

Family/Last name

Date of birth

Given name(s)

Patient identifiers

Date of request

Accession/Laboratory number

All molecular elements are NON-CORE.

DATASET SCOPE

OVERVIEW OF SELECTED MOLECULAR MARKERS

ADEQUACY OF SPECIMEN FOR MOLECULAR ASSESSMENT



Specimen is adequate for analysis

Specimen is inadequate for analysis, give reason,
(select all that apply)

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

▼ Other, *specify*

ATRX MUTATION



ATRX mutation

- Negative
- Positive

Cannot be determined

TESTING METHOD (select all that apply)

- Sanger sequencing
- Next-generation sequencing
- PCR-based method
- Other, *specify*

ATRX expression (immunohistochemistry)

- Intact nuclear expression
- Loss of nuclear expression

BRAF ALTERATIONS



BRAF mutation

- | | |
|---|----------------------|
| Absent | Cannot be determined |
| BRAF V600E (c.1799T>A) mutation present | |
| Other BRAF mutation present, <i>specify</i> | |

MUTATIONS ASSESSED (select all that apply)

- V600E
- Any mutation in exon 15
- Other, *specify*

TESTING METHOD (select all that apply)

- Sanger sequencing
- Next-generation sequencing
- PCR-based method
- Other, *specify*

BRAF V600E expression (immunohistochemistry)

- | | |
|----------|----------------------|
| Negative | Cannot be determined |
| Positive | |

BRAF rearrangement/duplication

- | | |
|-------------------------|----------------------|
| Absent | Cannot be determined |
| Present, <i>specify</i> | |

MUTATIONS ASSESSED (select all that apply)

- 7q34 tandem duplication
- KIAA-BRAF fusion
- BRAF-RAF1 fusion
- Other, *specify*

TESTING METHOD (select all that apply)

- In situ hybridization (FISH)
- RT-PCR
- Array-based method
- RNA-sequencing
- Other, *specify*

CDKN2A/B HOMOZYGOUS DELETION 

- | | |
|-----------------------|----------------------|
| Absent | Cannot be determined |
| Homozygous deletion | |
| Heterozygous deletion | |
- TESTING METHOD (select all that apply)
- In situ hybridization (FISH, CISH)
 - Array-based method
 - Next-generation sequencing
 - Other, *specify*

CHROMOSOME 7 GAIN (combined with chromosome 10 loss) 

- | | |
|---------|----------------------|
| Absent | Cannot be determined |
| Present | |
- TESTING METHOD (select all that apply)
- In situ hybridization
 - Array-based method
 - Next-generation sequencing
 - Other, *specify*

C19MC ALTERATION 

- | | |
|--|----------------------|
| Absent | Cannot be determined |
| Absent with low level gain | |
| Present, <i>specify, including copy number</i> | |
- TESTING METHOD (select all that apply)
- In situ hybridization (FISH, CISH)
 - Array-based method
 - Next-generation sequencing
 - Other, *specify*

CHROMOSOME 10q23 (*PTEN* LOCUS) DELETION AND *PTEN* MUTATION **Chromosome 10q23 (*PTEN* Locus) deletion**

- | | |
|-------------------------------|----------------------|
| None detected | Cannot be determined |
| Interstitial deletion present | |
| Monosomy, <i>specify</i> | |
- ▼
- | | |
|--------------------------|--|
| Polysomy, <i>specify</i> | |
|--------------------------|--|

TESTING METHOD (select all that apply)

- In situ hybridization
- Array-based method
- PCR/Loss of heterozygosity assay
- Other, *specify*

***PTEN* mutation**

- | | |
|-------------------------|----------------------|
| Absent | Cannot be determined |
| Present, <i>specify</i> | |

TESTING METHOD (select all that apply)

- Sanger sequencing
- Next-generation sequencing
- PCR-based method
- Other, *specify*

CHROMOSOMAL ARM 1p/19q CODELETION 

- | | |
|--------------------------|----------------------|
| None detected | Cannot be determined |
| 1p/19q codeletion | |
| 1p only deletion | |
| 19q only deletion | |
| Polysomy, <i>specify</i> | |
- TESTING METHOD (select all that apply)
- In situ hybridization (FISH, CISH)
 - Array-based method
 - PCR/Loss of heterozygosity assay
 - Next-generation sequencing
 - Other, *specify*

EGFR AMPLIFICATION AND EGFRvIII MUTATION **EGFR amplification**

- | | |
|--|----------------------|
| Absent | Cannot be determined |
| Absent with low level gain | |
| Present, <i>specify, including copy number</i> | |

TESTING METHOD (select all that apply)

- In situ hybridization (FISH, CISH)
- Array-based method
- Next-generation sequencing
- Other, *specify*

