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| **SWGLH – Cancer Genomics Test Request Form: Neurological Tumours** |
| Patient name:       | Referring Consultant:       |
| Address:     Postcode:       | Department and Hospital:       |
| Report destination (e-mail/s):      |
| DOB:       | Sex:       | Pathologist:       |
| NHS number:       | Date of resection/biopsy:       |
| Pathology block number:       | Date test requested:       |
| Hospital number:       | Date sample sent to SWGLH:       |
|  | Date of MDT for discussion of result:       |

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| **Reason for referral:**       |
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| For further information refer to the National Genomics Test Directory for Cancer: <https://www.england.nhs.uk/publication/national-genomic-test-directories/>

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| **Clinical Indication** | **Test Code**  | **Test Directory Name** | **Sample\*** |
| **Adult Oligodendroglioma** | M35.1 [ ]  | Adult Oligodendroglioma Gene Panel – small variants *(ATRX, BRAF, H3F3A, HIST1H3B, IDH1, IDH2, TERT promoter)* | **A** |
|  | M35.2 [ ]  | 1p/19q codeletionFISH | **B** |
|  | M28.3 [ ]  | *EGFR* amplification FISH | **B** |
|  | M21.23 [ ]  | *CDKN2A/B* FISH | **B** |
|  | M189.11 [ ]  | *SNP array (1p/19q, EGFR amplification, CDKN2A/B)* | **D** |
|  | M31.1 [ ]  | *MGMT* promoter methylation analysis | **A** |
|  | M35.6 [ ]  | Methylation array | **E** |
|  | M35.8 [ ]  | RNA fusion panel\* | **C** |
| **Adult Astrocytoma** | M21.1 [ ]  | Adult Astrocytoma Gene Panel *– small variants (ATRX, BRAF, CIC, H3F3A, HIST1H3B, IDH1, IDH2, NF1, NOTCH1, PDGFRA, PIK3CA, PTEN, SMARCA4, TP53, TERT promoter)* | **A** |
|  | M28.3 [ ]  | *EGFR* amplification FISH | **B** |
|  | M21.23 [ ]  | *CDKN2A/B* FISH | **B** |
|  | M189.11 [ ]  | *SNP array (EGFR amplification, CDKN2A/B)* | **D** |
|  | M31.1 [ ]  | *MGMT* promoter methylation analysis | **A** |
|  | M21.20 [ ]  | Methylation array | **E** |
|  | M22.9 [ ]  | RNA fusion panel\* | **C** |
| **Adult High Grade Glioma** | M192.1 [ ]  | Adult High Grade Glioma Panel – small variants *(IDH1, IDH2, ATRX, BRAF, CDKN2B, CIC, FGFR1, FGFR2, FGFR3, H3F3A, H3F3B, H3F3C, HIST1H3B, HIST1H3C, HIST2H3C, HRAS, KRAS, NRAS,* *MDM2, MDM4, NF1, PDGFRA, PIK3CA, PTEN, RB1, SETD2, TERT promoter, TP53, VHL)* | **A** |
|  | M192.14 [ ]  | *EGFR* amplification FISH | **B** |
|  M192.13 [ ]  | *CDKN2A/B* FISH | **B** |
| M189.11 [ ]  | *SNP array (EGFR amplification, CDKN2A/B)* | **D** |
| M29.2 [ ]  | *MGMT* promoter methylation analysis | **A** |
|  | M29.6 [ ]  | Methylation array | **E** |
|  | M192.21 [ ]  | RNA fusion panel\* | **C** |
| **Meningiomas** | M33.3 [ ]  | Meningioma Gene Panel – small variants *(BAP1, NF1, NF2, TERT)* | **A** |
|  M193.13 [ ]  | *CDKN2A/B* FISH | **B** |
|  | M189.11 [ ]  | *SNP array (CDKN2A/B)* | **D** |
|  | M33.4 [ ]  | Methylation array | **E** |
| **Embryonal Tumours** Note: Medulloblastomas  | M194.1 [ ]  | Embryonal Tumours Gene Panel – small variants (*ALK, BCOR, CTNNB1, DICER1, EZH2, MYCN, NOTCH1, PIK3CA, PTCH1, PTEN, SMARCA4, SMARCB1, SMO, SUFU, TERT promoter, TP53, YAP1)* | **A** |
| to be sent directly to Newcastle | M194.13 [ ]  | *MYC* copy number FISH | **B** |
| M194.14 [ ]   | *MYCN* copy number FISH | **B** |
|  | M194.8 [ ]  | *SNP array (MYC and MYCN copy number)* | **D** |
| M194.23 [ ]  | Methylation array | **E** |
|  | M190.2[ ]  | RNA fusion panel\* | **C** |
| **Ependymal Tumours** | M25.10 [ ]  | *MYCN* copy number FISH | **B** |
| M189.11 [ ]  | *SNP array (MYCN copy number)* | **D** |
