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Landscape of cancer biomarker testing in England following genomic services reconfiguration: insights from a nationwide pathologist survey

Phillipe Taniere [ID],[1] Andrew G Nicholson,[2,3] John R Gosney,[4] Maria Angeles Montero Fernandez,[5] Danielle Bury,[6] David Allan Moore [ID],[7] Eldo Verghese,[8] Irshad Soomro,[9] Leena Joseph,[5] Nidhi Bhatt,[10] Patrizia Viola,[11] Rozinder Bains,[12] Adrienne G Lanctot,[12] Jacqueline Ryan[12]

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ABSTRACT

Aims Cancer diagnostics have been evolving rapidly. In England, the new National Health Service Genomic Medicine Service (GMS) provides centralised access to genomic testing via seven regional Genomic Laboratory Hubs. The PATHways survey aimed to capture pathologists' experience with current diagnostic pathways and opportunities for optimisation to ensure equitable and timely access to biomarker testing.
Methods A nationwide survey was conducted with consultant pathologists from regional laboratories, via direct interviews based on a structured questionnaire. Descriptive analysis of responses was undertaken using quantitative and qualitative methods.
Results Fifteen regional centres completed the survey covering a median population size of 2.5 (1.9–3.6) million (each for n=12). The median estimated turnaround time (calendar days) for standard molecular markers in melanoma, breast and lung cancers ranged from 2 to 3 days by immunohistochemistry (excluding NTRKfus in breast and lung cancers, and PD-L1 in melanoma) and 6–15 days by real-time-PCR (excluding KIT for melanoma), to 17.5–24.5 days by next-generation sequencing (excluding *PIK3CA* for breast cancer). Tests were mainly initiated by pathologists and oncologists. All respondents discussed the results at multidisciplinary team (MDT) meetings. The GMS roll-out was perceived to have high impact on services by 53% of respondents, citing logistical and technical issues. Enhanced education on new pathways, tissue requirements, report interpretation, providing patient information and best practice sharing was suggested for pathologists and other MDT members.
Conclusion Our survey highlighted the role of regional pathology within the evolving diagnostic landscape in England. Notable recommendations included improved communication and education, active stakeholder engagement, and tackling informatics barriers.

INTRODUCTION
Over the past decade, transformative advances in genomic sequencing technologies and the corresponding increase in potentially actionable oncogenic targets have facilitated a vast expansion of genomic testing in cancer. Use of technologies such as next-generation sequencing (NGS) and whole-genome sequencing for routine diagnosis

WHAT IS ALREADY KNOWN ON THIS TOPIC
⇒ Genomics testing is a rapidly evolving cornerstone of cancer treatment, allowing clinicians to offer personalised medicines to patients. In England, the recent implementation of the Genomics Medicines Services has transformed the solid tumour molecular diagnostics pathway.

WHAT THIS STUDY ADDS
⇒ The PATHways survey captured the real-world experience of pathologists involved in biomarker testing and the challenges and opportunities of transition towards expanded and centralised genomic services. Our findings highlight the important role of pathology within this new model.

HOW THIS STUDY MIGHT AFFECT RESEARCH, PRACTICE OR POLICY
⇒ The recommendations provided by the authors will help clinical teams review and optimise their local genomic testing pathways to ultimately improve patient care.

and patient management brings great opportunities alongside some challenges. A personalised approach to optimal therapy selection based on molecular markers relies on equitable and timely access to the tests.

The UK has been at the forefront of integrating genomics into routine healthcare following the success of Genomics England's 100 000 Genome Project, which laid the foundation for the National Health Service (NHS) England Genomic Medicine Service (GMS) launched in 2018. Delivery of the GMS is underpinned by consolidation of genomic testing to seven regional Genomic Laboratory Hubs (GLHs) and the publication of a National Genomic Test Directory. This directory specifies the genomic tests commissioned by the NHS, its technology and the patient eligibility criteria.[1 2]

Consolidation of genomic testing requires effective collaboration among multiple stakeholders (figure 1). In optimising diagnostic pathways from pathology through to regional genomic laboratories, there are several technical and logistical
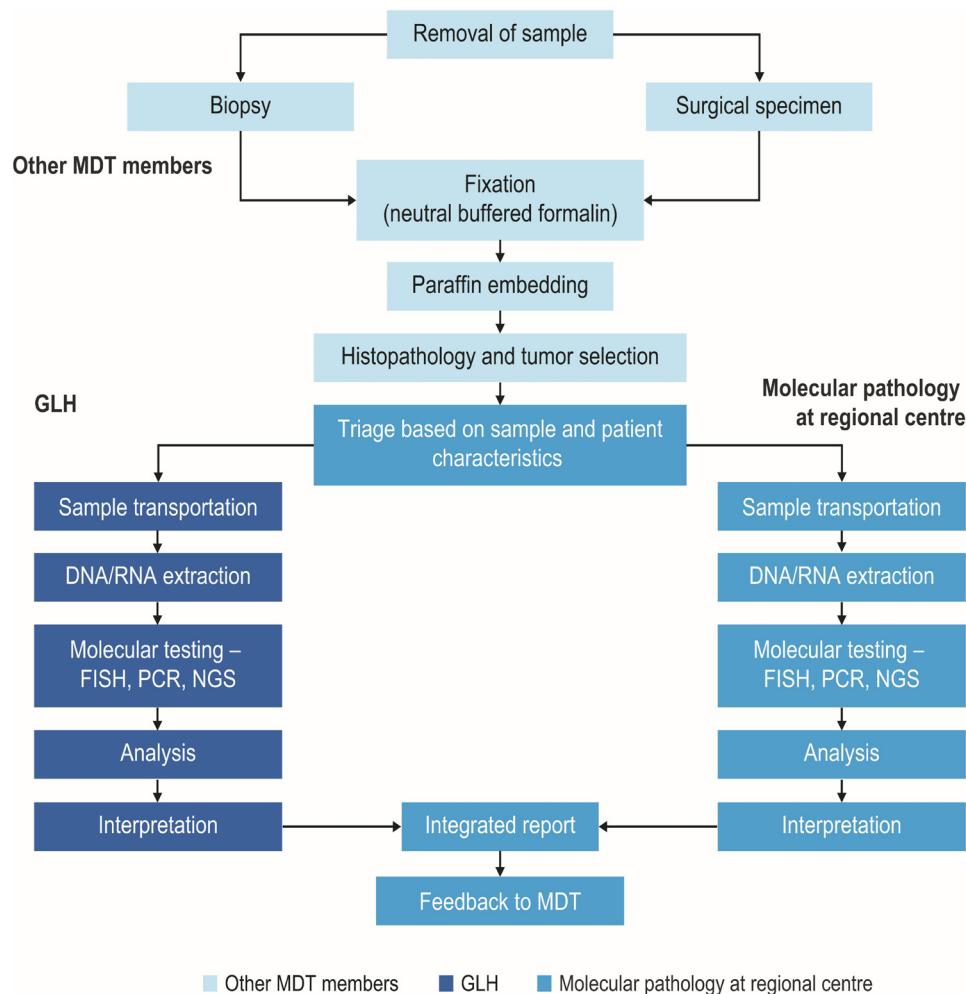
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Figure 1 Workflow for genetic testing within the NHS England Genomic Medicine Service Regional pathology plays a central role in supporting the delivery of genomic services. Pathologists have the critical responsibility in driving the evolving diagnostic pathways by integrating and interpreting morphological, immunohistochemical and molecular data from sources alongside other clinical information to offer expert opinions on diagnostic and prognostic information. FISH, fluorescence in situ hybridisation; GLH, Genomic Laboratory Hub; MDT, multidisciplinary team; NGS, next-generation sequencing; NHS, National Health Service.

