetti L, Mucilli F and Buttitta F (2016). ALK Protein Analysis by IHC Staining after Recent Regulatory Changes: A Comparison of Two Widely Used Approaches, Revision of the Literature, and a New Testing Algorithm. *J Thorac Oncol* 11(4):487-495.
- 17 Capper D, Reifenberger G, French PJ, Schweizer L, Weller M, Touat M, Niclou SP, Euskirchen P, Haberler C, Hegi ME, Brandner S, Le Rhun E, Rudà R, Sanson M, Tabatabai G, Sahm F, Wen PY, Wesseling P, Preusser M and van den Bent MJ (2023). EANO guideline on rational molecular testing of gliomas, glioneuronal and neuronal tumors in adults for targeted therapy selection. *Neuro Oncol* 25(5):813-826.
- 18 Deckert M, Batchelor T, Ferry JA, Paulus W, Weller M, Hoang-Xuan K and Nagane M (2021). Anaplastic large cell lymphoma (ALK+/ALK-). In: *Central Nervous System Tumours. WHO Classification of Tumours, 5th Edition*, Reifenberger G and Soffiotti R (eds), IARC Press, Lyon, France.
- 19 Lucas CG, Gilani A, Solomon DA, Liang X, Maher OM, Chamyam G, Kleinschmidt-Demasters BK and Perry A (2019). ALK-positive histiocytosis with KIF5B-ALK fusion in the central nervous system. *Acta Neuropathol* 138(2):335-337.

- 20 Pearson ADJ, Barry E, Mossé YP, Ligas F, Bird N, de Rojas T, Zimmerman ZF, Wilner K, Woessmann W, Weiner S, Weigel B, Venkatramani R, Valteau D, Trahair T, Smith M, Singh S, Selvaggi G, Scobie N, Schleiermacher G, Richardson N, Park J, Nysom K, Norga K, Merino M, McDonough J, Matloub Y, Marshall LV, Lowe E, Lesa G, Irwin M, Karres D, Gajjar A, Doz F, Fox E, DuBois SG, Donoghue M, Casanova M, Caron H, Buenger V, Bradford D, Blanc P, Barone A, Reaman G and Vassal G (2021). Second Paediatric Strategy Forum for anaplastic lymphoma kinase (ALK) inhibition in paediatric malignancies: ACCELERATE in collaboration with the European Medicines Agency with the participation of the Food and Drug Administration. *Eur J Cancer* 157:198-213.
- 21 Davies KD, Le AT, Sheren J, Nijmeh H, Gowan K, Jones KL, Varella-Garcia M, Aisner DL and Doebele RC (2018). Comparison of Molecular Testing Modalities for Detection of ROS1 Rearrangements in a Cohort of Positive Patient Samples. *J Thorac Oncol* 13(10):1474-1482.
- 22 Mayr L, Guntner AS, Madlener S, Schmook MT, Peyrl A, Azizi AA, Dieckmann K, Reisinger D, Stepien NM, Schramm K, Laemmerer A, Jones DTW, Ecker J, Sahm F, Milde T, Pajtler KW, Blattner-Johnson M, Strbac M, Dorfer C, Czech T, Kirchhofer D, Gabler L, Berger W, Haberler C, Müllauer L, Buchberger W, Slavic I, Lötsch-Gojo D and Gojo J (2020). Cerebrospinal Fluid Penetration and Combination Therapy of Entrectinib for Disseminated ROS1/NTRK-Fusion Positive Pediatric High-Grade Glioma. *J Pers Med* 10(4).
- 23 Papusha L, Zaytseva M, Panferova A, Druy A, Valiakhmetova A, Artemov A, Salnikova E, Kislyakov A, Imyanitov E, Karachunsky A, Maschan A, Hwang EI, Novichkova G and Packer RJ (2022). Two clinically distinct cases of infant hemispheric glioma carrying ZCCHC8:ROS1 fusion and responding to entrectinib. *Neuro Oncol* 24(6):1029-1031.
- 24 Wu G, Diaz AK, Paugh BS, Rankin SL, Ju B, Li Y, Zhu X, Qu C, Chen X, Zhang J, Easton J, Edmonson M, Ma X, Lu C, Nagahawatte P, Hedlund E, Rusch M, Pounds S, Lin T, Onar-Thomas A, Huether R, Kriwacki R, Parker M, Gupta P, Becksfort J, Wei L, Mulder HL, Boggs K, Vadodaria B, Yergeau D, Russell JC, Ochoa K, Fulton RS, Fulton LL, Jones C, Boop FA, Broniscer A, Wetmore C, Gajjar A, Ding L, Mardis ER, Wilson RK, Taylor MR, Downing JR, Ellison DW, Zhang J and Baker SJ (2014). The genomic landscape of diffuse intrinsic pontine glioma and pediatric non-brainstem high-grade glioma. *Nat Genet* 46(5):444-450.
- 25 Gambella A, Senetta R, Collelli G, Vallero SG, Monticelli M, Cofano F, Zeppa P, Garbossa D, Pellerino A, Rudà R, Soffietti R, Fagioli F, Papotti M, Cassoni P and Bertero L (2020). NTRK Fusions in Central Nervous System Tumors: A Rare, but Worthy Target. *Int J Mol Sci* 21(3).
- 26 Tihan T, Figarella-Branger D, Giannini C, Pfister SM, Rodriguez FJ, Jacques TS, Hawkins CE, Tabori U, Varlet P, Gupta K and DTW J (2021). Pilocytic astrocytoma. In: *Central Nervous System Tumours. WHO Classification of Tumours, 5th Edition*, Reifenberger G and Perry A (eds), IARC Press, Lyon, France.
- 27 Ryall S, Zapotocky M, Fukuoka K, Nobre L, Guerreiro Stucklin A, Bennett J, Siddaway R, Li C, Pajovic S, Arnoldo A, Kowalski PE, Johnson M, Sheth J, Lassaletta A, Tatevossian RG, Orisme W, Qaddoumi I, Surrey LF, Li MM, Waanders AJ, Gilheeneey S, Rosenblum M, Bale T, Tsang DS, Laperriere N, Kulkarni A, Ibrahim GM, Drake J, Dirks P, Taylor MD, Rutka JT, Laughlin S, Shroff M, Shago M, Hazrati LN, D'Arcy C, Ramaswamy V, Bartels U, Huang A, Bouffet E, Karajannis MA, Santi M, Ellison DW, Tabori U and Hawkins C (2020). Integrated Molecular and Clinical Analysis of 1,000 Pediatric Low-Grade Gliomas. *Cancer Cell* 37(4):569-583.e565.
- 28 Marchiò C, Scaltriti M, Ladanyi M, Iafrate AJ, Bibeau F, Dietel M, Hechtman JF, Troiani T, López-Rios F, Douillard JY, André F and Reis-Filho JS (2019). ESMO recommendations on the standard methods to detect NTRK fusions in daily practice and clinical research. *Ann Oncol* 30(9):1417-1427.

- 29 Cheng F and Guo D (2019). MET in glioma: signaling pathways and targeted therapies. *J Exp Clin Cancer Res* 38(1):270.
- 30 Guo R, Luo J, Chang J, Rekhtman N, Arcila M and Drilon A (2020). MET-dependent solid tumours - molecular diagnosis and targeted therapy. *Nat Rev Clin Oncol* 17(9):569-587.
- 31 Brennan CW, Verhaak RG, McKenna A, Campos B, Nounshmehr H, Salama SR, Zheng S, Chakravarty D, Sanborn JZ, Berman SH, Beroukhir R, Bernard B, Wu CJ, Genovese G, Shmulevich I, Barnholtz-Sloan J, Zou L, Vegesna R, Shukla SA, Ciriello G, Yung WK, Zhang W, Sougnez C, Mikkelsen T, Aldape K, Bigner DD, Van Meir EG, Prados M, Sloan A, Black KL, Eschbacher J, Finocchiaro G, Friedman W, Andrews DW, Guha A, Iacocca M, O'Neill BP, Foltz G, Myers J, Weisenberger DJ, Penny R, Kucherlapati R, Perou CM, Hayes DN, Gibbs R, Marra M, Mills GB, Lander E, Spellman P, Wilson R, Sander C, Weinstein J, Meyerson M, Gabriel S, Laird PW, Haussler D, Getz G and Chin L (2013). The somatic genomic landscape of glioblastoma. *Cell* 155(2):462-477.
- 32 Kwak Y, Kim SI, Park CK, Paek SH, Lee ST and Park SH (2015). C-MET overexpression and amplification in gliomas. *Int J Clin Exp Pathol* 8(11):14932-14938.
- 33 International Cancer Genome Consortium PedBrain Tumor Project (2016). Recurrent MET fusion genes represent a drug target in pediatric glioblastoma. *Nat Med* 22(11):1314-1320.
- 34 Shirahata M, Ono T, Stichel D, Schrimpf D, Reuss DE, Sahm F, Koelsche C, Wefers A, Reinhardt A, Huang K, Sievers P, Shimizu H, Nanjo H, Kobayashi Y, Miyake Y, Suzuki T, Adachi JI, Mishima K, Sasaki A, Nishikawa R, Bewerunge-Hudler M, Ryzhova M, Absalyamova O, Golanov A, Sinn P, Platten M, Jungk C, Winkler F, Wick A, Hänggi D, Unterberg A, Pfister SM, Jones DTW, van den Bent M, Hegi M, French P, Baumert BG, Stupp R, Gorlia T, Weller M, Capper D, Korshunov A, Herold-Mende C, Wick W, Louis DN and von Deimling A (2018). Novel, improved grading system(s) for IDH-mutant astrocytic gliomas. *Acta Neuropathol* 136(1):153-166.
- 35 Woo HY, Na K, Yoo J, Chang JH, Park YN, Shim HS and Kim SH (2020). Glioblastomas harboring gene fusions detected by next-generation sequencing. *Brain Tumor Pathol* 37(4):136-144.
- 36 Hu H, Mu Q, Bao Z, Chen Y, Liu Y, Chen J, Wang K, Wang Z, Nam Y, Jiang B, Sa JK, Cho HJ, Her NG, Zhang C, Zhao Z, Zhang Y, Zeng F, Wu F, Kang X, Liu Y, Qian Z, Wang Z, Huang R, Wang Q, Zhang W, Qiu X, Li W, Nam DH, Fan X, Wang J and Jiang T (2018). Mutational Landscape of Secondary Glioblastoma Guides MET-Targeted Trial in Brain Tumor. *Cell* 175(6):1665-1678.e1618.

