North East and Yorkshire Genomic Laboratory Hub

Solid Cancer Genomics Referral Form

Testing Lab Use Only

Lab No:
Date received:
Reporting Lab: LDS NCL SHF

Patient Information – use sticker if available				**Referring clinician:**	
Surname:		**D.O.B:**		**Department and Hospital:**	
Forename(s):		**Sex:**		**Report destination (NHS.net email):**	
Patient's address and postcode:		**Date of biopsy or resection:**		**Copies of reports to (NHS.net email):**	
NHS no.:		**Date sample sent for testing:**		**Pathologist:**	
Hospital no.:		**NHS** ☐ **Private** ☐		**Billing details if not NHS:**	

Clinical details - e.g. tumour type and disease stage (if available)

Test(s) Required and test code (M code) – please refer to National Genomic Test Directory (https://www.england.nhs.uk/publication/national-genomic-test-directories/).

Please tick	Test type	Further testing details - specify gene targets and M code if known
☐	**DNA analysis**	
☐	**RNA analysis (gene fusions, eg NTRK)**	
☐	**DNA and RNA analysis**	
☐	**FISH (please specify probes)**	
☐	**Methylation analysis (MGMT or MLH1)**	
☐	**SNP arrays**	
☐	**Methylation (EPIC) arrays**	
☐	**Other (please specify)**	

Please see solid cancer genomics guidance notes overleaf for details on requesting testing for DPYD, cell free DNA, whole genome sequencing & HRD/somatic BRCA

Sample information (please see sample requirements in the solid cancer genomics guidance notes overleaf)

FFPE curls ☐ FFPE sections ☐ Fresh tissue ☐ DNA ☐
Histopath. no Block no.

Assessing Histopathologist

Estimated tumour cell percentage
Cellularity (Very High/High/Medium/Low/Very Low)
Percentage necrosis

Sample Type:
☐ Biopsy ☐ Resection ☐ Cytology
☐ Primary ☐ Metastasis ☐ Other

Once taken, samples should be sent to your <u>local</u> genomics Laboratory (see below for contact information).
For queries, please use contact details below.

Newcastle Genetics Laboratory	Newcastle Genetics Laboratory Central Parkway Newcastle upon Tyne Tyne and Wear NE1 3BZ	nuth.cancer.genomics@nhs.net **0191 241 8786** www.newcastlelaboratories.com/lab_service/laboratory-cancer-services/
Sheffield Genetics Laboratory	Sheffield Diagnostic Genetics Service Sheffield Children's NHS Foundation Trust Western Bank Sheffield S10 2TH	sheffield.diagnosticgenetics@nhs.net **0114 271 7014** www.sheffieldchildrens.nhs.uk/SDGS.htm
Leeds Genetics Laboratory	Leeds Genetics Laboratory, Genomic Specimen Reception Bexley Wing (Level 5) St James's University Hospital Beckett Street Leeds, LS9 7TF	mod.lth@nhs.net **0113 206 5205** www.leedsth.nhs.uk/a-z-of-services/the-leeds-genetics-laboratory/

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Solid Cancer Genomics guidance notes

Please take note of these specific referral & sample guidelines to ensure that the correct testing is carried out and delays are avoided

1. For further information on NEY GLH Services – please visit https://ney-genomics.org.uk/
2. For DPYD referrals please use the NEY GLH DPYD referral form at https://ney-genomics.org.uk/wp-content/uploads/2022/02/411.028-DYPD-Referral-Form-v2.0web.pdf
3. For Whole Genome Sequencing referrals please use the NHSE referral forms at NHS England » NHS Genomic Medicine Service test order forms and the record of discussion form at NHS England » NHS Genomic Medicine Service record of discussion form
4. For blood plasma cell free DNA testing, please use the NEY GLH circulating tumour DNA referral form at The Leeds Genetics Laboratory, Referral Forms (leedsth.nhs.uk)
5. For HRD and somatic BRCA testing in ovarian carcinoma, please use the NEY GLH HRD and somatic BRCA referral form at GLH-tBRCA-and-HRD-request-form-v1.0web.pdf (ney-genomics.org.uk)

Sample Requirements

FFPE material:

1. FISH

Send 2-3 x 4µm FFPE sections on 'APES' or 'sticky' slides per test required with marked H&E slide with tumour rich area(s) marked.
Minimum estimated tumour cell percentage 20%.

2. For DNA or RNA extraction only – DNA NGS panels, Trusight RNA fusion panel, MGMT methylation testing, Sanger sequencing

Samples with >20% estimated tumour cell percentage: send one tube (Eppendorf or Universal) containing 5-10 x 10µm FFPE curls
Samples with lower overall tumour percentage, if there is a region of the block with >20% tumour, please either;
a. macro dissect tumour-rich regions and send in a single tube (preferred), or
b. send 10 x 5µm slide mounted sections along with marked H&E with tumour rich area(s) marked.
If it is not possible to macrodissect out a tumour rich region >20%, please contact the laboratory for further guidance as to whether the sample can still be tested.

***Exceptions:**

a. For MLH1 methylation testing, please send 10 x 5µm slide mounted sections along with marked H&E with tumour rich area(s) marked. Samples should have >20% estimated tumour cell percentage. Curls are not acceptable. If tumour content is <20%, please contact the laboratory for further guidance as to whether the sample can still be tested
b. Where methylation arrays are also required, please send an additional 5-10 x 10 µm FFPE curls, as above

3. For DNA and RNA extraction – Oncomine Focus, Genexus or Trusight Oncology 500 (TSO500) panel

Samples with >20% estimated tumour cell percentage: send two tubes (Eppendorf or Universal): each containing 5-10 x 10µm FFPE curls
Samples with lower overall estimated tumour cell percentage, if there is a region of the block with >20% tumour, please either;
a. macro dissect tumour-rich regions and split into two tube (preferred), or
b. send 20 x 5µm slide mounted sections along with marked H&E with tumour rich area(s) marked
If it is not possible to macrodissect out a tumour rich region >20%, please contact the laboratory for further guidance as to whether the sample can still be tested

Testing pathways may change and updated guidance will be given on the NEY GLH Solid Tumour testing website – please click here

Fresh frozen tissue:

Send either frozen tumour in dry ice or if refrigerated in stabilisation buffer (e.g. 'RNA later' or RLT buffer)
Please send at least 5mm^3 tumour tissue