challenges that require transformation via collaboration across all members involved in the delivery of clinical diagnostics.[3]

In the view of ongoing centralisation of genomic services in England, the PATHways survey aimed to understand the current and evolving molecular pathology services from the perspective of pathologists, with a focus on testing in breast cancer, lung cancer and melanoma. We aimed to highlight the challenges and support required for pathology laboratories, as a key stakeholder in establishing a diagnostic infrastructure, to ensure all required biomarker results are delivered in clinically relevant timeframes for optimal patient management.

METHODS
Survey design and dissemination
Consultant pathologists (CPs) from regional pathology laboratories across England were invited to participate in a nationwide survey (January–March 2022). Each participating pathology laboratory was engaged in one-to-one remote interviews with members of the Novartis Medical Science Liaison (MSL) team. The interviews were facilitated with a structured questionnaire developed in collaboration with an expert steering committee (SC) comprising of three leading UK pathologists. The involvement of the SC ensured the survey was clinically

accurate and relevant to the healthcare community. A virtual interview method was selected to allow capture of the nuances of CPs experiences, and as it allowed for rapid data collection considering the temporal relevance of the data. The survey was conducted in accordance with the British Healthcare Business Intelligence Association (BHBIA) guidance for the conduct of market research. The survey included 34 multiple-choice questions, some with free-text fields. The questions were grouped into the following five sections: referring centre profile, testing for specific cancers of interest, diagnostic pathway and logistics, impact of the COVID-19 pandemic as well as the GMS and GLH on current and future services, and lastly, barriers and support for optimal delivery of the GMS. Each pathology laboratory was administered with one questionnaire. However, multiple CPs from each site may have contributed to the responses based on their subspecialist expertise.

Centre recruitment
The expert SC connected with a network of pathology laboratories in England, configured in 29 pathology networks, to enquire about their interest to participate. The survey aimed to include a sample size of 29 centres across England for geographical representation. Recruitment was completed after 2.5 months of data

collection, with agreed participation of 15 labs across the 29 networks.

Data analysis

Descriptive analysis of survey responses was undertaken by a third party, OPEN Health. A data quality check was performed for identifying missing/incorrect responses. Queries were resolved with the respondents and/or with the MSL. Data capture was impacted by some respondents providing free-text response, more than one answer or no answers. Quantitative data were analysed using appropriate descriptive statistics; categorical variables were described by frequency and percentages (denominator is 15, unless otherwise stated). For free-text responses, important concepts were identified and categorised into themes with assistance from the SC.

Patient and public involvement

No patient or the public was involved in the development of research questions and design, conduct or reporting of the study. The results of this research will be disseminated to stakeholders across the molecular diagnostic pathway after being published in a scientific journal to facilitate wider access.

RESULTS

The analysis of the survey responses was divided into five sections in alignment with the questionnaire. The total number of centres involved was 15 unless specified otherwise.

Section 1: referring centre profile

In total, 15 centres from England completed the survey. Of these, 93% reported as regional centres, and all the centres managed samples from referral networks. Twelve of these centres covered an estimated median (IQR) population size of 2.5 (1.9–3.6) million each. Respondents were aligned to six of seven GLHs in England (online supplemental figure S1). In their current practice, pathologists reported using the following technologies in-house: immunohistochemistry (IHC; 100%), real-time PCR (RT-PCR; 60%), fluorescence in-situ hybridisation (27%), as well as Sanger sequencing and NGS (13% each, online supplemental figure S2). Biomarker testing was also performed in coordination with external laboratories and GLHs.

Section 2: specific cancer testing in focus

The estimated median samples received per month for breast cancer, lung cancer and melanoma were 130, 65 and 52.5, respectively (online supplemental table S1). The median estimated turnaround time (TAT, calendar days), which was the time from receipt of sample to test results, for standard markers in breast cancer, lung cancer and melanoma ranged from 2 to 3 days by IHC (excluding NTRKfus in breast and lung cancers and BRAF in melanoma), 6–15 days by RT-PCR (excluding KIT for melanoma) to 17.5–24.5 days by NGS (excluding *PIK3CA* for breast cancer; table 1). In-house technologies such as IHC and RT-PCR were the preferred methods by 60% of laboratories for samples requiring results outside of the NGS time frame. Sixty-seven per cent of laboratories also sent these samples to GLH for NGS, if possible, following local testing. The testing of these samples was most often funded by the NHS trust (60%) or a combination of NHS Trust and NHS England (20%).