- 37 Brat DJ, Verhaak RG, Aldape KD, Yung WK, Salama SR, Cooper LA, Rheinbay E, Miller CR, Vitucci M, Morozova O, Robertson AG, Noushmehr H, Laird PW, Cherniack AD, Akbani R, Huse JT, Ciriello G, Poisson LM, Barnholtz-Sloan JS, Berger MS, Brennan C, Colen RR, Colman H, Flanders AE, Giannini C, Grifford M, Iavarone A, Jain R, Joseph I, Kim J, Kasaian K, Mikkelsen T, Murray BA, O'Neill BP, Pachter L, Parsons DW, Sougnez C, Sulman EP, Vandenberg SR, Van Meir EG, von Deimling A, Zhang H, Crain D, Lau K, Mallery D, Morris S, Paulauskis J, Penny R, Shelton T, Sherman M, Yena P, Black A, Bowen J, Dicostanzo K, Gastier-Foster J, Leraas KM, Lichtenberg TM, Pierson CR, Ramirez NC, Taylor C, Weaver S, Wise L, Zmuda E, Davidsen T, Demchok JA, Eley G, Ferguson ML, Hutter CM, Mills Shaw KR, Ozenberger BA, Sheth M, Sofia HJ, Tarnuzzer R, Wang Z, Yang L, Zenklusen JC, Ayala B, Baboud J, Chudamani S, Jensen MA, Liu J, Pihl T, Raman R, Wan Y, Wu Y, Ally A, Auman JT, Balasundaram M, Balu S, Baylin SB, Beroukheim R, Bootwalla MS, Bowlby R, Bristow CA, Brooks D, Butterfield Y, Carlsen R, Carter S, Chin L, Chu A, Chuah E, Cibulskis K, Clarke A, Coetzee SG, Dhalla N, Fennell T, Fisher S, Gabriel S, Getz G, Gibbs R, Guin R, Hadjipanayis A, Hayes DN, Hinoue T, Hoadley K, Holt RA, Hoyle AP, Jefferys SR, Jones S, Jones CD, Kucherlapati R, Lai PH, Lander E, Lee S, Lichtenstein L, Ma Y, Maglinte DT, Mahadeshwar HS, Marra MA, Mayo M, Meng S, Meyerson ML, Mieczkowski PA, Moore RA, Mose LE, Mungall AJ, Pantazi A, Parfenov M, Park PJ, Parker JS, Perou CM, Protopopov A, Ren X, Roach J, Sabedot TS, Schein J, Schumacher SE, Seidman JG, Seth S, Shen H, Simons JV, Sipahimalani P, Soloway MG, Song X, Sun H, Tabak B, Tam A, Tan D, Tang J, Thiessen N, Triche T, Jr., Van Den Berg DJ, Veluvolu U, Waring S, Weisenberger DJ, Wilkerson MD, Wong T, Wu J, Xi L, Xu AW, Yang L, Zack TI, Zhang J, Aksoy BA, Arachchi H, Benz C, Bernard B, Carlin D, Cho J, DiCara D, Frazer S, Fuller GN, Gao J, Gehlenborg N, Haussler D, Heiman DI, Iype L, Jacobsen A, Ju Z, Katzman S, Kim H, Knijnenburg T, Kreisberg RB, Lawrence MS, Lee W, Leinonen K, Lin P, Ling S, Liu W, Liu Y, Liu Y, Lu Y, Mills G, Ng S, Noble MS, Paull E, Rao A, Reynolds S, Saksena G, Sanborn Z, Sander C, Schultz N, Senbabaoglu Y, Shen R, Shmulevich I, Sinha R, Stuart J, Sumer SO, Sun Y, Tasman N, Taylor BS, Voet D, Weinhold N, Weinstein JN, Yang D, Yoshihara K, Zheng S, Zhang W, Zou L, Abel T, Sadeghi S, Cohen ML, Eschbacher J, Hattab EM, Raghunathan A, Schniederjan MJ, Aziz D, Barnett G, Barrett W, Bigner DD, Boice L, Brewer C, Calatuzzolo C, Campos B, Carlotti CG, Jr., Chan TA, Cuppini L, Curley E, Cuzzubbo S, Devine K, DiMeco F, Duell R, Elder JB, Fehrenbach A, Finocchiaro G, Friedman W, Fulop J, Gardner J, Hermes B, Herold-Mende C, Jungk C, Kandler A, Lehman NL, Lipp E, Liu O, Mandt R, McGraw M, McLendon R, McPherson C, Neder L, Nguyen P, Noss A, Nunziata R, Ostrom QT, Palmer C, Perin A, Pollo B, Potapov A, Potapova O, Rathmell WK, Rotin D, Scarpacci L, Schilero C, Senecal K, Shimmel K, Shurkhay V, Sifri S, Singh R, Sloan AE, Smolenski K, Staugaitis SM, Steele R, Thorne L, Tirapelli DP, Unterberg A, Vallurupalli M, Wang Y, Warnick R, Williams F, Wolinsky Y, Bell S, Rosenberg M, Stewart C, Huang F, Grimsby JL, Radenbaugh AJ and Zhang J (2015). Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. *N Engl J Med* 372(26):2481-2498.
- 38 Ceccarelli M, Barthel FP, Malta TM, Sabedot TS, Salama SR, Murray BA, Morozova O, Newton Y, Radenbaugh A, Pagnotta SM, Anjum S, Wang J, Manyam G, Zoppoli P, Ling S, Rao AA, Grifford M, Cherniack AD, Zhang H, Poisson L, Carlotti CG, Jr., Tirapelli DP, Rao A, Mikkelsen T, Lau CC, Yung WK, Rabadan R, Huse J, Brat DJ, Lehman NL, Barnholtz-Sloan JS, Zheng S, Hess K, Rao G, Meyerson M, Beroukheim R, Cooper L, Akbani R, Wensch M, Haussler D, Aldape KD, Laird PW, Gutmann DH, Noushmehr H, Iavarone A and Verhaak RG (2016). Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. *Cell* 164(3):550-563.
- 39 Reuss DE, Sahm F, Schrimpf D, Wiestler B, Capper D, Koelsche C, Schweizer L, Korshunov A, Jones DT, Hovestadt V, Mittelbronn M, Schittenhelm J, Herold-Mende C, Unterberg A, Platten M, Weller M, Wick W, Pfister SM and von Deimling A (2015). ATRX and IDH1-R132H immunohistochemistry with subsequent copy number analysis and IDH sequencing as a basis for an "integrated" diagnostic approach for adult astrocytoma, oligodendroglioma and glioblastoma. *Acta Neuropathol* 129(1):133-146.

- 40 Purkait S, Miller CA, Kumar A, Sharma V, Pathak P, Jha P, Sharma MC, Suri V, Suri A, Sharma BS, Fulton RS, Kale SS, Dahiya S and Sarkar C (2017). ATRX in Diffuse Gliomas With its Mosaic/Heterogeneous Expression in a Subset. *Brain Pathol* 27(2):138-145.
- 41 Nakata S, Yuan M, Rubens JA, Kahlert UD, Maciaczyk J, Raabe EH and Eberhart CG (2021). BCOR Internal Tandem Duplication Expression in Neural Stem Cells Promotes Growth, Invasion, and Expression of PRC2 Targets. *Int J Mol Sci* 22(8).
- 42 Bouchoucha Y, Tauziède-Espariat A, Gauthier A, Guillemot D, Bochaton D, Vibert J, Carton M, Watson S, Grossetête S, Quignot C, Orbach D, Corradini N, Schleiermacher G, Bourdeaut F, Simbozel M, Dufour C, Minard-Colin V, Brahmi M, Tirode F, Pissaloux D, Karanian M, Machet MC, Masliah-Planchon J, Delattre O, Cardoen L, Pierron G and Doz F (2022). Intra- and extra-cranial BCOR-ITD tumours are separate entities within the BCOR-rearranged family. *J Pathol Clin Res* 8(3):217-232.
- 43 Mardi L, Tauziède-Espariat A, Guillemot D, Pierron G, Gigant P, Mehdi L, Berthaud C, Pucelle N, Lacombe J, Hasty L, Wahler E, Chrétien F, Lechapt E and Varlet P (2021). BCOR immunohistochemistry, but not SATB2 immunohistochemistry, is a sensitive and specific diagnostic biomarker for central nervous system tumours with BCOR internal tandem duplication. *Histopathology* 79(5):891-894.
- 44 Sturm D, Orr BA, Toprak UH, Hovestadt V, Jones DTW, Capper D, Sill M, Buchhalter I, Northcott PA, Leis I, Ryzhova M, Koelsche C, Pfaff E, Allen SJ, Balasubramanian G, Worst BC, Pajtler KW, Brabetz S, Johann PD, Sahm F, Reimand J, Mackay A, Carvalho DM, Remke M, Phillips JJ, Perry A, Cowdrey C, Drissi R, Fouladi M, Giangaspero F, Łastowska M, Grajkowska W, Scheurlen W, Pietsch T, Hagel C, Gojo J, Löttsch D, Berger W, Slavc I, Haberler C, Jouvett A, Holm S, Hofer S, Prinz M, Keohane C, Fried I, Mawrin C, Scheie D, Mobley BC, Schniederjan MJ, Santi M, Buccoliero AM, Dahiya S, Kramm CM, von Bueren AO, von Hoff K, Rutkowski S, Herold-Mende C, Frühwald MC, Milde T, Hasselblatt M, Wesseling P, Rößler J, Schüller U, Ebinger M, Schittenhelm J, Frank S, Grobholz R, Vajtai I, Hans V, Schneppenheim R, Zitterbart K, Collins VP, Aronica E, Varlet P, Puget S, Dufour C, Grill J, Figarella-Branger D, Wolter M, Schuhmann MU, Shalaby T, Grotzer M, van Meter T, Monoranu CM, Felsberg J, Reifenberger G, Snuderl M, Forrester LA, Koster J, Versteeg R, Volckmann R, van Sluis P, Wolf S, Mikkelsen T, Gajjar A, Aldape K, Moore AS, Taylor MD, Jones C, Jabado N, Karajannis MA, Eils R, Schlesner M, Lichter P, von Deimling A, Pfister SM, Ellison DW, Korshunov A and Kool M (2016). New Brain Tumor Entities Emerge from Molecular Classification of CNS-PNETs. *Cell* 164(5):1060-1072.
- 45 Tauziède-Espariat A, Pierron G, Guillemot D, Bochaton D, Watson S, Masliah-Planchon J, Vasiljevic A, Meurgey A, Chotard G, Hasty L, Wahler E, Lechapt E, Chrétien F, Grill J, Bourdeaut F, Bouchoucha Y, Puget S, Icher-de-Bouyn C, Jecko V, Cardoen L, Dangouloff-Ros V, Boddaert N and Varlet P (2021). CNS tumors with YWHAE:NUTM2 and KDM2B-fusions present molecular similarities to extra-CNS tumors having BCOR internal tandem duplication or alternative fusions. *Acta Neuropathol Commun* 9(1):176.
- 46 Tauziède-Espariat A, Uro-Coste E, Sievers P, Nicaise Y, Mariet C, Siegfried A, Pierron G, Guillemot D, Benzakoun J, Pallud J, Roques M, Bonneville F, Larrieu-Ciron D, Chaynes P, Saffroy R, Hamelin J, Hasty L, Métails A, Chrétien F, Kool M, Gojo J and Varlet P (2023). CNS tumor with EP300::BCOR fusion: discussing its prevalence in adult population. *Acta Neuropathol Commun* 11(1):26.
- 47 Sugino H, Satomi K, Mori T, Mukai Y, Honda-Kitahara M, Matsushita Y, Ichimura K, Narita Y and Yoshida A (2023). High-grade neuroepithelial tumor with EP300::BCOR fusion and negative BCOR immunohistochemical expression: a case report. *Brain Tumor Pathol* 40(2):133-141.