|  | M25.7 [ ]  | Methylation array | **E** |
|  | M25.9 [ ]  | RNA fusion panel\* | **C** |
| **Glioneuronal Tumours/LEATs** | M32.1 [ ]  | Low Grade Glioma/Glioneuronal Gene Panel – small variants (*AKT1, AKT2, AKT3, BRAF, EGFR, H3F3A, HIST1H3B, FGFR1, FGFR2, FGFR3, IDH1, IDH2, NF1, NOTCH1, NOTCH2, NOTCH3, NRAS, PDGFRA, PIK3CA, PTEN, RAF1, TERT* promoter*, TSC1, TSC2*) | **A** |
|  | M213.23 [ ]  | 1p/19q codeletionFISH | **B** |
| M36.11 [ ]  | *CDKN2A/B* FISH | **B** |
|  | M189.11 [ ]  | *SNP array (1p/19q, CDKN2A/B)* | **D** |
| M213.2[ ]  | RNA fusion panel\* | **C** |
|  | M213.38 [ ]  | Methylation array | **E** |
| **Paediatric Diffuse Low Grade Glioma** | M213.1 [ ]  | Paediatric Diffuse Low Grade Glioma Gene Panel – small variants(*ALK, ATRX, BRAF, CDKN2A, CTNNB1, FGFR1, FGFR2, FGFR3, FGFR4, HIST1H3B, H3F3A, H3F3B, H3F3C, KIT, NRAS, PDGFRA, PHOX2B, PIK3CA, RAF1, SMARCA4, SMARCB1, TP53*) | **A** |
|  | M36.11 [ ]  | *CDKN2A/B* FISH | **B** |
|  | M189.11 [ ]  | *SNP array (CDKN2A/B)* | **D** |
|  | M22.7 [ ]  | Methylation array | **E** |
|  | M186.8[ ]  | RNA fusion panel\* | **C** |
| **Paediatric Circumscribed Low**  | M36.12[ ]  | Pilocytic Astrocytoma Gene Panel – small variants (*BRAF, CDKN2A, FGFR1, FGFR2, FGFR3, NF1, RAF1*) | **A** |
| M36.11 [ ]  | *CDKN2A/B* FISH | **B** |
| **Grade Glioma** | M189.11 [ ]  | *SNP array (CDKN2A/B)* | **D** |
| M36.14 [ ]  | RNA fusion panel\* | **C** |
|  | M36.13 [ ]  | Methylation array | **E** |
| **Paediatric High Grade Glioma** | M184.1[ ]  | Paediatric Glioma Gene Panel – small variants (*ATRX, BRAF, FGFR1, FGFR2, FGFR3, H3F3A, H3F3B, H3F3C, HIST1H3B, HIST1H3C, HIST2H3C, IDH1, IDH2, NF1, TP53, VHL*) | **A** |
|  | M36.11 [ ]  | *CDKN2A/B* FISH | **B** |
| M213.27 [ ]  | *EGFR* amplification FISH | **B** |
|  | M189.11 [ ]  | *SNP array (EGFR amplification, CDKN2A/B)* | **D** |
| M184.8 [ ]  | RNA fusion panel\* | **C** |
|  | M189.16 [ ]  | *MGMT* promoter methylation analysis | **A** |
|  | M185.4 [ ]  | Methylation array | **E** |
| **Paediatric Midline Diffuse Glioma** | M183.1 [ ]  | Paediatric Midline Diffuse Glioma Gene Panel – small variants (*ACVR1, ATRX, BRAF, CDK4, CDK6, EGFR, FGFR1, H3F3A, HIST1H3C, HIST1H3B, PDGFRA, PIK3CA, PPM1D, PTEN, TP53, NF1, TERT promoter)* | **A** |
|  |  M183.3 [ ]  | *MYC* copy number FISH | **B** |
| M183.4 [ ]   | *MYCN* copy number FISH | **B** |
|  | M36.11 [ ]  | *CDKN2A/B* FISH | **B** |
| M189.11 [ ]  | *SNP array (MYC, MYCN, CDKN2A/B)* | **D** |
|  | M183.7 [ ]  | Methylation array | **E** |
| M183.9 [ ]  | RNA fusion panel\* | **C** |
| **Infantile Hemispheric Glioma** | M184.8 [ ]  | RNA fusion panel\* | **C** |
| M185.4 [ ]  | Methylation array | **E** |
| **Pineoblastoma** | M37.1 [ ]  | Pineoblastoma Gene Panel – small variants *(DICER1, MYC)* | **A** |
| M37.3 [ ]  | Methylation array | **E** |
|  | M37.4 [ ]  | RNA fusion panel\* | **C** |

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| **Mesenchymal Tumours** | Refer to sarcoma request form |
| **Solid Tumours** | Refer to solid tumours request form |
| **Haematological** | Refer to BHODS request form |
| **Neuroblastoma** | Send directly to Newcastle |