Four of 15 laboratories performed molecular testing using liquid biopsy samples, of which 2 laboratories used this only for EGFR analysis in lung cancer. The potential applications of liquid biopsy suggested from this survey were: testing to complement tissue sample results (87%) and as an alternative where suitable tissue was not available (60%). In addition, panel testing (53%) was preferred to single gene testing with liquid biopsies. The reported challenges associated with liquid biopsies included technical issues (86%) such as poor clinical sensitivity due to variable levels of circulating tumour DNA (ctDNA) in sample, and limited testing options, and logistical issues (50%) such as additional administrative work, pathway integration, funding and results interpretation. The challenges associated with the use of archival tissue are explained in online supplemental figure S3. Six of 15 laboratories were implementing in-house NGS capabilities for lung cancer, breast cancer or melanoma for future developments.

Section 3: diagnostic pathway and logistics

Funding/resource allocation (87%), test validation (80%), administration (60%) and timelines for implementation (53%) were reported to be the main challenges with implementing a new test. The CPs from all regional laboratories involved in this survey discussed results at standard multidisciplinary team meetings (MDTs). Only 20% of respondents attended and participated in genomic tumour advisory board (GTABs). It was reported by 100% and 67% of laboratories that tests were initiated by pathologists and oncologists, and to a lesser extent by MDT members such as respiratory physicians, surgeons, clinical scientists and others (details on contact and communication with the MDT are in online supplemental figures S4A,B). Most respondents (60%) stated that clinical interpretation of the molecular results was reported with reference to both published disease area management recommendations and available targeted therapies.

Section 4: impact of the GMS

The roll-out of the GMS was perceived to have a high impact on current services by 53% of respondents. The attributes leading to perceived negative impact were primarily logistical issues (80%) including funding, higher resource requirement, poor information technology (IT) system compatibility, absence of streamlined pathways and suboptimal information sharing and communication, all these potentially leading to increased TAT. Technical issues (20%) included higher tissue requirements leading to high failure rates and incomplete results. Factors associated with perceived positive impact included logistical aspects (33%) such as formally funded pathways, streamlined pathways and improved communication. Technical aspects (13%) included improved TAT, reduced failure rates and higher scope of genetic analysis (figure 2A). The recent COVID-19 pandemic was also perceived to have a high impact on the current services (online supplemental figure S5).

Similarly, it was perceived that the GMS roll-out would have a high impact on future services, indicated by 67% of respondents, highlighting logistical issues (47%) as well as potential benefits (27%) (figure 2B). Thirty-three per cent of respondents reported being unsure of the future impact of the GMS on the service.

Respondents highlighted that their responsibilities included sample preparation (87%), education/training (87%) and reflex test requests (80%) (online supplemental figure S6). All respondents indicated that conducting at least some form of testing including urgent or first-line testing as critical responsibilities of pathology laboratories.

Section 5: optimal delivery of the GMS—barriers and support

The high-impact barriers to the optimal delivery of the GMS are detailed in figure 3. The most frequently identified educational

Table 1 Biomarker testing for breast cancer, lung cancer, melanoma

Test	Biomarkers	Current estimated turnaround time (calendar days)			Test location			
		n*	Median	IQR	n*	Pathology	External lab	GLH
Biomarker testing for breast cancer								
IHC	HR	8	2.0	2.0–2.2	9	9	0	0
	HER2	8	2.8	2.0–3.2	9	7	2	0
	PgR	8	2.0	2.0–2.6	9	9	0	0
	PD-L1	7	3.0	2.2–11.2	8	6	2	0
	NTRKfus	4	19.2	12.4–25.9	4	1	1	2
FISH	HER2	7	7.0	3.5–10.2	8	4	1	3
	NTRKfus	4	24.5	21.9–25.9	4	0	1	3
RT-PCR	PIK3CA	3	14.0	10.8–22	4	1	0	3
	BRCA1/2	1	15.0	15.0–15.0	2	0	0	2
	NTRKfus	3	15.0	11.2–22.5	4	1	0	3
NGS	PIK3CA	1	40.0	40.0–40.0	2	0	0	2
	NTRKfus	4	24.5	22.2–28.4	5	1	0	4
	BRCA1/2	3	24.5	24.5–32.2	4	0	0	4
Other	Ki67 (IHC)	–	NA	NA	1	1	0	0
	Oncotype Dx	1	24.5	24.5–24.5	3	0	3	0
Biomarker testing for lung cancer								
IHC	PD-L1	14	2.5	2.0–3.0	15	14	1	0
	ROS1fus	12	2.8	2.0–7.0	13	11	2	0
	ALKfus	13	2.5	2.0–3.0	15	14	1	0
	BRAF	1	3.0	3.0–3.0	1	1	0	0
	NTRKfus	3	7.5	5.2–18.8	3	2	1	0
FISH	ALKfus	8	7.2	5.5–10.0	8	5	0	3
	ROS1fus	8	7.2	5.5–10.0	8	5	0	3
	METamp	5	10.0	7.5–21.0	5	2	1	2
	HER2amp	4	8.8	6.1–12.8	4	2	0	2
	RETfus	6	8.8	4.9–18.2	6	3	1	2
	NTRKfus	4	7.0	3.5–12.8	4	2	0	2
RT-PCR	EGFR	11	6.0	2.0–7.2	11	9	1	1
	ROS1fus	2	4.8	3.4–6.1	2	2	0	0
	ALKfus	2	4.8	3.4–6.1	2	2	0	0
	ALK	2	4.8	3.4–6.1	2	2	0	0
	BRAF	9	7.0	2.0–14.0	9	6	2	1
	KRAS	7	7.5	3.0–21.0	7	4	2	1
	METex14	6	10.8	4.9–24.5	6	3	2	1
	HER2	3	7.5	5.8–18.8	3	2	1	0
	RETfus	5	7.5	4.0–14.0	5	3	1	1
	NTRKfus	5	7.5	4.0–14.0	6	3	2	1
NGS	EGFR	11	17.5	13.0–21.8	12	2	0	10
	ROS1fus	9	19.0	14.0–24.5	10	0	0	10
	ALKfus	10	18.5	14.0–24.5	11	0	0	11
	BRAF	11	17.5	13.0–21.8	12	1	0	11
	KRAS	11	17.5	13.0–21.8	12	1	0	11
	METex14	10	17.8	14.0–23.1	11	1	0	10
	HER2	7	17.5	14.0–21.2	8	0	0	8
	RETfus	10	18.5	14.0–24.5	11	0	0	11
	NTRKfus	9	19.0	14.0–24.5	10	0	0	10
Other	PIK3CA, TP53	–	NA	NA	1	0	0	1
Biomarker testing for melanoma								
IHC	BRAF	3	7.0	4.5 to 18.5	3	1	2	0
	PD-L1	2	17.0	10.5 to 23.5	2	1	1	0
Sanger sequencing	BRAF	1	7.0	7.0 to 7.0	1	0	1	0
	NRAS	–	NA	NA	–	–	–	–
Pyrosequencing	BRAF	–	NA	NA	–	–	–	–