- 48 Wu Z, Rajan S, Chung HJ, Raffeld M, Panneer Selvam P, Schweizer L, Perry A, Samuel D, Giannini C, Ragnathan A, Frosch MP, Marshall MS, Boué DR, Donev K, Neill SG, Fernandes I, Resnick A, Rood B, Cummings TJ, Buckley AF, Szymanski L, Neto OLA, Zach L, Colman H, Cheshier S, Ziskin J, Tyagi M, Capper D, Abdullaev Z, Cimino PJ, Quezado M, Pratt D and Aldape K (2022). Molecular and clinicopathologic characteristics of gliomas with EP300::BCOR fusions. *Acta Neuropathol* 144(6):1175-1178.
- 49 Brastianos PK, Taylor-Weiner A, Manley PE, Jones RT, Dias-Santagata D, Thorner AR, Lawrence MS, Rodriguez FJ, Bernardo LA, Schubert L, Sunkavalli A, Shillingford N, Calicchio ML, Lidov HG, Taha H, Martinez-Lage M, Santi M, Storm PB, Lee JY, Palmer JN, Adappa ND, Scott RM, Dunn IF, Laws ER, Jr., Stewart C, Ligon KL, Hoang MP, Van Hummelen P, Hahn WC, Louis DN, Resnick AC, Kieran MW, Getz G and Santagata S (2014). Exome sequencing identifies BRAF mutations in papillary craniopharyngiomas. *Nat Genet* 46(2):161-165.
- 50 Schindler G, Capper D, Meyer J, Janzarik W, Omran H, Herold-Mende C, Schmieder K, Wesseling P, Mawrin C, Hasselblatt M, Louis DN, Korshunov A, Pfister S, Hartmann C, Paulus W, Reifenberger G and von Deimling A (2011). Analysis of BRAF V600E mutation in 1,320 nervous system tumors reveals high mutation frequencies in pleomorphic xanthoastrocytoma, ganglioglioma and extra-cerebellar pilocytic astrocytoma. *Acta Neuropathol* 121(3):397-405.
- 51 Kleinschmidt-DeMasters BK, Aisner DL, Birks DK and Foreman NK (2013). Epithelioid GBMs show a high percentage of BRAF V600E mutation. *Am J Surg Pathol* 37(5):685-698.
- 52 Lassaletta A, Zapotocky M, Mistry M, Ramaswamy V, Honnorat M, Krishnatry R, Guerreiro Stucklin A, Zhukova N, Arnoldo A, Ryall S, Ling C, McKeown T, Loukides J, Cruz O, de Torres C, Ho CY, Packer RJ, Tatevossian R, Qaddoumi I, Harreld JH, Dalton JD, Mulcahy-Levy J, Foreman N, Karajannis MA, Wang S, Snuderl M, Nageswara Rao A, Giannini C, Kieran M, Ligon KL, Garre ML, Nozza P, Mascelli S, Raso A, Mueller S, Nicolaidis T, Silva K, Perbet R, Vasiljevic A, Faure Conter C, Frappaz D, Leary S, Crane C, Chan A, Ng HK, Shi ZF, Mao Y, Finch E, Eisenstat D, Wilson B, Carret AS, Hauser P, Sumerauer D, Krskova L, Larouche V, Fleming A, Zelcer S, Jabado N, Rutka JT, Dirks P, Taylor MD, Chen S, Bartels U, Huang A, Ellison DW, Bouffet E, Hawkins C and Tabori U (2017). Therapeutic and Prognostic Implications of BRAF V600E in Pediatric Low-Grade Gliomas. *J Clin Oncol* 35(25):2934-2941.
- 53 Ihle MA, Fassunke J, Konig K, Grunewald I, Schlaak M, Kreuzberg N, Tietze L, Schildhaus HU, Buttner R and Merkelbach-Bruse S (2014). Comparison of high resolution melting analysis, pyrosequencing, next generation sequencing and immunohistochemistry to conventional Sanger sequencing for the detection of p.V600E and non-p.V600E BRAF mutations. *BMC Cancer* 14:13.
- 54 Ritterhouse LL and Barletta JA (2015). BRAF V600E mutation-specific antibody: A review. *Semin Diagn Pathol* 32(5):400-408.
- 55 Stichel D, Schrimpf D, Sievers P, Reinhardt A, Suwala AK, Sill M, Reuss DE, Korshunov A, Casalini BM, Sommerkamp AC, Ecker J, Selt F, Sturm D, Gnekow A, Koch A, Simon M, Hernáiz Driever P, Schüller U, Capper D, van Tilburg CM, Witt O, Milde T, Pfister SM, Jones DTW, von Deimling A, Sahm F and Wefers AK (2021). Accurate calling of KIAA1549-BRAF fusions from DNA of human brain tumours using methylation array-based copy number and gene panel sequencing data. *Neuropathol Appl Neurobiol* 47(3):406-414.
- 56 Ceccom J, Bourdeaut F, Loukh N, Rigau V, Milin S, Takin R, Richer W, Uro-Coste E, Couturier J, Bertozzi AI, Delattre O and Delisle MB (2014). Embryonal tumor with multilayered rosettes: diagnostic tools update and review of the literature. *Clin Neuropathol* 33(1):15-22.

- 57 Vaubel RA, Caron AA, Yamada S, Decker PA, Eckel Passow JE, Rodriguez FJ, Nageswara Rao AA, Lachance D, Parney I, Jenkins R and Giannini C (2018). Recurrent copy number alterations in low-grade and anaplastic pleomorphic xanthoastrocytoma with and without BRAF V600E mutation. *Brain Pathol* 28(2):172-182.
- 58 Maragkou T, Reinhard S, Jungo P, Pasquier B, Neuenschwander M, Schucht P, Vassella E and Hewer E (2023). Evaluation of MTAP and p16 immunohistochemical deficiency as surrogate marker for CDKN2A/B homozygous deletion in gliomas. *Pathology* 55(4):466-477.
- 59 Vogazianou AP, Chan R, Backlund LM, Pearson DM, Liu L, Langford CF, Gregory SG, Collins VP and Ichimura K (2010). Distinct patterns of 1p and 19q alterations identify subtypes of human gliomas that have different prognoses. *Neuro Oncol* 12(7):664-678.
- 60 Wiens AL, Cheng L, Bertsch EC, Johnson KA, Zhang S and Hattab EM (2012). Polysomy of chromosomes 1 and/or 19 is common and associated with less favorable clinical outcome in oligodendrogliomas: fluorescent in situ hybridization analysis of 84 consecutive cases. *J Neuropathol Exp Neurol* 71(7):618-624.
- 61 Wiestler B, Capper D, Hovestadt V, Sill M, Jones DT, Hartmann C, Felsberg J, Platten M, Feiden W, Keyvani K, Pfister SM, Wiestler OD, Meyermann R, Reifenberger G, Pietsch T, von Deimling A, Weller M and Wick W (2014). Assessing CpG island methylator phenotype, 1p/19q codeletion, and MGMT promoter methylation from epigenome-wide data in the biomarker cohort of the NOA-04 trial. *Neuro Oncol* 16(12):1630-1638.
- 62 Filipski K, Braun Y, Zinke J, Roller B, Baumgarten P, Wagner M, Senft C, Zeiner PS, Ronellenfitsch MW, Steinbach JP, Plate KH, Gasparoni G, Mittelbronn M, Capper D and Harter PN (2019). Lack of H3K27 trimethylation is associated with 1p/19q codeletion in diffuse gliomas. *Acta Neuropathol* 138(2):331-334.
- 63 Felix M, Friedel D, Jayavelu AK, Filipski K, Reinhardt A, Warnken U, Stichel D, Schrimpf D, Korshunov A, Wang Y, Kessler T, Etminan N, Unterberg A, Herold-Mende C, Heikaus L, Sahm F, Wick W, Harter PN, von Deimling A and Reuss DE (2022). HIP1R and vimentin immunohistochemistry predict 1p/19q status in IDH-mutant glioma. *Neuro Oncol* 24(12):2121-2132.
- 64 Brat DJ, Aldape K, Colman H, Holland EC, Louis DN, Jenkins RB, Kleinschmidt-DeMasters BK, Perry A, Reifenberger G, Stupp R, von Deimling A and Weller M (2018). cIMPACT-NOW update 3: recommended diagnostic criteria for "Diffuse astrocytic glioma, IDH-wildtype, with molecular features of glioblastoma, WHO grade IV". *Acta Neuropathol* 136(5):805-810.
- 65 Stichel D, Ebrahimi A, Reuss D, Schrimpf D, Ono T, Shirahata M, Reifenberger G, Weller M, Hänggi D, Wick W, Herold-Mende C, Westphal M, Brandner S, Pfister SM, Capper D, Sahm F and von Deimling A (2018). Distribution of EGFR amplification, combined chromosome 7 gain and chromosome 10 loss, and TERT promoter mutation in brain tumors and their potential for the reclassification of IDHwt astrocytoma to glioblastoma. *Acta Neuropathol* 136(5):793-803.
- 66 Kallen ME and Hornick JL (2022). From the ashes of "Ewing-like" sarcoma: A contemporary update of the classification, immunohistochemistry, and molecular genetics of round cell sarcomas. *Semin Diagn Pathol* 39(1):29-37.
- 67 Hung YP, Fletcher CD and Hornick JL (2016). Evaluation of ETV4 and WT1 expression in CIC-rearranged sarcomas and histologic mimics. *Mod Pathol* 29(11):1324-1334.

- 68 Mangray S, Kelly DR, LeGuellec S, Fridman E, Aggarwal S, Shago M, Matoso A, Madison R, Pramanik S, Zhong S, Li R, Lombardo KA, Cramer S, Pressey J, Ross JS, Corona RJ, Bratslavsky G, Argani P, Coindre JM, Somers GR, Ali SM and Yakirevich E (2018). Clinicopathologic Features of a Series of Primary Renal CIC-rearranged Sarcomas With Comprehensive Molecular Analysis. *Am J Surg Pathol* 42(10):1360-1369.
- 69 Schaefer IM, Dal Cin P, Landry LM, Fletcher CDM, Hanna GJ and French CA (2018). CIC-NUTM1 fusion: A case which expands the spectrum of NUT-rearranged epithelioid malignancies. *Genes Chromosomes Cancer* 57(9):446-451.
- 70 Siegele B, Roberts J, Black JO, Rudzinski E, Vargas SO and Galambos C (2017). DUX4 Immunohistochemistry Is a Highly Sensitive and Specific Marker for CIC-DUX4 Fusion-positive Round Cell Tumor. *Am J Surg Pathol* 41(3):423-429.
- 71 Tauziède-Espariat A, Hasty L, Métais A and Varlet P (2023). Mesenchymal non-meningothelial tumors of the central nervous system: a literature review and diagnostic update of novelties and emerging entities. *Acta Neuropathol Commun* 11(1):22.
- 72 Yoshida A, Goto K, Kodaira M, Kobayashi E, Kawamoto H, Mori T, Yoshimoto S, Endo O, Kodama N, Kushima R, Hiraoka N, Motoi T and Kawai A (2016). CIC-rearranged Sarcomas: A Study of 20 Cases and Comparisons With Ewing Sarcomas. *Am J Surg Pathol* 40(3):313-323.
- 73 Pratt D, Kumar-Sinha C, Ciešlik M, Mehra R, Xiao H, Shao L, Franson A, Cantor E, Chinnaiyan AM, Mody R, Abdullaev Z, Aldape K, Quezado M and Camelo-Piragua S (2021). A novel ATXN1-DUX4 fusion expands the spectrum of 'CIC-rearranged sarcoma' of the CNS to include non-CIC alterations. *Acta Neuropathol* 141(4):619-622.
- 74 Bettegowda C, Agrawal N, Jiao Y, Sausen M, Wood LD, Hruban RH, Rodriguez FJ, Cahill DP, McLendon R, Riggins G, Velculescu VE, Oba-Shinjo SM, Marie SK, Vogelstein B, Bigner D, Yan H, Papadopoulos N and Kinzler KW (2011). Mutations in CIC and FUBP1 contribute to human oligodendroglioma. *Science* 333(6048):1453-1455.
- 75 Jiao Y, Killela PJ, Reitman ZJ, Rasheed AB, Heaphy CM, de Wilde RF, Rodriguez FJ, Rosemberg S, Oba-Shinjo SM, Nagahashi Marie SK, Bettegowda C, Agrawal N, Lipp E, Pirozzi C, Lopez G, He Y, Friedman H, Friedman AH, Riggins GJ, Holdhoff M, Burger P, McLendon R, Bigner DD, Vogelstein B, Meeker AK, Kinzler KW, Papadopoulos N, Diaz LA and Yan H (2012). Frequent ATRX, CIC, FUBP1 and IDH1 mutations refine the classification of malignant gliomas. *Oncotarget* 3(7):709-722.
- 76 Wong D and Yip S (2020). Making heads or tails - the emergence of capicua (CIC) as an important multifunctional tumour suppressor. *J Pathol* 250(5):532-540.
- 77 Aldape K, Zadeh G, Mansouri S, Reifenberger G and von Deimling A (2015). Glioblastoma: pathology, molecular mechanisms and markers. *Acta Neuropathol* 129(6):829-848.