EGFRvIII mutation	Absent Present	Cannot be determined	Ki-67 IMMUNOHISTOCHEMISTRY 	Percentage of positive nuclei
TESTING METHOD (select all that apply)	Next-generation sequencing PCR-based method Immunohistochemistry Other, specify	Cannot be determined		Cannot be determined
HISTONE H3 MUTATION AND H3 K27 TRIMETHYLATION (me3)			L1CAM EXPRESSION (IMMUNOHISTOCHEMISTRY) 	Negative Positive
Histone H3 gene family mutation	Negative Positive for K27M Positive for G34R or G34V Positive, for other H3 mutation, specify	Cannot be determined		Cannot be determined
TESTING METHOD (select all that apply)	Sanger sequencing Next-generation sequencing PCR-based method Other, specify		LIN28A EXPRESSION (IMMUNOHISTOCHEMISTRY) 	Negative Positive
Histone H3 K27M expression (immunohistochemistry)	Negative Positive	Cannot be determined	MEDULLOBLASTOMA IMMUNOHISTOCHEMISTRY 	
Histone H3 G34R expression (immunohistochemistry)	Negative Positive	Cannot be determined	β-catenin expression (immunohistochemistry)	Absence of nuclear expression Positive nuclear expression
Histone H3 K27me3 expression (immunohistochemistry)	Intact expression Loss of expression	Cannot be determined	GAB1 expression (immunohistochemistry)	Negative Positive
IDH1/IDH2 MUTATION 			YAP1 expression (immunohistochemistry)	Negative Positive
IDH1/IDH2 mutation	Absent Present, specify	Cannot be determined	MGMT PROMOTER METHYLATION 	Absent Present
TESTING METHOD (select all that apply)	Sanger sequencing Next-generation sequencing PCR-based method Other, specify		TESTING METHOD (select all that apply)	Cannot be determined
IDH1 R132H expression (immunohistochemistry)	Negative Positive	Cannot be determined	MONOSOMY 6 	Absent Present, specify
			TESTING METHOD (select all that apply)	Cannot be determined
			In situ hybridization Multiplex ligation-dependent probe amplification (MLPA) Array-based method Microsatellite analysis	

MYC GENE FAMILY AMPLIFICATION (MYC and/or MYCN) 

Absent Cannot be determined
Absent with low level gain
Present, specify, including copy number

TESTING METHOD (select all that apply)

In situ hybridization (FISH, CISH)
Array-based method
Next-generation sequencing
Other, specify

NAB2-STAT6 FUSION **NAB2-STAT6 fusion**

Negative Cannot be determined
Positive

TESTING METHOD (select all that apply)

FISH
Next generation sequencing
Other, specify

STAT6 expression (immunohistochemistry)

Absence of nuclear expression Cannot be determined
Positive nuclear expression

PITUITARY HORMONES AND TRANSCRIPTION FACTORS IMMUNOHISTOCHEMISTRY 

Tumour cells are reactive for (select all that apply)

Prolactin Cannot be determined
Human growth hormone
β-TSH
β-FSH
β-LH
Alpha subunit
ACTH
PIT1
TPIT
SF1
Other, specify

RELA FUSION 

Negative Cannot be determined
Positive

TESTING METHOD (select all that apply)

FISH
Next generation sequencing
Other, specify

SMARCA4/BRG1 ALTERATION **SMARCA4/BRG1 mutation**

Absent Cannot be determined
Present, specify

TESTING METHOD (select all that apply)

Sanger sequencing
Next-generation sequencing
PCR-based method
Other, specify

BRG1 loss of expression (immunohistochemistry)

Intact nuclear expression Cannot be determined
Loss of nuclear expression

SMARCB1/INI1/HSNF5 ALTERATION **SMARCB1/INI1/HSNF5 mutation**

Absent Cannot be determined
Present, specify

TESTING METHOD (select all that apply)

Sanger sequencing
Next-generation sequencing
PCR-based method
Other, specify

INI1 (BAF47) loss of expression (immunohistochemistry)

Intact nuclear expression Cannot be determined
Loss of nuclear expression

TERT PROMOTER MUTATION 

Absent Cannot be determined
Hotspot mutation (C228T or C250T)
Other mutation, specify

TESTING METHOD (select all that apply)

Sanger sequencing
Next-generation sequencing
PCR-based method
Other, specify

TP53 MUTATION **TP53 mutation**

Absent

Cannot be determined

Present, *specify***EXONS ANALYSED**

Exons 5-8

All exons

Other, *specify***TESTING METHOD** (select all that apply)

Sanger sequencing

Next-generation sequencing

PCR-based method

Other, *specify***p53 expression (immunohistochemistry)**

Negative or rare, lightly positive cells

Cannot be determined

Intermediate (intermediate numbers of predominantly lightly positive cells)

Positive (diffuse and strong nuclear positivity)

OTHER FINDINGS **Other immunohistochemical findings, specify****Other molecular findings, specify test, testing method and findings****YAP1 FUSION** 

Negative

Cannot be determined

Positive

TESTING METHOD (select all that apply)

FISH

Next generation sequencing

Other, *specify*