Continued

Table 1 Continued

| Test | Biomarkers | Current estimated turnaround time (calendar days) | | | Test location | | | |
		n*	Median	IQR	n*	Pathology	External lab	GLH
RT-PCR	BRAF	9	6.0	2.5 to 7.5	9	6	2	1
	NRAS	3	7.5	5.8 to 24.8	2	1	1	0
	KIT	2	23.0	13.5 to 32.5	2	0	2	0
NGS	BRAF	7	21.5	15.8 to 26.2	7	1	0	6
	NRAS	7	21.5	15.8 to 26.2	8	1	1	6
	KIT	7	21.5	15.8 to 26.2	8	1	1	6
Others	Pyrosequencing (KIT)	–	NA	NA	1	1	0	0
	NTRK1-3	–	NA	NA	1	0	0	1
	FISH (BRAF)	1	0	0	1	0	1	0

*The n values represent the total number of responses received for the corresponding questionnaire field on test location and estimated TAT. The median estimated TAT was the time from receipt of sample to test results.
ALKfus, ALK fusion; FISH, fluorescence in situ hybridisation; GLH, Genomic Laboratory Hub; HER2amp, HER2 amplification; HR, hormone receptor, which may include ER or PgR; IHC, immunohistochemistry; METamp, MET amplification; METex14, MET exon 14; NA, not applicable; NGS, next-generation sequencing; NTRKfus, NTRK fusion; PD-L1, programmed death ligand-1; PgR, progesterone receptor; RETfus, RET fusion; ROS1fus, ROS1 fusion; RT-PCR, real-time PCR; TAT, turnaround times.

needs for pathologists included understanding the new molecular testing pathways and best practice sharing (figure 4A). Educational support suggested for clinical colleagues primarily comprised patient information of testing and results and tissue