- 78 Sturm D, Witt H, Hovestadt V, Khuong-Quang DA, Jones DT, Konermann C, Pfaff E, Tonjes M, Sill M, Bender S, Kool M, Zapatka M, Becker N, Zucknick M, Hielscher T, Liu XY, Fontebasso AM, Ryzhova M, Albrecht S, Jacob K, Wolter M, Ebinger M, Schuhmann MU, van Meter T, Fruhwald MC, Hauch H, Pekrun A, Radlwimmer B, Niehues T, von Komorowski G, Durken M, Kulozik AE, Madden J, Donson A, Foreman NK, Drissi R, Fouladi M, Scheurlen W, von Deimling A, Monoranu C, Roggendorf W, Herold-Mende C, Unterberg A, Kramm CM, Felsberg J, Hartmann C, Wiestler B, Wick W, Milde T, Witt O, Lindroth AM, Schwartzentruber J, Faury D, Fleming A, Zakrzewska M, Liberski PP, Zakrzewski K, Hauser P, Garami M, Klekner A, Bogner L, Morrissy S, Cavalli F, Taylor MD, van Sluis P, Koster J, Versteeg R, Volckmann R, Mikkelsen T, Aldape K, Reifenberger G, Collins VP, Majewski J, Korshunov A, Lichter P, Plass C, Jabado N and Pfister SM (2012). Hotspot mutations in H3F3A and IDH1 define distinct epigenetic and biological subgroups of glioblastoma. *Cancer Cell* 22(4):425-437.
- 79 Weller M, Kaulich K, Hentschel B, Felsberg J, Gramatzki D, Pietsch T, Simon M, Westphal M, Schackert G, Tonn JC, von Deimling A, Davis T, Weiss WA, Loeffler M and Reifenberger G (2014). Assessment and prognostic significance of the epidermal growth factor receptor vIII mutation in glioblastoma patients treated with concurrent and adjuvant temozolomide radiochemotherapy. *Int J Cancer* 134(10):2437-2447.
- 80 Gan HK, Cvrljevic AN and Johns TG (2013). The epidermal growth factor receptor variant III (EGFRvIII): where wild things are altered. *Febs j* 280(21):5350-5370.
- 81 Weller M, Butowski N, Tran DD, Recht LD, Lim M, Hirte H, Ashby L, Mechtler L, Goldlust SA, Iwamoto F, Drappatz J, O'Rourke DM, Wong M, Hamilton MG, Finocchiaro G, Perry J, Wick W, Green J, He Y, Turner CD, Yellin MJ, Keler T, Davis TA, Stupp R and Sampson JH (2017). Rindopepimut with temozolomide for patients with newly diagnosed, EGFRvIII-expressing glioblastoma (ACT IV): a randomised, double-blind, international phase 3 trial. *Lancet Oncol* 18(10):1373-1385.
- 82 Desai R, Suryadevara CM, Batich KA, Farber SH, Sanchez-Perez L and Sampson JH (2016). Emerging immunotherapies for glioblastoma. *Expert Opin Emerg Drugs* 21(2):133-145.
- 83 Thorne AH, Zanca C and Furnari F (2016). Epidermal growth factor receptor targeting and challenges in glioblastoma. *Neuro Oncol* 18(7):914-918.
- 84 Masui K, Mischel PS and Reifenberger G (2016). Molecular classification of gliomas. *Handb Clin Neurol* 134:97-120.
- 85 Hübner JM, Müller T, Papageorgiou DN, Mauermann M, Krijgsveld J, Russell RB, Ellison DW, Pfister SM, Pajtler KW and Kool M (2019). EZHIP/CXorf67 mimics K27M mutated oncohistones and functions as an intrinsic inhibitor of PRC2 function in aggressive posterior fossa ependymoma. *Neuro Oncol* 21(7):878-889.
- 86 Jain SU, Rashoff AQ, Krabbenhoft SD, Hoelper D, Do TJ, Gibson TJ, Lundgren SM, Bondra ER, Deshmukh S, Harutyunyan AS, Juretic N, Jabado N, Harrison MM and Lewis PW (2020). H3 K27M and EZHIP Impede H3K27-Methylation Spreading by Inhibiting Allosterically Stimulated PRC2. *Mol Cell* 80(4):726-735.e727.
- 87 Antin C, Tauziède-Espariat A, Debily MA, Castel D, Grill J, Pagès M, Ayrault O, Chrétien F, Gareton A, Andreiuolo F, Lechapt E and Varlet P (2020). EZHIP is a specific diagnostic biomarker for posterior fossa ependymomas, group PFA and diffuse midline gliomas H3-WT with EZHIP overexpression. *Acta Neuropathol Commun* 8(1):183.

- 88 Panwalkar P, Clark J, Ramaswamy V, Hawes D, Yang F, Dunham C, Yip S, Hukin J, Sun Y, Schipper MJ, Chavez L, Margol A, Pekmezci M, Chung C, Banda A, Bayliss JM, Curry SJ, Santi M, Rodriguez FJ, Snuderl M, Karajannis MA, Saratsis AM, Horbinski CM, Carret AS, Wilson B, Johnston D, Lafay-Cousin L, Zelcer S, Eisenstat D, Silva M, Scheinemann K, Jadoo N, McNeely PD, Kool M, Pfister SM, Taylor MD, Hawkins C, Korshunov A, Judkins AR and Venneti S (2017). Immunohistochemical analysis of H3K27me3 demonstrates global reduction in group-A childhood posterior fossa ependymoma and is a powerful predictor of outcome. *Acta Neuropathol* 134(5):705-714.
- 89 Sloan EA, Chiang J, Villanueva-Meyer JE, Alexandrescu S, Eschbacher JM, Wang W, Mafra M, Ud Din N, Carr-Boyd E, Watson M, Punsoni M, Oviedo A, Gilani A, Kleinschmidt-DeMasters BK, Coss DJ, Lopes MB, Raffel C, Berger MS, Chang SM, Reddy A, Ramani B, Ferris SP, Lee JC, Hofmann JW, Cho SJ, Horvai AE, Pekmezci M, Tihan T, Bollen AW, Rodriguez FJ, Ellison DW, Perry A and Solomon DA (2021). Intracranial mesenchymal tumor with FET-CREB fusion-A unifying diagnosis for the spectrum of intracranial myxoid mesenchymal tumors and angiomatoid fibrous histiocytoma-like neoplasms. *Brain Pathol* 31(4):e12918.
- 90 Sloan EA, Gupta R, Koelsche C, Chiang J, Villanueva-Meyer JE, Alexandrescu S, Eschbacher JM, Wang W, Mafra M, Ud Din N, Carr-Boyd E, Watson M, Punsoni M, Oviedo A, Gilani A, Kleinschmidt-DeMasters BK, Coss DJ, Lopes MB, Reddy A, Mueller S, Cho SJ, Horvai AE, Lee JC, Pekmezci M, Tihan T, Bollen AW, Rodriguez FJ, Ellison DW, Perry A, von Deimling A, Chang SM, Berger MS and Solomon DA (2022). Intracranial mesenchymal tumors with FET-CREB fusion are composed of at least two epigenetic subgroups distinct from meningioma and extracranial sarcomas. *Brain Pathol* 32(4):e13037.
- 91 Vizcaino MA, Giannini C, Chang HT, Kipp BR, Fritchie K and Vaubel R (2021). Intracranial angiomatoid fibrous histiocytoma with rhabdoid features: a mimic of rhabdoid meningioma. *Brain Tumor Pathol* 38(2):138-144.
- 92 Bale TA (2020). FGFR- gene family alterations in low-grade neuroepithelial tumors. *Acta Neuropathol Commun* 8(1):21.
- 93 Métais A, Tauziède-Espariat A, Garcia J, Appay R, Uro-Coste E, Meyronet D, Maurage CA, Vandebos F, Rigau V, Chiforeanu DC, Pallud J, Senova S, Saffroy R, Colin C, Edjlali M, Varlet P and Figarella-Branger D (2023). Clinico-pathological and epigenetic heterogeneity of diffuse gliomas with FGFR3::TACC3 fusion. *Acta Neuropathol Commun* 11(1):14.
- 94 Ardizzone A, Scuderi SA, Giuffrida D, Colarossi C, Puglisi C, Campolo M, Cuzzocrea S, Esposito E and Paterniti I (2020). Role of Fibroblast Growth Factors Receptors (FGFRs) in Brain Tumors, Focus on Astrocytoma and Glioblastoma. *Cancers (Basel)* 12(12):3825.
- 95 Chioni AM and Grose RP (2021). Biological Significance and Targeting of the FGFR Axis in Cancer. *Cancers (Basel)* 13(22):5681.
- 96 Korshunov A, Okonechnikov K, Schmitt-Hoffner F, Ryzhova M, Sahm F, Stichel D, Schrimpf D, Reuss DE, Sievers P, Suwala AK, Kumirova E, Zheludkova O, Golanov A, Jones DTW, Pfister SM, Kool M and von Deimling A (2021). Molecular analysis of pediatric CNS-PNET revealed nosologic heterogeneity and potent diagnostic markers for CNS neuroblastoma with FOXR2-activation. *Acta Neuropathol Commun* 9(1):20.

