

CNS Somatic Testing Request Form

North West Genomic Laboratory Hub (MANCHESTER), Manchester Centre for Genomic Medicine (MCGM)

Patient Details		Payment Status:	NHS	Private	Referring Cli	nicia	n	UKAS MEDICAL
Surname:				Consultant (in full):			9865	
Forename:				Hospital (in full):				
DoB :	NHS No:			Department:		Tel:		
Sex:	Hospital No:			Email:				
Address:			Copy report to (if applicable):					
Postcode:								

 3. TEST REQUEST (please select options by placing a tick or cross next to each test required) See overleaf for minimum sample requirements and additional information on sample preparation. 1. Please note that all genes are tested and reported and this test may identify pathogenic germline variants. 2. NGS panel testing also available for research or clinical trial support. 	For GDL red use ONLY			
1p19q FISH				
EGFR amplification	гізп			
MGMT promoter hypermethylation	Bisulphite treatment			
KIAA1549:BRAF fusion				
C11orf95:RELA fusion	RNA extraction			
EGFRvIII transcript				
BRAF codon 600 mutation testing				
Meningioma/schwannoma panel ¹ (NF2, SMARCB1, SMARCE1, SMARCA4, LZTR1)				
NGS CNS tumour sub-panel ^{1,2} – please circle any genes where analysis is a priority (AKT1; ALK; AR; ATRX; BRAF;				
CDKN2A; CTNNB1; DDR2; EGFR; ERBB2; FGFR3; GNA11; GNAQ; H3F3A; H3F3B; HIST1H3B; HIST1H3C; IDH1;	DNA extraction			
IDH2; KIT; KRAS; MAP2K1; MET; NRAS; PDGFRA; PIK3CA; PTEN; RET; STK11; TERT (including promoter); TP53;				
VHL)				
Methylation arrays (please send an additional 4 x 5uM unmounted sections)				

4. PATHOLOGY AND CLINICAL DETAILS

Tumour Type/origin of organ: Pathologist: Hospital/Trust: Pathology Block/Sample No: Date sections sent to Genetics lab:

Please indicate the approximate % nuclei that are neoplastic in the sample sent for analysis:

(this information	is important and is us	sed to ensure the test of	carried out is appro	priately sensitive)
<10%*	10-20%*	20-30%*	>30%	

*If sample is suitable for macrodissection, please send slide mounted sections and include an H&E stained section with area(s) of tumour clearly circled and an estimate of % nuclei that are neoplastic within marked area ______%

PLEASE COMPLETE SECTION 1-3 AND EITHER FORWARD TO THE PATHOLOGY LABORATORY HOLDING THE SAMPLE, OR IF YOU REQUIRETHEGENOMICDIAGNOSTICSLABORATORYTOOBTAINTHESPECIMENPLEASEFORWARDTOmft.Pharmaco.GeneticsRequests@nhs.net.SECTION 4 IS INTENDED TO BE COMPLETED BY THE PATHOLOGY LABORATORY.

INFORMATION FOR PATHOLOGY LAB (ALL SAMPLES)

Minimum sample requirements for each individual test:

- o FISH test: 4 x 3uM unstained slide mounted sections (see below for information on sample preparation)
- o MGMT Hypermethylation test: 2 x 5uM unstained sections
- o Fusion test or EGFRvIII transcript: 4 x 5uM unstained slide unmounted rolls
- $\circ~$ BRAF codon 600 or NGS panel: 5 x 5uM unstained sections
- Formalin fixed paraffin embedded (FFPE) material should be reviewed by a histo/cyto-pathologist to identify areas containing neoplastic cells and determine suitability for testing.
- Sections should be cut under conditions that prevent cross contamination from other specimens.
- Scrolls should be sent in a sterile tube labelled with at least 2 patient identifiers, one of which should be the pathology sample number. Containers and slides should also be labelled with at least 2 patient identifiers one of which should be the pathology sample number.
- For each additional test indicated to need additional material please send an additional tube of scrolls.
- Please avoid baking slides or heating samples
- Please send appropriate corresponding paperwork with the samples
- Please contact the laboratory for additional guidance or if you are unsure whether a sample is suitable

FISH TEST

- Prepare 4 unstained sections (3uM thick) floated on the surface of a purified water bath set at 40°C (+/-2°C).
- Mount on positively charged slides and allow to air-dry
- Also include 1 H&E slide with regions enriched for nuclei that are neoplastic marked by a Pathologist along with an estimate % nuclei that are neoplastic within the marked area(s)