requirements (figure 4B; additional resource requirements are detailed in online supplemental figure S7). The preferred mode of information dissemination suggested by the respondents were digital education (80%), virtual educational meeting (73%)
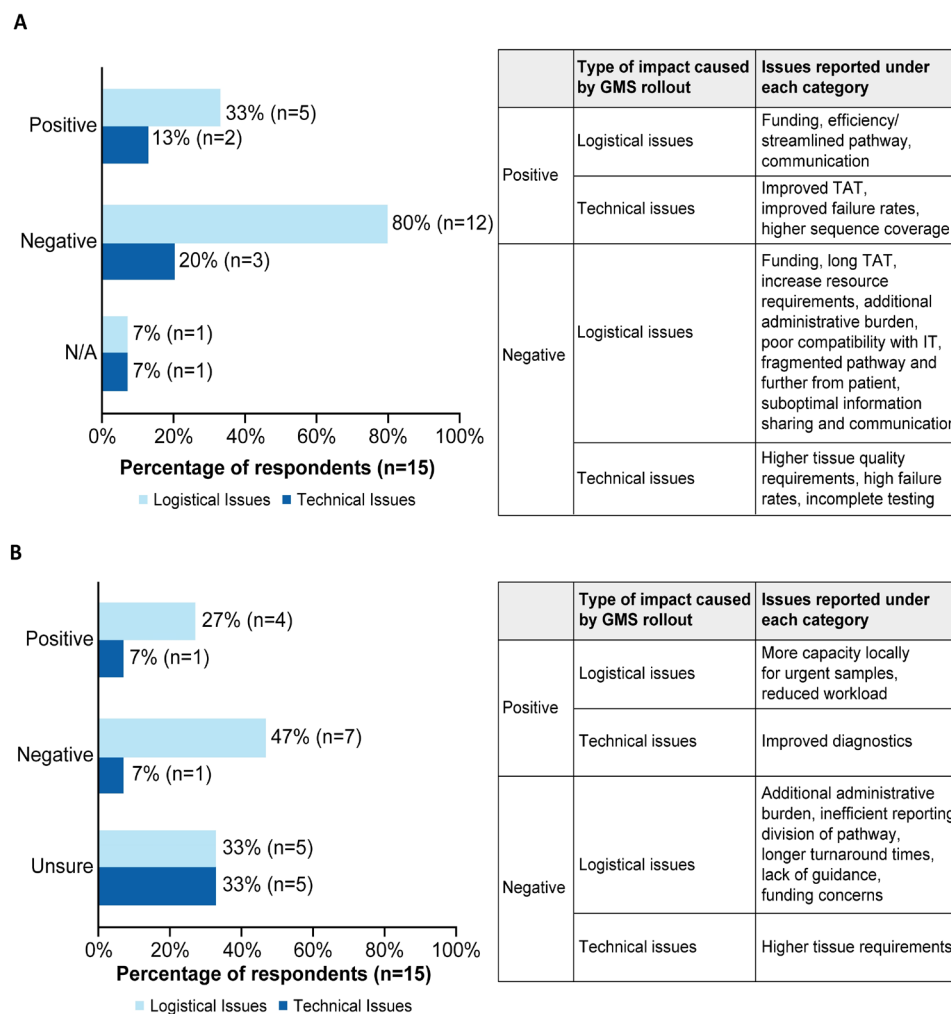
Figure 2 (A) Perceived impact of the GMS roll-out on current services. (B) Perceived impact of the GMS roll-out on future services Responses are not mutually exclusive. GMS, Genomic Medicine Service; IT, information technology; n, number of respondents; TAT, turnaround time.
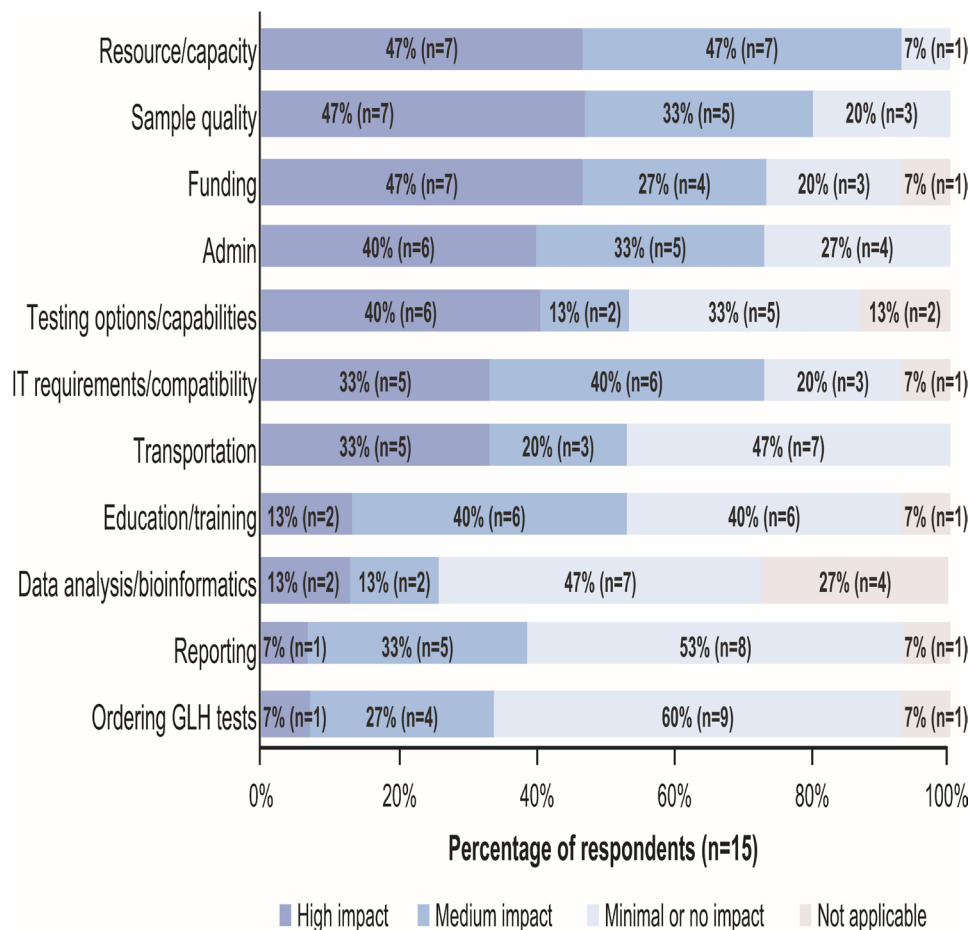
Figure 3 Barriers for optimal delivery of the GMS responses are not mutually exclusive. GLH, genomic laboratory hub; GMS, Genomic Medicine Service; IT, information technology; n, number of respondents.

and in-person educational meeting (60%) (online supplemental figure S8).

DISCUSSION

The centralisation of genomic testing to seven GLHs in England aims to ensure equitable access of tests specified in the national test directory.[2] The consolidation of genomic testing to GLHs is also aimed at standardisation of these tests to improve cost efficiency of laboratories as well as facilitating a broader scope of analysis to inform clinical trial eligibility.[4] The role of CPs has become increasingly complex with recent advances in the genomic testing landscape. Our survey results provide an overview of the current services and challenges for cancer diagnostics in pathology laboratories in England and highlight the areas requiring further support to facilitate a diagnostic infrastructure for optimal and equitable patient management.

Fifteen geographically spread regional pathology laboratories in England participated, 12 of which reported to cover a median estimated population of 2.5 million each. This would roughly indicate that the survey covered services for 37.5 of 56 million residents of England.[5]

Our survey highlighted the pivotal activities of the pathologist within this complex molecular testing pathway. In addition to conducting diagnostic tests, pathologists are also involved in interpretation of test results within the clinicopathological context of the case, attending standard disease-specific MDTs as well as increasingly participating in GTABs. This practice is in alignment with evolving international practice and recommendations.[6] With

rapid consolidation of genomic testing to GLHs, the pathologists have a central role in facilitating closer collaboration between the regional centres and the GLHs as they hold both the patient's clinical information and the tissue, and can guide appropriate diagnostic and downstream testing, particularly where small sample size may limit testing. The survey results exemplify the vital role of pathology laboratory teams in tissue provision for genomic tests. In their current practice, regional pathology centres reported working with their GLHs through activities such as initiation of test requests, sample preparation, interpretation of results and integration of GLH reports into local systems.