- 97 Tauziède-Espariat A, Figarella-Branger D, Métais A, Uro-Coste E, Maurage CA, Lhermitte B, Aline-Fardin A, Hasty L, Vasiljevic A, Chiforeanu D, Chotard G, Adle-Biassette H, Meurgey A, Saffroy R, Guillemot D, Pierron G, Sievers P and Varlet P (2023). CNS neuroblastoma, FOXR2-activated and its mimics: a relevant panel approach for work-up and accurate diagnosis of this rare neoplasm. *Acta Neuropathol Commun* 11(1):43.
- 98 Seal RL, Denny P, Bruford EA, Gribkova AK, Landsman D, Marzluff WF, McAndrews M, Panchenko AR, Shaytan AK and Talbert PB (2022). A standardized nomenclature for mammalian histone genes. *Epigenetics Chromatin* 15(1):34.
- 99 Vuong HG, Ngo TNM, Le HT, Jea A, Hrachova M, Battiste J, McNall-Knapp R and Dunn IF (2022). Prognostic Implication of Patient Age in H3K27M-Mutant Midline Gliomas. *Front Oncol* 12:858148.
- 100 Pratt D, Natarajan SK, Banda A, Giannini C, Vats P, Koschmann C, Mody R, Chinnaiyan A and Venneti S (2018). Circumscribed/non-diffuse histology confers a better prognosis in H3K27M-mutant gliomas. *Acta Neuropathol* 135(2):299-301.
- 101 Ryall S, Krishnatry R, Arnoldo A, Buczkowicz P, Mistry M, Siddaway R, Ling C, Pajovic S, Yu M, Rubin JB, Hukin J, Steinbok P, Bartels U, Bouffet E, Tabori U and Hawkins C (2016). Targeted detection of genetic alterations reveal the prognostic impact of H3K27M and MAPK pathway aberrations in paediatric thalamic glioma. *Acta Neuropathol Commun* 4(1):93.
- 102 Mariet C, Castel D, Grill J, Saffroy R, Dangouloff-Ros V, Boddaert N, Llamas-Guttierrez F, Chappé C, Puget S, Hasty L, Chrétien F, Métais A, Varlet P and Tauziède-Espariat A (2022). Posterior fossa ependymoma H3 K27-mutant: an integrated radiological and histomolecular tumor analysis. *Acta Neuropathol Commun* 10(1):137.
- 103 Mackay A, Burford A, Carvalho D, Izquierdo E, Fazal-Salom J, Taylor KR, Bjerke L, Clarke M, Vinci M, Nandhabalan M, Temelso S, Popov S, Molinari V, Raman P, Waanders AJ, Han HJ, Gupta S, Marshall L, Zacharoulis S, Vaidya S, Mandeville HC, Bridges LR, Martin AJ, Al-Sarraj S, Chandler C, Ng HK, Li X, Mu K, Trabelsi S, Brahim DH, Kisljakov AN, Konovalov DM, Moore AS, Carcaboso AM, Sunol M, de Torres C, Cruz O, Mora J, Shats LI, Stavale JN, Bidinotto LT, Reis RM, Entz-Werle N, Farrell M, Cryan J, Crimmins D, Caird J, Pears J, Monje M, Debily MA, Castel D, Grill J, Hawkins C, Nikbakht H, Jabado N, Baker SJ, Pfister SM, Jones DTW, Fouladi M, von Bueren AO, Baudis M, Resnick A and Jones C (2017). Integrated Molecular Meta-Analysis of 1,000 Pediatric High-Grade and Diffuse Intrinsic Pontine Glioma. *Cancer Cell* 32(4):520-537.e525.
- 104 Bayliss J, Mukherjee P, Lu C, Jain SU, Chung C, Martinez D, Sabari B, Margol AS, Panwalkar P, Parolia A, Pekmezci M, McEachin RC, Cieslik M, Tamrazi B, Garcia BA, La Rocca G, Santi M, Lewis PW, Hawkins C, Melnick A, David Allis C, Thompson CB, Chinnaiyan AM, Judkins AR and Venneti S (2016). Lowered H3K27me3 and DNA hypomethylation define poorly prognostic pediatric posterior fossa ependymomas. *Sci Transl Med* 8(366):366ra161.
- 105 Chapman RJ, Ghasemi DR, Andreiuolo F, Zschoernack V, Tauziède-Espariat A, Buttarelli FR, Giangaspero F, Grill J, Haberler C, Paine SML, Scott I, Jacques TS, Sill M, Pfister S, Kilday JP, Leblond P, Massimino M, Witt H, Modena P, Varlet P, Pietsch T, Grundy RG, Pajtler KW and Ritzmann TA (2023). Optimising biomarkers for accurate ependymoma diagnosis, prognostication and stratification within International Clinical Trials: A BIOMECA study. *Neuro Oncol* 25(10):1871-1882.

- 106 Banan R, Stichel D, Bleck A, Hong B, Lehmann U, Suwala A, Reinhardt A, Schrimpf D, Buslei R, Stadelmann C, Ehlert K, Prinz M, Acker T, Schittenhelm J, Kaul D, Schweizer L, Capper D, Harter PN, Etminan N, Jones DTW, Pfister SM, Herold-Mende C, Wick W, Sahm F, von Deimling A, Hartmann C and Reuss DE (2020). Infratentorial IDH-mutant astrocytoma is a distinct subtype. *Acta Neuropathol* 140(4):569-581.
- 107 Brandner S and von Deimling A (2015). Diagnostic, prognostic and predictive relevance of molecular markers in gliomas. *Neuropathol Appl Neurobiol* 41(6):694-720.
- 108 Louis DN, Perry A, Reifenberger G, von Deimling A, Figarella-Branger D, Cavenee WK, Ohgaki H, Wiestler OD, Kleihues P and Ellison DW (2016). The 2016 World Health Organization Classification of Tumors of the Central Nervous System: a summary. *Acta Neuropathologica* 131(6):803-820.
- 109 Capper D, Jones DTW, Sill M, Hovestadt V, Schrimpf D, Sturm D, Koelsche C, Sahm F, Chavez L, Reuss DE, Kratz A, Wefers AK, Huang K, Pajtler KW, Schweizer L, Stichel D, Olar A, Engel NW, Lindenberg K, Harter PN, Braczynski AK, Plate KH, Dohmen H, Garvalov BK, Coras R, Holsken A, Hewer E, Bewerunge-Hudler M, Schick M, Fischer R, Beschorner R, Schittenhelm J, Staszewski O, Wani K, Varlet P, Pages M, Temming P, Lohmann D, Selt F, Witt H, Milde T, Witt O, Aronica E, Giangaspero F, Rushing E, Scheurlen W, Geisenberger C, Rodriguez FJ, Becker A, Preusser M, Haberler C, Bjerkvig R, Cryan J, Farrell M, Deckert M, Hench J, Frank S, Serrano J, Kannan K, Tsirigos A, Bruck W, Hofer S, Brehmer S, Seiz-Rosenhagen M, Hanggi D, Hans V, Rozsnoki S, Hansford JR, Kohlhof P, Kristensen BW, Lechner M, Lopes B, Mawrin C, Ketter R, Kulozik A, Khatib Z, Heppner F, Koch A, Jouvet A, Keohane C, Muhleisen H, Mueller W, Pohl U, Prinz M, Benner A, Zapatka M, Gottardo NG, Driever PH, Kramm CM, Muller HL, Rutkowski S, von Hoff K, Fruhwald MC, Gnekow A, Fleischhack G, Tippelt S, Calaminus G, Monoranu CM, Perry A, Jones C, Jacques TS, Radlwimmer B, Gessi M, Pietsch T, Schramm J, Schackert G, Westphal M, Reifenberger G, Wesseling P, Weller M, Collins VP, Blumcke I, Bendszus M, Debus J, Huang A, Jabado N, Northcott PA, Paulus W, Gajjar A, Robinson GW, Taylor MD, Jaunmuktane Z, Ryzhova M, Platten M, Unterberg A, Wick W, Karajannis MA, Mittelbronn M, Acker T, Hartmann C, Aldape K, Schuller U, Buslei R, Lichter P, Kool M, Herold-Mende C, Ellison DW, Hasselblatt M, Snuderl M, Brandner S, Korshunov A, von Deimling A and Pfister SM (2018). DNA methylation-based classification of central nervous system tumours. *Nature* 555(7697):469-474.
- 110 Capper D, Stichel D, Sahm F, Jones DTW, Schrimpf D, Sill M, Schmid S, Hovestadt V, Reuss DE, Koelsche C, Reinhardt A, Wefers AK, Huang K, Sievers P, Ebrahimi A, Scholer A, Teichmann D, Koch A, Hanggi D, Unterberg A, Platten M, Wick W, Witt O, Milde T, Korshunov A, Pfister SM and von Deimling A (2018). Practical implementation of DNA methylation and copy-number-based CNS tumor diagnostics: the Heidelberg experience. *Acta Neuropathol* 136(2):181-210.
- 111 Euskirchen P, Bielle F, Labreche K, Kloosterman WP, Rosenberg S, Daniau M, Schmitt C, Masliah-Planchon J, Bourdeaut F, Dehais C, Marie Y, Delattre J-Y and Idbaih A (2017). Same-day genomic and epigenomic diagnosis of brain tumors using real-time nanopore sequencing. *Acta Neuropathol* 134(5):691-703.
- 112 Wu Z, Abdullaev Z, Pratt D, Chung HJ, Skarshaug S, Zgonc V, Perry C, Pack S, Saidkhodjaeva L, Nagaraj S, Tyagi M, Gangalapudi V, Valdez K, Turakulov R, Xi L, Raffeld M, Papanicolau-Sengos A, O'Donnell K, Newford M, Gilbert MR, Sahm F, Suwala AK, von Deimling A, Mamatjan Y, Karimi S, Nassiri F, Zadeh G, Ruppin E, Quezado M and Aldape K (2022). Impact of the methylation classifier and ancillary methods on CNS tumor diagnostics. *Neuro Oncol* 24(4):571-581.

- 113 Louis DN, Perry A, Wesseling P, Brat DJ, Cree IA, Figarella-Branger D, Hawkins C, Ng HK, Pfister SM, Reifenberger G, Soffietti R, von Deimling A and Ellison DW (2021). The 2021 WHO Classification of Tumors of the Central Nervous System: a summary. *Neuro Oncol* 23(8):1231-1251.
- 114 Hielscher T, Sill M, Sievers P, Stichel D, Brandner S, Jones DTW, von Deimling A, Sahm F and Maas SLN (2023). Clinical implementation of integrated molecular-morphologic risk prediction for meningioma. *Brain Pathol* 33(3):e13132.
- 115 Bady P, Sciuscio D, Diserens AC, Bloch J, van den Bent MJ, Marosi C, Dietrich PY, Weller M, Mariani L, Heppner FL, McDonald DR, Lacombe D, Stupp R, Delorenzi M and Hegi ME (2012). MGMT methylation analysis of glioblastoma on the Infinium methylation BeadChip identifies two distinct CpG regions associated with gene silencing and outcome, yielding a prediction model for comparisons across datasets, tumor grades, and CIMP-status. *Acta Neuropathol* 124(4):547-560.
- 116 Braczynski AK, Capper D, Jones DTW, Schittenhelm J, Stichel D, von Deimling A, Harter PN and Mittelbronn M (2020). High density DNA methylation array is a reliable alternative for PCR-based analysis of the MGMT promoter methylation status in glioblastoma. *Pathol Res Pract* 216(1):152728.
- 117 Tzaridis T, Schafer N, Weller J, Steinbach JP, Schlegel U, Seidel S, Sabel M, Hau P, Seidel C, Krex D, Goldbrunner R, Tonn JC, Grauer O, Kebir S, Schneider M, Schaub C, Vatter H, Coch C, Glas M, Fimmers R, Pietsch T, Reifenberger G, Herrlinger U and Felsberg J (2021). MGMT promoter methylation analysis for allocating combined CCNU/TMZ chemotherapy: Lessons learned from the CeTeG/NOA-09 trial. *Int J Cancer* 148(7):1695-1707.
- 118 Brandner S, McAleenan A, Kelly C, Spiga F, Cheng HY, Dawson S, Schmidt L, Faulkner CL, Wragg C, Jefferies S, Higgins JPT and Kurian KM (2021). MGMT promoter methylation testing to predict overall survival in people with glioblastoma treated with temozolomide: a comprehensive meta-analysis based on a Cochrane Systematic Review. *Neuro Oncol* 23(9):1457-1469.
- 119 Heuser M, Argiropoulos B, Kuchenbauer F, Yung E, Piper J, Fung S, Schlenk RF, Dohner K, Hinrichsen T, Rudolph C, Schambach A, Baum C, Schlegelberger B, Dohner H, Ganser A and Humphries RK (2007). MN1 overexpression induces acute myeloid leukemia in mice and predicts ATRA resistance in patients with AML. *Blood* 110(5):1639-1647.
- 120 Lekanne Deprez RH, Riegman PH, Groen NA, Warringa UL, van Biezen NA, Molijn AC, Bootsma D, de Jong PJ, Menon AG, Kley NA and et al. (1995). Cloning and characterization of MN1, a gene from chromosome 22q11, which is disrupted by a balanced translocation in a meningioma. *Oncogene* 10(8):1521-1528.
- 121 Lehman NL, Spassky N, Sak M, Webb A, Zumbar CT, Usubalieva A, Alkhateeb KJ, McElroy JP, Maclean KH, Fadda P, Liu T, Gangalapudi V, Carver J, Abdullaev Z, Timmers C, Parker JR, Pierson CR, Mobley BC, Gokden M, Hattab EM, Parrett T, Cooke RX, Lehman TD, Costinean S, Parwani A, Williams BJ, Jensen RL, Aldape K and Mistry AM (2022). Astroblastomas exhibit radial glia stem cell lineages and differential expression of imprinted and X-inactivation escape genes. *Nat Commun* 13(1):2083.
- 122 Ellison DW, Hawkins C, Jones DTW, Onar-Thomas A, Pfister SM, Reifenberger G and Louis DN (2019). cIMPACT-NOW update 4: diffuse gliomas characterized by MYB, MYBL1, or FGFR1 alterations or BRAF(V600E) mutation. *Acta Neuropathol* 137(4):683-687.

