



Solid Cancer Genomics Referral Form

Lab No:
Date received:
Reporting Lab:

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 <input type="checkbox"/> Private <input type="checkbox"/>		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
<input type="checkbox"/>	DNA analysis	
<input type="checkbox"/>	RNA analysis (gene fusions, eg NTRK)	
<input type="checkbox"/>	DNA and RNA analysis	
<input type="checkbox"/>	FISH (please specify probes)	
<input type="checkbox"/>	Methylation analysis (MGMT or MLH1)	
<input type="checkbox"/>	SNP arrays	
<input type="checkbox"/>	Methylation (EPIC) arrays	
<input type="checkbox"/>	Other (please specify)	

Please see solid cancer genomics guidance notes overleaf for details on requesting testing for DPYD, cell free DNA, whole genome sequencing, and tumour HRD/BRCA testing in ovarian carcinoma

Sample information (please see sample requirements in the solid cancer genomics guidance notes overleaf)			
FFPE curls <input type="checkbox"/>	FFPE sections <input type="checkbox"/>	Fresh tissue <input type="checkbox"/>	DNA <input type="checkbox"/>
Histopath. no	Block no.	Assessing Histopathologist	
Estimated tumour cell percentage		Sample Type:	
Cellularity (Very High/High/Medium/Low/Very Low)		<input type="checkbox"/> Biopsy	<input type="checkbox"/> Resection <input type="checkbox"/> Cytology
Percentage necrosis		<input type="checkbox"/> Primary	<input type="checkbox"/> Metastasis <input type="checkbox"/> Other

Once taken, samples should be sent to your local 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	scn-tr.sdgs.oncology@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/

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 tumour 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 other than prostate cancer** 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 (discouraged for Trusight RNA fusion panel).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.
- **c. For **prostate cancers**, only FFPE curls will be accepted for testing - requirement is therefore one tube (Eppendorf or Universal) containing 5-10 x 10µm FFPE curls

3. For DNA and RNA extraction – OncoPrint 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 5mm³ tumour tissue