Our survey indicated a perceived high impact of the GMS implementation on current and future pathology services. Potential positive impacts of the GMS were highlighted, such as improved and standardised diagnoses, handling of complex cases by GLHs ensuring more capacity for routine testing and reduced workloads. However, most respondents expressed concerns around logistical issues including funding, increased pathologist/laboratory/administrative workload, poor IT compatibility and the need to streamline pathways, all potentially leading to increased TAT. The authors welcome the intention stated in the recently published NHS 5-year Genomic Medicine Strategy to optimise cancer tissue pathways by working with stakeholders such as NHS England and NHS Improvement pathology networks and the Royal College of Pathologists to address concerns including those mentioned in the survey. Further, the plan acknowledges the need for pathway redesign via collaboration across clinical specialties, and between the GMS and Cancer Alliances.[7]
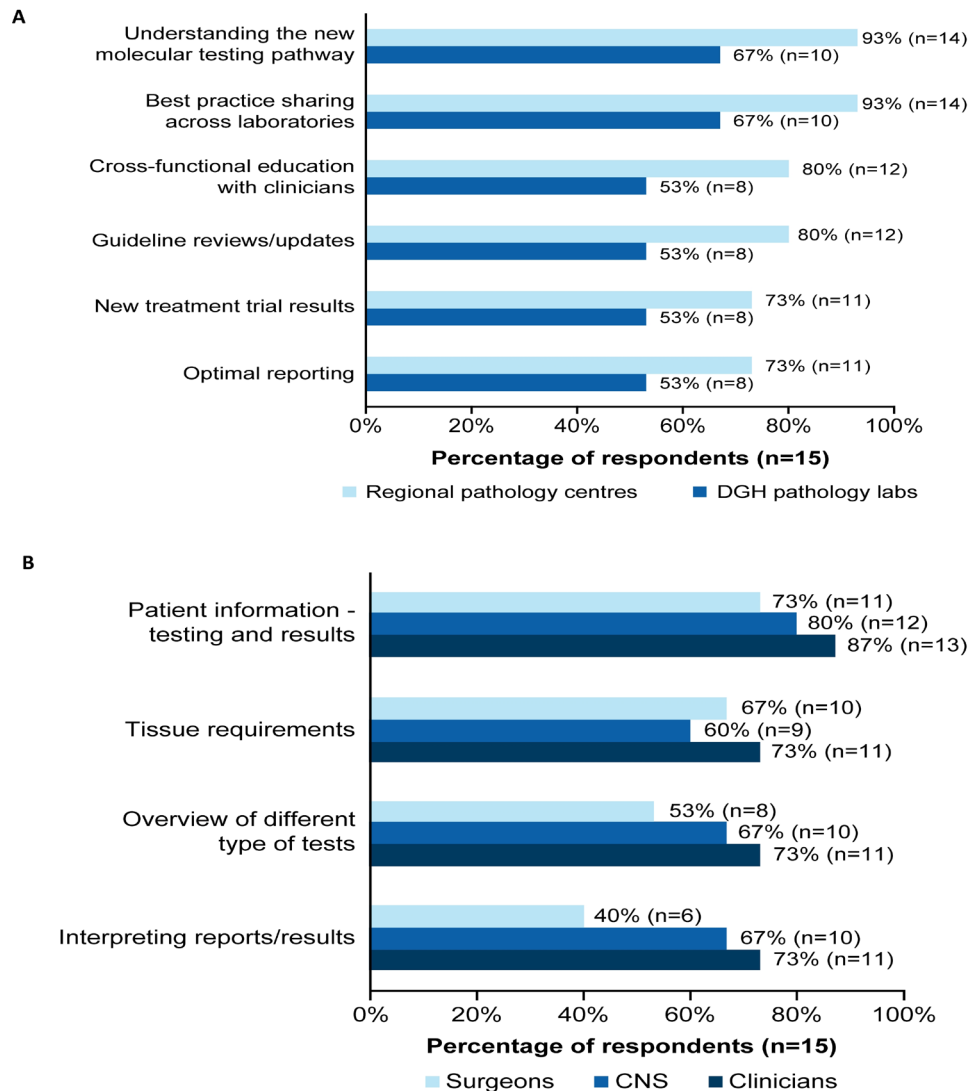
Figure 4 (A) Educational support for pathologists from different sites. (B) Educational support for surgeons, clinical nurse specialist and clinicians. Responses are not mutually exclusive. CNS, clinical nurse specialist; n, number of respondents.

The tests covered in the national genomic test directories are funded centrally by NHS England leading to potential savings for local pathology laboratories, delivering or funding these tests from their own budgets. However, increased costs may be incurred for tissue preparation with repeat biopsies, as and when the test directory offering and uptake expand and when there are changes in practice.[7] To ensure equitable access to required testing for patients across all regions, consideration should be made for national commissioning of all required biomarkers (via all techniques, including predictive IHC) in addition to ongoing resources supporting sample preparation for downstream molecular testing.

The need for a robust bioinformatics infrastructure in handling high-volume data generated at each step of the pathway has been emphasised in previous studies.[8] The development of an integrated IT system across regional centres and GLHs is recommended to aid efficient access to full clinical information and reduce the duplication of effort and risk of transcription errors from one laboratory's system into another. To this end, the NHS 5-year Genomics Medicine Strategy aims to develop an interoperable informatics and data infrastructure.[7]

Our survey respondents suggested that pathologists would benefit from additional education on changes to the molecular testing pathway and from best practice sharing. Opportunities for information sharing and educational support via digital or in-person meetings may enable more effective communication regarding GMS developments. Respondents also highlighted an educational need for other clinicians in the cancer MDT. While current resources such as the Health Education England Genomics Education Programme are available, a more proactive approach to education, especially focused on junior doctors, may facilitate understanding of and enthusiasm for this increasingly important field early in their careers.[9]

Biomarker-based treatment planning is the cornerstone of precision oncology. The biomarkers assessed in our survey, for melanoma, lung cancer and breast cancer based on IHC, RT-PCR and NGS techniques were in line with the guideline recommendations.[10–15] Limited molecular testing was performed routinely for breast cancer at the time of survey, while PIK3CA testing was nationally commissioned since April 2022.[16] Delays in test results potentially lead to greater morbidity, higher costs of care and lower likelihood of survival

in patients with solid tumours.[17] As a baseline, NHS England has recommended a timeline of 21 calendar days for standard panel testing of somatic cancers (currently under review by disease type).[18] Moreover, there are differing recommendations between NHS England and other national guidelines such as the National Optimal Lung Cancer Pathway that suggests 10 days for molecular marker testing to inform first-line therapy.[19] In our survey, although several sites reported TATs within these timelines, the upper limit often exceeded the 21 days recommendation. Such variations in guidance and between regions may have an impact on patient care.