- 123 Chiang J, Harreld JH, Tinkle CL, Moreira DC, Li X, Acharya S, Qaddoumi I and Ellison DW (2019). A single-center study of the clinicopathologic correlates of gliomas with a MYB or MYBL1 alteration. *Acta Neuropathol* 138(6):1091-1092.
- 124 Tatevossian RG, Tang B, Dalton J, Forsheo T, Lawson AR, Ma J, Neale G, Shurtleff SA, Bailey S, Gajjar A, Baker SJ, Sheer D and Ellison DW (2010). MYB upregulation and genetic aberrations in a subset of pediatric low-grade gliomas. *Acta Neuropathol* 120(6):731-743.
- 125 Wefers AK, Stichel D, Schrimpf D, Coras R, Pages M, Tauziède-Espariat A, Varlet P, Schwarz D, Söylemezoglu F, Pohl U, Pimentel J, Meyer J, Hewer E, Japp A, Joshi A, Reuss DE, Reinhardt A, Sievers P, Casalini MB, Ebrahimi A, Huang K, Koelsche C, Low HL, Rebelo O, Marnoto D, Becker AJ, Staszewski O, Mittelbronn M, Hasselblatt M, Schittenhelm J, Cheesman E, de Oliveira RS, Queiroz RGP, Valera ET, Hans VH, Korshunov A, Olar A, Ligon KL, Pfister SM, Jaunmuktane Z, Brandner S, Tatevossian RG, Ellison DW, Jacques TS, Honavar M, Aronica E, Thom M, Sahm F, von Deimling A, Jones DTW, Blumcke I and Capper D (2020). Isomorphic diffuse glioma is a morphologically and molecularly distinct tumour entity with recurrent gene fusions of MYBL1 or MYB and a benign disease course. *Acta Neuropathol* 139(1):193-209.
- 126 Dang CV (2013). MYC, metabolism, cell growth, and tumorigenesis. *Cold Spring Harb Perspect Med* 3(8).
- 127 Northcott PA, Shih DJ, Peacock J, Garzia L, Morrissy AS, Zichner T, Stutz AM, Korshunov A, Reimand J, Schumacher SE, Beroukhir R, Ellison DW, Marshall CR, Lionel AC, Mack S, Dubuc A, Yao Y, Ramaswamy V, Luu B, Rolider A, Cavalli FM, Wang X, Remke M, Wu X, Chiu RY, Chu A, Chuah E, Corbett RD, Hoad GR, Jackman SD, Li Y, Lo A, Mungall KL, Nip KM, Qian JQ, Raymond AG, Thiessen NT, Varhol RJ, Birol I, Moore RA, Mungall AJ, Holt R, Kawauchi D, Roussel MF, Kool M, Jones DT, Witt H, Fernandez LA, Kenney AM, Wechsler-Reya RJ, Dirks P, Aviv T, Grajkowska WA, Perek-Polnik M, Haberler CC, Delattre O, Reynaud SS, Doz FF, Pernet-Fattet SS, Cho BK, Kim SK, Wang KC, Scheurlen W, Eberhart CG, Fevre-Montange M, Jouvett A, Pollack IF, Fan X, Muraszko KM, Gillespie GY, Di Rocco C, Massimi L, Michiels EM, Kloosterhof NK, French PJ, Kros JM, Olson JM, Ellenbogen RG, Zitterbart K, Kren L, Thompson RC, Cooper MK, Lach B, McLendon RE, Bigner DD, Fontebasso A, Albrecht S, Jabado N, Lindsey JC, Bailey S, Gupta N, Weiss WA, Bogner L, Klekner A, Van Meter TE, Kumabe T, Tominaga T, Elbabaa SK, Leonard JR, Rubin JB, Liao LM, Van Meir EG, Fouladi M, Nakamura H, Cinalli G, Garami M, Hauser P, Saad AG, Iolascon A, Jung S, Carlotti CG, Vibhakar R, Ra YS, Robinson S, Zollo M, Faria CC, Chan JA, Levy ML, Sorensen PH, Meyerson M, Pomeroy SL, Cho YJ, Bader GD, Tabori U, Hawkins CE, Bouffet E, Scherer SW, Rutka JT, Malkin D, Clifford SC, Jones SJ, Korbel JO, Pfister SM, Marra MA and Taylor MD (2012). Subgroup-specific structural variation across 1,000 medulloblastoma genomes. *Nature* 488(7409):49-56.
- 128 Roussel MF and Robinson GW (2013). Role of MYC in Medulloblastoma. *Cold Spring Harb Perspect Med* 3(11).
- 129 Shatara M, Schieffer KM, Klawinski D, Thomas DL, Pierson CR, Sribnick EA, Jones J, Rodriguez DP, Deeg C, Hamelberg E, LaHaye S, Miller KE, Fitch J, Kelly B, Leraas K, Pfau R, White P, Magrini V, Wilson RK, Mardis ER, Abdelbaki MS, Finlay JL, Boué DR, Cottrell CE, Ghasemi DR, Pajtler KW and Osorio DS (2021). Clinically aggressive pediatric spinal ependymoma with novel MYC amplification demonstrates molecular and histopathologic similarity to newly described MYCN-amplified spinal ependymomas. *Acta Neuropathol Commun* 9(1):192.

- 130 Korshunov A, Schrimpf D, Ryzhova M, Sturm D, Chavez L, Hovestadt V, Sharma T, Habel A, Burford A, Jones C, Zheludkova O, Kumirova E, Kramm CM, Golanov A, Capper D, von Deimling A, Pfister SM and Jones DTW (2017). H3-/IDH-wild type pediatric glioblastoma is comprised of molecularly and prognostically distinct subtypes with associated oncogenic drivers. *Acta Neuropathol* 134(3):507-516.
- 131 Khuong-Quang DA, Buczkowicz P, Rakopoulos P, Liu XY, Fontebasso AM, Bouffet E, Bartels U, Albrecht S, Schwartzenruber J, Letourneau L, Bourgey M, Bourque G, Montpetit A, Bourret G, Lepage P, Fleming A, Lichter P, Kool M, von Deimling A, Sturm D, Korshunov A, Faury D, Jones DT, Majewski J, Pfister SM, Jabado N and Hawkins C (2012). K27M mutation in histone H3.3 defines clinically and biologically distinct subgroups of pediatric diffuse intrinsic pontine gliomas. *Acta Neuropathol* 124(3):439-447.
- 132 Chen CCL, Deshmukh S, Jessa S, Hadjadj D, Lisi V, Andrade AF, Faury D, Jawhar W, Dali R, Suzuki H, Pathania M, A D, Dubois F, Woodward E, Hébert S, Coutelier M, Karamchandani J, Albrecht S, Brandner S, De Jay N, Gayden T, Bajic A, Harutyunyan AS, Marchione DM, Mikael LG, Juretic N, Zeinieh M, Russo C, Maestro N, Bassenden AV, Hauser P, Virga J, Bognar L, Klekner A, Zapotocky M, Vicha A, Krskova L, Vanova K, Zamecnik J, Sumerauer D, Ekert PG, Ziegler DS, Ellezam B, Filbin MG, Blanchette M, Hansford JR, Khuong-Quang DA, Berghuis AM, Weil AG, Garcia BA, Garzia L, Mack SC, Beroukhim R, Ligon KL, Taylor MD, Bandopadhyay P, Kramm C, Pfister SM, Korshunov A, Sturm D, Jones DTW, Salomoni P, Kleinman CL and Jabado N (2020). Histone H3.3G34-Mutant Interneuron Progenitors Co-opt PDGFRA for Gliomagenesis. *Cell* 183(6):1617-1633.e1622.
- 133 Fujimoto K, Arita H, Satomi K, Yamasaki K, Matsushita Y, Nakamura T, Miyakita Y, Umehara T, Kobayashi K, Tamura K, Tanaka S, Higuchi F, Okita Y, Kanemura Y, Fukai J, Sakamoto D, Uda T, Machida R, Kuchiba A, Maehara T, Nagane M, Nishikawa R, Suzuki H, Shibuya M, Komori T, Narita Y and Ichimura K (2021). TERT promoter mutation status is necessary and sufficient to diagnose IDH-wildtype diffuse astrocytic glioma with molecular features of glioblastoma. *Acta Neuropathol* 142(2):323-338.
- 134 Wong QH, Li KK, Wang WW, Malta TM, Noushmehr H, Grabovska Y, Jones C, Chan AK, Kwan JS, Huang QJ, Wong GC, Li WC, Liu XZ, Chen H, Chan DT, Mao Y, Zhang ZY, Shi ZF and Ng HK (2021). Molecular landscape of IDH-mutant primary astrocytoma Grade IV/glioblastomas. *Mod Pathol* 34(7):1245-1260.
- 135 Chiang JCH, Harreld JH, Tanaka R, Li X, Wen J, Zhang C, Boué DR, Rauch TM, Boyd JT, Chen J, Corbo JC, Bouldin TW, Elton SW, Liu LL, Schofield D, Lee SC, Bouffard JP, Georgescu MM, Dossani RH, Aguiar MA, Sances RA, Saad AG, Boop FA, Qaddoumi I and Ellison DW (2019). Septal dysembryoplastic neuroepithelial tumor: a comprehensive clinical, imaging, histopathologic, and molecular analysis. *Neuro Oncol* 21(6):800-808.
- 136 Lucas CG, Villanueva-Meyer JE, Whipple N, Oberheim Bush NA, Cooney T, Chang S, McDermott M, Berger M, Cham E, Sun PP, Putnam A, Zhou H, Bollo R, Cheshier S, Poppe MM, Fung KM, Sung S, Glenn C, Fan X, Bannykh S, Hu J, Danielpour M, Li R, Alva E, Johnston J, Van Ziffle J, Onodera C, Devine P, Grenert JP, Lee JC, Pekmezci M, Tihan T, Bollen AW, Perry A and Solomon DA (2020). Myxoid glioneuronal tumor, PDGFRA p.K385-mutant: clinical, radiologic, and histopathologic features. *Brain Pathol* 30(3):479-494.
- 137 Solomon DA, Korshunov A, Sill M, Jones DTW, Kool M, Pfister SM, Fan X, Bannykh S, Hu J, Danielpour M, Li R, Johnston J, Cham E, Cooney T, Sun PP, Oberheim Bush NA, McDermott M, Van Ziffle J, Onodera C, Grenert JP, Bastian BC, Villanueva-Meyer JE, Pekmezci M, Bollen AW and Perry A (2018). Myxoid glioneuronal tumor of the septum pellucidum and lateral ventricle is defined by a recurrent PDGFRA p.K385 mutation and DNT-like methylation profile. *Acta Neuropathol* 136(2):339-343.