**Neuropathology Report**: (please include a copy of the neuropathology report for this patient) [ ] **\*Sample Requirements Key:****A DNA extraction**[ ]  Sample with **>30%** neoplastic cells: send one tube (Eppendorf or Universal): containing 5 x 10µm sections (curls/scrolls) OR[ ]  Sample with **<30%** neoplastic cells: send 10 x 5µm slide mounted sections along with H&E with regions of >30% neoplastic cells highlighted OR[ ]  Frozen Tissue (approx.4mm3)if neoplastic cell content is >30% Note: if two ‘A’ tests are required e.g. a Gene Panel and *MGMT* testing, it is not necessary to send double the material. However extra material is required for FISH (B), RNA (C), SNP array (D) or methylation array (E) testing as below.**B FISH**[ ]  2 x 4µm and 2 x 2µm sections on 'APES' or 'sticky' slides **per test** required with an accompanying H&E slide with the appropriate tumour rich area(s) marked. Please also send frozen tissue for SNP array (see section D below).**C RNA extraction**[ ]  Sample with **>30%** neoplastic cells: send one tube (Eppendorf or Universal): containing 5 x 10µm sections (curls/scrolls) OR[ ]  Sample with **<30%** neoplastic cells: send 10 x 5µm slide mounted sections along with H&E with regions of >30% neoplastic cells highlightedNote: frozen tissue is not currently suitable for RNA extraction\* RNA fusion panel analyses the following genes (key fusion genes in Neurological Tumours in bold): ***AGK****,* ***AKAP9****, AKT3,* ***ALK****, AR, ASPSCR1, AXL, BCL9,* ***BCOR****,* ***BRAF****, BRCA1, BRCA2, BRD2, BRD3, BRD4, CAMTA1,* ***CCDC6****,* ***CCNB3****, CDK4,* ***CIC****, COL1A1, CPNE1, CPSF6, CTNNB1, DDIT3, DNAJB1, EGFR, ELM4, EPC1, ERBB2, ERG, ESR1, ETS1, ETV1, ETV4, ETV5, ETV6,* ***EWSR1****,* ***FAM118B****,* ***FGFR1****,* ***FGFR2****,* ***FGFR3****,* ***FGFR4****, FLI1, FLT1, FMR1, FN1, FOSB, FOXO1, FUS,* ***FXR1****, GNA11, HEY1, HNRNPH1, IDH1, IDH2, JAZF1, KDR,* ***KIAA1549****, KIT, LGR5,* ***MACF1****, MALAT1, MAML2, MET, MITF,* ***MN1****, MSH2,* ***MYB****,* ***MYBL1****,* ***MYC****, NAB2, NCOA2,* ***NFIA****, NFIB, NOTCH1, NOTCH2, NOTCH3, NPM1, NR4A3, NRG1,* ***NTRK1****,* ***NTRK2****,* ***NTRK3****, NUP107, NUTM1, NUTM2B, NUTM2E, OGA, PAX3, PAX7, PDGFB, PDGFRA, PDGFRB, PHF1, PIK3CA, PLAG1, PPARG, PRCC, PRKACA, PTPRK,* ***PVT1****,* ***RAF1****, RARG,* ***RELA****,* ***RET****,* ***ROS1****, RPS6KB1, RSPO3, SERPINE1, SRGAP3, SS18, STAT6, SUZ12, TCL1B,* ***TFE3****, TFEB, TGFBR3, TMP3, TMPRSS2, TPM4,* ***TTYH1****, USP6, WT1, WWTR1,* ***YAP1****, YWHAE,* ***ZFTA*****D SNP array**[ ]  Frozen Tissue (approx.4mm3)if neoplastic cell content is >30% **E Methylation array**[ ]  Sample with **>30%** neoplastic cells: send one tube (Eppendorf or Universal): containing 5 x 10µm sections (curls/scrolls) OR[ ]  Sample with **<30%** neoplastic cells: send 10 x 5µm slide mounted sections along with H&E with regions of >30% neoplastic cells highlighted OR[ ]  Frozen Tissue (approx.4mm3)if neoplastic cell content is >30% Note: a separate DNA extraction is required for methylation array testing**Please indicate the percentage neoplastic cell content in the curls/marked region of the H&E/frozen tissue:**[ ]  <30% (not recommended due to risk of false negative result but please specify reason and neoplastic cell content if sending       )[ ]  31-40% [ ]  41-50% [ ]  51-60% [ ]  61-70% [ ]  71-80% [ ]  81-90% [ ]  91-100%**Please send paperwork and sample to:** Bristol Genetics Laboratory, Pathology Sciences, Southmead Hospital, Bristol, BS10 5NB. **Phone:** 0117 414 6168 **Email:** SWGLHcancer@nbt.nhs.uk***CONSENT STATEMENT It is the referring clinician’s responsibility to ensure that the patient/carer knows the purpose of the test and that the DNA sample will be retained in long term storage and may be used for future diagnostic tests. Completing this form is an indication that the clinician has obtained consent for testing and storage. The patient should be advised that the sample may be used anonymously for quality assurance and training purposes. Please advise us of any restrictions.*** |