Advances in technologies have increasingly indicated the appropriateness of plasma ctDNA analysis (liquid biopsies) for solid tumours in clinical practice, which is considered complementary to tissue biopsies, in guiding therapeutic decisions.[20] Most pathology centres agreed on the positive contribution of the use of liquid biopsies, particularly when tissue samples were not suitable or available, with openness to its future wider adoption. A close collaboration between the clinical team performing liquid biopsies and laboratory scientists and pathologists will be required to facilitate optimal sample handling as well as integration of liquid biopsy results within complete molecular profiling of the cases for accurate and complete assessment.

The PATHways survey was designed to capture the views of pathologists involved in biomarker testing, the current challenges and the opportunities to optimise the transition towards expanded and centralised genomic services. However, there were some limitations to the design:

► The data reflect the conditions at the time of the survey, and there may have been further developments.
► The survey results were based on self-reported practice, subject to recall bias. The questionnaire design, and the conduct of the survey, by Novartis medical department personnel may have resulted in potential response bias.

CONCLUSION

Our survey highlighted the pathologists' views on challenges and opportunities in the centralisation of genomic services. The findings further highlight the concerns that need to be addressed for wider implementation of genomic testing, in alignment with the recent 5-year strategy of the NHS for accelerated uptake of genomic services.[7]

Notable recommendations from our survey included the following:

► Wider proactive engagement and effective communication between oncologists, physicians, surgeons, clinical nurse specialists, scientists and pathologists, to optimise the MDT approach to patient management.
► A pragmatic approach to biomarker detection, ensuring optimal use of technologies for early diagnosis.
► Access to broader profiling for all eligible patients, also supporting clinical trials and research opportunities for patients.
► Multistakeholder pathway review to achieve clinically meaningful TATs for all required biomarkers.
► Upgradation of IT infrastructure to support faster integration of diagnostic, prognostic and predictive information from all relevant sources for analysis and interpretation.
► Further proactive educational training programmes, on areas such as new diagnostic and predictive markers, optimised sample handling and tumour content assessment to facilitate smooth implementation of the GMS.

► Centralised directory and funding of all required cancer biomarker tests beyond genomics and inclusion of protein-based tests such as predictive IHC.

Author affiliations
¹Histopathology, University Hospitals Birmingham NHS Foundation Trust, Birmingham, UK
²Respiratory Pathology, National Heart and Lung Institute, Imperial College London, London, UK
³Histopathology, Royal Brompton and Harefield Hospitals, Guy's and St Thomas' NHS Foundation Trust, London, UK
⁴Cellular Pathology, Royal Liverpool University Hospital, Liverpool, UK
⁵Histopathology, Manchester University NHS Foundation Trust, Manchester, UK
⁶Histopathology, Blackpool Teaching Hospitals NHS Foundation Trust, Blackpool, UK
⁷Cellular Pathology, University College London Cancer Institute, London, UK
⁸Histopathology, St James's University Hospital, Leeds, UK
⁹Histopathology, Nottingham University Hospitals NHS Trust, Nottingham, UK
¹⁰Cellular Pathology, North Bristol NHS Trust, Westbury on Trym, UK
¹¹Cellular Pathology, Imperial College Healthcare NHS Trust, London, UK
¹²Novartis Pharmaceuticals UK Ltd, London, UK

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Patient consent for publication Not applicable.

Ethics approval As the PATHways survey does not require divulging of sensitive or patient-identifiable data and does not raise material ethical issues, ethics committee approval was not required.

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Data availability statement All data relevant to the study are included in the article or uploaded as online supplemental information.

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ORCID iDs
Phillipe Taniere http://orcid.org/0000-0002-4638-4551
David Allan Moore http://orcid.org/0000-0001-9116-346X

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The landscape of cancer biomarker testing in England following genomic reconfiguration: Insights from a nationwide pathologist survey

Philippe Taniere[1], Andrew G. Nicholson[2], John Gosney[3], Angeles Montero[4], Danielle Bury[5], David Moore[6], Eldo Verghese[7], Emily Shaw[8], Irshad Soomro[9], Leena Joseph[10], Nidhi Bhatt[11], Patrizia Viola[12], Rozinder Bains[13], Adrienne G. Lanctot[13], Jacqueline Ryan[13]

[1]Department of Histopathology, University Hospitals Birmingham NHS Foundation Trust, Birmingham, United Kingdom

[2]Department of Histopathology, Royal Brompton and Harefield Hospitals, Guy's and St Thomas' NHS Foundation Trust; Honorary Professor of Respiratory Pathology, National Heart and Lung Institute, Imperial College, London, United Kingdom

[3]Department of Cellular Pathology, Royal Liverpool University Hospital, Liverpool, United Kingdom

[4]Department of Histopathology, Manchester University Foundation Trust, Manchester, United Kingdom

[5]Blackpool Teaching Hospitals NHS Foundation Trust, Blackpool; Department of Cellular Pathology, Royal Liverpool University Hospital, Liverpool, United Kingdom

[6]Cancer Research UK Lung Cancer Centre of Excellence, UCL Cancer Institute, London; Department of Cellular Pathology, University College London Hospital NHS Foundation Trust, London, United Kingdom

[7]Department of Histopathology, St James University Hospital, Leeds LS9 7TF, United Kingdom

[8]Department of Histopathology, University Hospital Southampton NHS Foundation Trust, Southampton, United Kingdom

[9]Department of Histopathology, Nottingham University Hospital, Nottingham, United Kingdom