- 138 Asa SL, Mete O, Perry A and Osamura RY (2022). Overview of the 2022 WHO Classification of Pituitary Tumors. *Endocr Pathol* 33(1):6-26.
- 139 Lopes MBS, Asa SL, Kleinschmidt-DeMasters BK, Mete O, Osamura Y and Villa C (2021). Pituitary adenoma/pituitary neuroendocrine tumour. In: *Central Nervous System Tumours. WHO Classification of Tumours, 5th Edition*, DJ B (ed), IARC Press, Lyon, France.
- 140 McDonald WC (2024). Pituitary adenoma classification: Tools to improve the current system. *Free Neuropathol* 5.
- 141 McDonald WC, Banerji N, McDonald KN, Ho B, Macias V and Kajdacsy-Balla A (2017). Steroidogenic Factor 1, Pit-1, and Adrenocorticotrophic Hormone: A Rational Starting Place for the Immunohistochemical Characterization of Pituitary Adenoma. *Arch Pathol Lab Med* 141(1):104-112.
- 142 Lenders NF, Chui J, Low J, Inder WJ, Earls PE and McCormack AI (2022). Development of a cost-effective diagnostic algorithm incorporating transcription factor immunohistochemistry in the evaluation of pituitary tumours. *Pituitary* 25(6):997-1003.
- 143 McDonald WC, McDonald KN, Helmer JA, Ho B, Wang A and Banerji N (2021). The Role of T-box Transcription Factor in a Pituitary Adenoma Diagnostic Algorithm. *Arch Pathol Lab Med* 145(5):592-598.
- 144 Villa C, Vasiljevic A, Jaffrain-Rea ML, Ansorge O, Asioli S, Barresi V, Chinezu L, Gardiman MP, Lania A, Lapshina AM, Poliani L, Reiniger L, Righi A, Saeger W, Soukup J, Theodoropoulou M, Uccella S, Trouillas J and Roncaroli F (2019). A standardised diagnostic approach to pituitary neuroendocrine tumours (PitNETs): a European Pituitary Pathology Group (EPPG) proposal. *Virchows Arch* 475(6):687-692.
- 145 Casar-Borota O, Boldt HB, Engström BE, Andersen MS, Baussart B, Bengtsson D, Berinder K, Ekman B, Feldt-Rasmussen U, Höybye C, Jørgensen JOL, Kolnes AJ, Korbonits M, Rasmussen Å K, Lindsay JR, Loughrey PB, Maiter D, Manojlovic-Gacic E, Pahnke J, Poliani PL, Popovic V, Ragnarsson O, Schalin-Jääntti C, Scheie D, Tóth M, Villa C, Wirenfeldt M, Kunicki J and Burman P (2021). Corticotroph Aggressive Pituitary Tumors and Carcinomas Frequently Harbor ATRX Mutations. *J Clin Endocrinol Metab* 106(4):1183-1194.
- 146 Trouillas J, Jaffrain-Rea ML, Vasiljevic A, Raverot G, Roncaroli F and Villa C (2020). How to Classify the Pituitary Neuroendocrine Tumors (PitNET)s in 2020. *Cancers (Basel)* 12(2):514.
- 147 WHO Classification of Tumours Editorial Board (2022). *Endocrine and Neuroendocrine Tumours, WHO Classification of Tumours, 5th Edition, Volume 10*. IARC Press, Lyon, France.
- 148 Lopes MB, Kleinschmidt-DeMasters BK, Mete O, Roncaroli F and Shibuya M (2021). Pituicytoma, granular cell tumour of the sellar region, and spindle cell oncocytoma. In: *Central Nervous System Tumours. WHO Classification of Tumours, 5th Edition*, Brat DJ and Wesseling P (eds), IARC Press, Lyon, France.
- 149 Schaefer IM, Fletcher CD and Hornick JL (2016). Loss of H3K27 trimethylation distinguishes malignant peripheral nerve sheath tumors from histologic mimics. *Mod Pathol* 29(1):4-13.
- 150 Wang L, Zehir A, Sadowska J, Zhou N, Rosenblum M, Busam K, Agaram N, Travis W, Arcila M, Dogan S, Berger MF, Cheng DT, Ladanyi M, Nafa K and Hameed M (2015). Consistent copy number changes and recurrent PRKAR1A mutations distinguish Melanotic Schwannomas from Melanomas: SNP-array and next generation sequencing analysis. *Genes Chromosomes Cancer* 54(8):463-471.

- 151 Hou Y, Pinheiro J, Sahm F, Reuss DE, Schimpf D, Stichel D, Casalini B, Koelsche C, Sievers P, Wefers AK, Reinhardt A, Ebrahimi A, Fernández-Klett F, Pusch S, Meier J, Schweizer L, Paulus W, Prinz M, Hartmann C, Plate KH, Reifenberger G, Pietsch T, Varlet P, Pagès M, Schüller U, Scheie D, de Stricker K, Frank S, Hench J, Pollo B, Brandner S, Unterberg A, Pfister SM, Jones DTW, Korshunov A, Wick W, Capper D, Blümcke I, von Deimling A and Bertero L (2019). Papillary glioneuronal tumor (PGNT) exhibits a characteristic methylation profile and fusions involving PRKCA. *Acta Neuropathol* 137(5):837-846.
- 152 Begemann M, Waszak SM, Robinson GW, Jäger N, Sharma T, Knopp C, Kraft F, Moser O, Mynarek M, Guerrini-Rousseau L, Brugieres L, Varlet P, Pietsch T, Bowers DC, Chintagumpala M, Sahm F, Korbel JO, Rutkowski S, Eggermann T, Gajjar A, Northcott P, Elbracht M, Pfister SM, Kontny U and Kurth I (2020). Germline GPR161 Mutations Predispose to Pediatric Medulloblastoma. *J Clin Oncol* 38(1):43-50.
- 153 Pietsch T and Haberler C (2016). Update on the integrated histopathological and genetic classification of medulloblastoma - a practical diagnostic guideline. *Clin Neuropathol* 35(6):344-352.
- 154 Waszak SM, Northcott PA, Buchhalter I, Robinson GW, Sutter C, Groebner S, Grund KB, Brugières L, Jones DTW, Pajtler KW, Morrissy AS, Kool M, Sturm D, Chavez L, Ernst A, Brabetz S, Hain M, Zichner T, Segura-Wang M, Weischenfeldt J, Rausch T, Mardin BR, Zhou X, Baciu C, Lawerenz C, Chan JA, Varlet P, Guerrini-Rousseau L, Fufts DW, Grajkowska W, Hauser P, Jabado N, Ra YS, Zitterbart K, Shringarpure SS, De La Vega FM, Bustamante CD, Ng HK, Perry A, MacDonald TJ, Hernáiz Driever P, Bendel AE, Bowers DC, McCowage G, Chintagumpala MM, Cohn R, Hassall T, Fleischhack G, Eggen T, Wesenberg F, Feychting M, Lannering B, Schüz J, Johansen C, Andersen TV, Rööslí M, Kuehni CE, Grotzer M, Kjaerheim K, Monoranu CM, Archer TC, Duke E, Pomeroy SL, Shelagh R, Frank S, Sumerauer D, Scheurlen W, Ryzhova MV, Milde T, Kratz CP, Samuel D, Zhang J, Solomon DA, Marra M, Eils R, Bartram CR, von Hoff K, Rutkowski S, Ramaswamy V, Gilbertson RJ, Korshunov A, Taylor MD, Lichter P, Malkin D, Gajjar A, Korbel JO and Pfister SM (2018). Spectrum and prevalence of genetic predisposition in medulloblastoma: a retrospective genetic study and prospective validation in a clinical trial cohort. *Lancet Oncol* 19(6):785-798.
- 155 Waszak SM, Robinson GW, Gudenas BL, Smith KS, Forget A, Kojic M, Garcia-Lopez J, Hadley J, Hamilton KV, Indersie E, Buchhalter I, Kerssemakers J, Jäger N, Sharma T, Rausch T, Kool M, Sturm D, Jones DTW, Vasilyeva A, Tatevossian RG, Neale G, Lombard B, Loew D, Nakitandwe J, Rusch M, Bowers DC, Bendel A, Partap S, Chintagumpala M, Crawford J, Gottardo NG, Smith A, Dufour C, Rutkowski S, Eggen T, Wesenberg F, Kjaerheim K, Feychting M, Lannering B, Schüz J, Johansen C, Andersen TV, Rööslí M, Kuehni CE, Grotzer M, Remke M, Puget S, Pajtler KW, Milde T, Witt O, Ryzhova M, Korshunov A, Orr BA, Ellison DW, Brugieres L, Lichter P, Nichols KE, Gajjar A, Wainwright BJ, Ayrault O, Korbel JO, Northcott PA and Pfister SM (2020). Germline Elongator mutations in Sonic Hedgehog medulloblastoma. *Nature* 580(7803):396-401.
- 156 Schweizer L, Koelsche C, Sahm F, Piro RM, Capper D, Reuss DE, Pusch S, Habel A, Meyer J, Gock T, Jones DT, Mawrin C, Schittenhelm J, Becker A, Heim S, Simon M, Herold-Mende C, Mechttersheimer G, Paulus W, König R, Wiestler OD, Pfister SM and von Deimling A (2013). Meningeal hemangiopericytoma and solitary fibrous tumors carry the NAB2-STAT6 fusion and can be diagnosed by nuclear expression of STAT6 protein. *Acta Neuropathol* 125(5):651-658.
- 157 Koelsche C, Schweizer L, Renner M, Warth A, Jones DT, Sahm F, Reuss DE, Capper D, Knosel T, Schulz B, Petersen I, Ulrich A, Renker EK, Lehner B, Pfister SM, Schirmacher P, von Deimling A and Mechttersheimer G (2014). Nuclear relocation of STAT6 reliably predicts NAB2-STAT6 fusion for the diagnosis of solitary fibrous tumour. *Histopathology* 65(5):613-622.

- 158 Nakada S, Minato H and Nojima T (2016). Clinicopathological differences between variants of the NAB2-STAT6 fusion gene in solitary fibrous tumors of the meninges and extra-central nervous system. *Brain Tumor Pathol* 33(3):169-174.
- 159 Koelsche C, Sahm F, Capper D, Reuss D, Sturm D, Jones DT, Kool M, Northcott PA, Wiestler B, Bohmer K, Meyer J, Mawrin C, Hartmann C, Mittelbronn M, Platten M, Brokinkel B, Seiz M, Herold-Mende C, Unterberg A, Schittenhelm J, Weller M, Pfister S, Wick W, Korshunov A and von Deimling A (2013). Distribution of TERT promoter mutations in pediatric and adult tumors of the nervous system. *Acta Neuropathol* 126(6):907-915.
- 160 Arita H, Narita Y, Takami H, Fukushima S, Matsushita Y, Yoshida A, Miyakita Y, Ohno M, Shibui S and Ichimura K (2013). TERT promoter mutations rather than methylation are the main mechanism for TERT upregulation in adult gliomas. *Acta Neuropathol* 126(6):939-941.
- 161 Berzero G, Di Stefano AL, Ronchi S, Bielle F, Villa C, Guillerm E, Capelle L, Mathon B, Laurence A, Giry M, Schmitt Y, Marie Y, Idbaih A, Hoang-Xuan K, Delattre JY, Mokhtari K and Sanson M (2021). IDH-wildtype lower-grade diffuse gliomas: the importance of histological grade and molecular assessment for prognostic stratification. *Neuro Oncol* 23(6):955-966.
- 162 Giannini C and Giangaspero F (2021). TERT promoter mutation: is it enough to call a WHO grade II astrocytoma IDH wild-type glioblastoma? *Neuro Oncol* 23(6):865-866.
- 163 Sahm F, Schrimpf D, Olar A, Koelsche C, Reuss D, Bissel J, Kratz A, Capper D, Schefzyk S, Hielscher T, Wang Q, Sulman EP, Adeberg S, Koch A, Okuducu AF, Brehmer S, Schittenhelm J, Becker A, Brokinkel B, Schmidt M, Ull T, Gousias K, Kessler AF, Lamszus K, Debus J, Mawrin C, Kim YJ, Simon M, Ketter R, Paulus W, Aldape KD, Herold-Mende C and von Deimling A (2016). TERT Promoter Mutations and Risk of Recurrence in Meningioma. *J Natl Cancer Inst* 108(5).
- 164 Takami H, Yoshida A, Fukushima S, Arita H, Matsushita Y, Nakamura T, Ohno M, Miyakita Y, Shibui S, Narita Y and Ichimura K (2015). Revisiting TP53 Mutations and Immunohistochemistry--A Comparative Study in 157 Diffuse Gliomas. *Brain Pathol* 25(3):256-265.
- 165 Gillet E, Alentorn A, Doukoure B, Mundwiler E, van Thuijl HF, Reijneveld JC, Medina JA, Liou A, Marie Y, Mokhtari K, Hoang-Xuan K, Sanson M, Delattre JY and Idbaih A (2014). TP53 and p53 statuses and their clinical impact in diffuse low grade gliomas. *J Neurooncol* 118(1):131-139.
- 166 Tanboon J, Williams EA and Louis DN (2016). The Diagnostic Use of Immunohistochemical Surrogates for Signature Molecular Genetic Alterations in Gliomas. *J Neuropathol Exp Neurol* 75(1):4-18.
- 167 Thorwarth A, Schnittert-Hübener S, Schrupf P, Müller I, Jyrch S, Dame C, Biebermann H, Kleinau G, Katchanov J, Schuelke M, Ebert G, Steininger A, Bönemann C, Brockmann K, Christen HJ, Crock P, deZegher F, Griese M, Hewitt J, Ivarsson S, Hübner C, Kapelari K, Plecko B, Rating D, Stoeva I, Ropers HH, Grüters A, Ullmann R and Krude H (2014). Comprehensive genotyping and clinical characterisation reveal 27 novel NKX2-1 mutations and expand the phenotypic spectrum. *J Med Genet* 51(6):375-387.
- 168 Lee EB, Tihan T, Scheithauer BW, Zhang PJ and Gonatas NK (2009). Thyroid transcription factor 1 expression in sellar tumors: a histogenetic marker? *J Neuropathol Exp Neurol* 68(5):482-488.

- 169 Bielle F, Villa C, Giry M, Bergemer-Fouquet AM, Polivka M, Vasiljevic A, Aubriot-Lorton MH, Bernier M, Lechapt-Zalcman E, Viennet G, Sazdovitch V, Duyckaerts C, Sanson M, Figarella-Branger D and Mokhtari K (2015). Chordoid gliomas of the third ventricle share TTF-1 expression with organum vasculosum of the lamina terminalis. *Am J Surg Pathol* 39(7):948-956.
- 170 Dutta R, Sharma MC, Suri V, Sarkar C, Garg A, Suri A and Kale SS (2022). TTF-1: A Well-Favored Addition to the Immunohistochemistry Armamentarium as a Diagnostic Marker of SEGA. *World Neurosurg* 159:e62-e69.
- 171 Hewer E, Beck J, Kellner-Weldon F and Vajtai I (2015). Suprasellar chordoid neoplasm with expression of thyroid transcription factor 1: evidence that chordoid glioma of the third ventricle and pituicytoma may form part of a spectrum of lineage-related tumors of the basal forebrain. *Hum Pathol* 46(7):1045-1049.
- 172 Hewer E and Vajtai I (2015). Consistent nuclear expression of thyroid transcription factor 1 in subependymal giant cell astrocytomas suggests lineage-restricted histogenesis. *Clin Neuropathol* 34(3):128-131.
- 173 Mete O, Lopes MB and Asa SL (2013). Spindle cell oncocytomas and granular cell tumors of the pituitary are variants of pituicytoma. *Am J Surg Pathol* 37(11):1694-1699.
- 174 Michotte A, Van Der Veken J, Huylebrouck M, Duerinck J, D'Haens J and Hoorens A (2014). Expression of thyroid transcription factor 1 in a chordoid glioma. *J Neurol Sci* 346(1-2):362-363.
- 175 Zamecnik J, Chanova M and Kodet R (2004). Expression of thyroid transcription factor 1 in primary brain tumours. *J Clin Pathol* 57(10):1111-1113.
- 176 Suwala AK, Stichel D, Schrimpf D, Maas SLN, Sill M, Dohmen H, Banan R, Reinhardt A, Sievers P, Hinz F, Blattner-Johnson M, Hartmann C, Schweizer L, Boldt HB, Kristensen BW, Schittenhelm J, Wood MD, Chotard G, Bjergvig R, Das A, Tabori U, Hasselblatt M, Korshunov A, Abdullaev Z, Quezado M, Aldape K, Harter PN, Snuderl M, Hench J, Frank S, Acker T, Brandner S, Winkler F, Wesseling P, Pfister SM, Reuss DE, Wick W, von Deimling A, Jones DTW and Sahm F (2021). Glioblastomas with primitive neuronal component harbor a distinct methylation and copy-number profile with inactivation of TP53, PTEN, and RB1. *Acta Neuropathol* 142(1):179-189.
- 177 Surun A, Varlet P, Brugières L, Lacour B, Faure-Contier C, Leblond P, Bertozzi-Salomon AI, Berger C, André N, Sariban E, Raimbault S, Prieur F, Desseigne F, Zattara H, Guimbaud R, Polivka M, Delisle MB, Vasiljevic A, Maurage CA, Figarella-Branger D, Coulet F, Guerrini-Rousseau L, Alapetite C, Dufour C, Colas C, Doz F and Bourdeaut F (2020). Medulloblastomas associated with an APC germline pathogenic variant share the good prognosis of CTNNB1-mutated medulloblastomas. *Neuro Oncol* 22(1):128-138.
- 178 Pajtler KW, Witt H, Sill M, Jones DT, Hovestadt V, Kratochwil F, Wani K, Tatevossian R, Punchihewa C, Johann P, Reimand J, Warnatz HJ, Ryzhova M, Mack S, Ramaswamy V, Capper D, Schweizer L, Sieber L, Wittmann A, Huang Z, van Sluis P, Volckmann R, Koster J, Versteeg R, Fults D, Toledano H, Avigad S, Hoffman LM, Donson AM, Foreman N, Hewer E, Zitterbart K, Gilbert M, Armstrong TS, Gupta N, Allen JC, Karajannis MA, Zagzag D, Hasselblatt M, Kulozik AE, Witt O, Collins VP, von Hoff K, Rutkowski S, Pietsch T, Bader G, Yaspo ML, von Deimling A, Lichter P, Taylor MD, Gilbertson R, Ellison DW, Aldape K, Korshunov A, Kool M and Pfister SM (2015). Molecular Classification of Ependymal Tumors across All CNS Compartments, Histopathological Grades, and Age Groups. *Cancer Cell* 27(5):728-743.

- 179 Parker M, Mohankumar KM, Punchihewa C, Weinlich R, Dalton JD, Li Y, Lee R, Tatevossian RG, Phoenix TN, Thiruvengadam R, White E, Tang B, Orisme W, Gupta K, Rusch M, Chen X, Li Y, Nagahawhatte P, Hedlund E, Finkelstein D, Wu G, Shurtleff S, Easton J, Boggs K, Yergeau D, Vadodaria B, Mulder HL, Becksfort J, Gupta P, Huether R, Ma J, Song G, Gajjar A, Merchant T, Boop F, Smith AA, Ding L, Lu C, Ochoa K, Zhao D, Fulton RS, Fulton LL, Mardis ER, Wilson RK, Downing JR, Green DR, Zhang J, Ellison DW and Gilbertson RJ (2014). C11orf95-RELA fusions drive oncogenic NF-kappaB signalling in ependymoma. *Nature* 506(7489):451-455.
- 180 Zheng T, Ghasemi DR, Okonechnikov K, Korshunov A, Sill M, Maass KK, Benites Goncalves da Silva P, Ryzhova M, Gojo J, Stichel D, Arabzade A, Kupp R, Benzel J, Taya S, Adachi T, Shiraishi R, Gerber NU, Sturm D, Ecker J, Sievers P, Selt F, Chapman R, Haberler C, Figarella-Branger D, Reifenberger G, Fleischhack G, Rutkowski S, Donson AM, Ramaswamy V, Capper D, Ellison DW, Herold-Mende CC, Schüller U, Brandner S, Driever PH, Kros JM, Snuderl M, Milde T, Grundy RG, Hoshino M, Mack SC, Gilbertson RJ, Jones DTW, Kool M, von Deimling A, Pfister SM, Sahm F, Kawauchi D and Pajtler KW (2021). Cross-Species Genomics Reveals Oncogenic Dependencies in ZFTA/C11orf95 Fusion-Positive Supratentorial Ependymomas. *Cancer Discov* 11(9):2230-2247.
- 181 Zschoernack V, Jünger ST, Mynarek M, Rutkowski S, Garre ML, Ebinger M, Neu M, Faber J, Erdlenbruch B, Claviez A, Bielack S, Brozou T, Frühwald MC, Dörner E, Dreschmann V, Stock A, Solymosi L, Hench J, Frank S, Vokuhl C, Waha A, Andreiuolo F and Pietsch T (2021). Supratentorial ependymoma in childhood: more than just RELA or YAP. *Acta Neuropathol* 141(3):455-466.