[10]Consultant Histopathologist, Honorary Lecturer, Manchester Medical School, Deputy Clinical Head of Division of Laboratory Medicine, Manchester Foundation Trust, Manchester, United Kingdom

[11]Cellular Pathology Department, North Bristol NHS Trust, Bristol, United Kingdom

[12]North West London Pathology based at Imperial College Healthcare NHS Trust, Charing Cross Hospital, London, United Kingdom

[13]Novartis Pharmaceuticals UK Ltd, London, United Kingdom

Address for Correspondence:

Dr. Phillipe Taniere
Consultant Histopathologist/Molecular Pathology
CLS/Cellular Pathology/Office 54
Histopathology - University Hospitals Birmingham NHS Foundation Trust, Birmingham,
B15 2TH, United Kingdom
Email: Phillipe.Taniere@uhb.nhs.uk

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Supplementary Online Material

Table S1. Estimated samples received per month

Cancer type	Estimated number of samples received per month at all centres		
	N*	Median	IQR
Breast cancer	8	130	40 to 425
Lung cancer	15	65	30 to 100
Melanoma skin	8	52.5	20 to 105
Other cancers	3	150	125 to 225

*Seven respondents were not able to provide the estimates for breast cancer and melanoma skin respectively; 12 respondents were not able to provide the estimates for other cancers.

IQR, interquartile range; N, number of respondents.

Supplementary figures

Figure S1. Regional GLH (n=15) of survey respondents
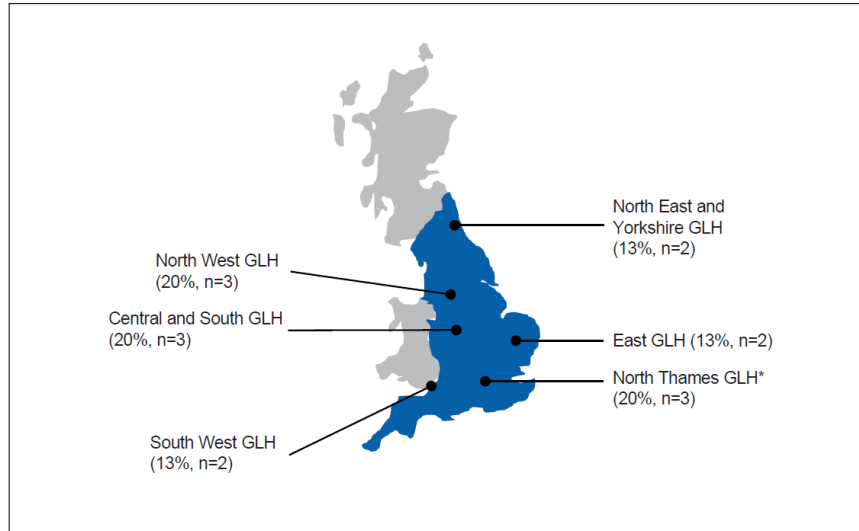
*n=1 also used the Central and South GLH
GLH, genomic laboratory hub; n, number of respondents.

Figure S2. Technologies in use by the respondents
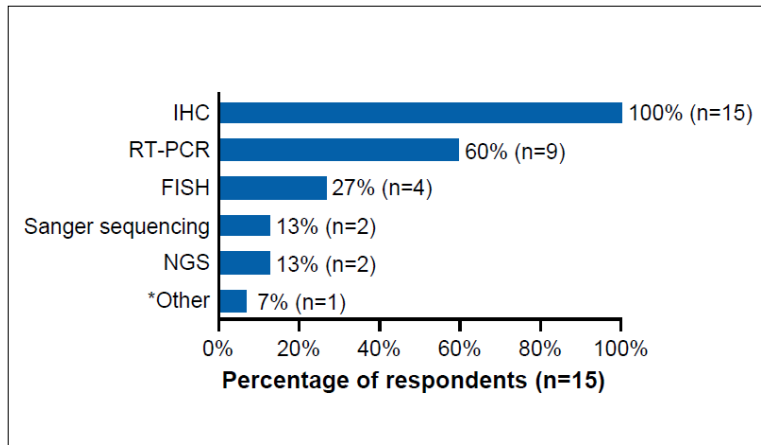
*Other included Pyrosequencing and digital-based (AI) assessment of proteins; Responses are not mutually exclusive.

AI, artificial intelligence; FISH, fluorescence in situ hybridization; IHC, immunohistochemistry; NGS, next-generation sequencing; n, number of respondents; RT-PCR, real-time polymerase chain reaction.

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Figure S3. Challenges with use of archival tissue
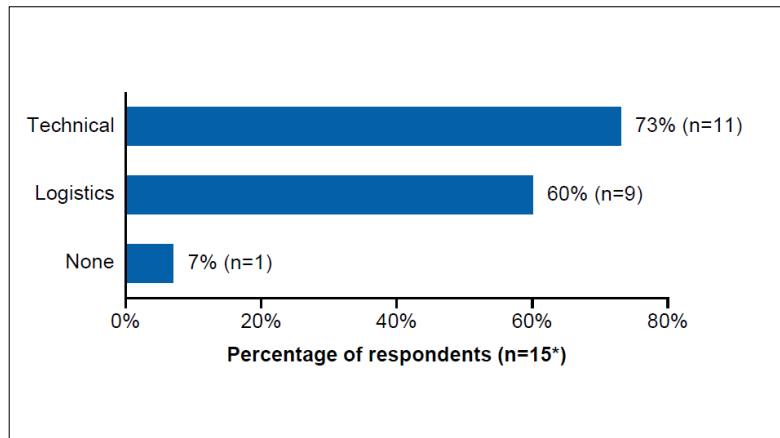
*Responses were not mutually exclusive.
n, number of respondents.
Technical challenges included sample quality, sample quantity and failure rates.
Logistical challenges included additional administrative resources, loss of sample, difficulty with retrieval, cost and turnaround time.

Figure S4A. Point of contact in the clinic
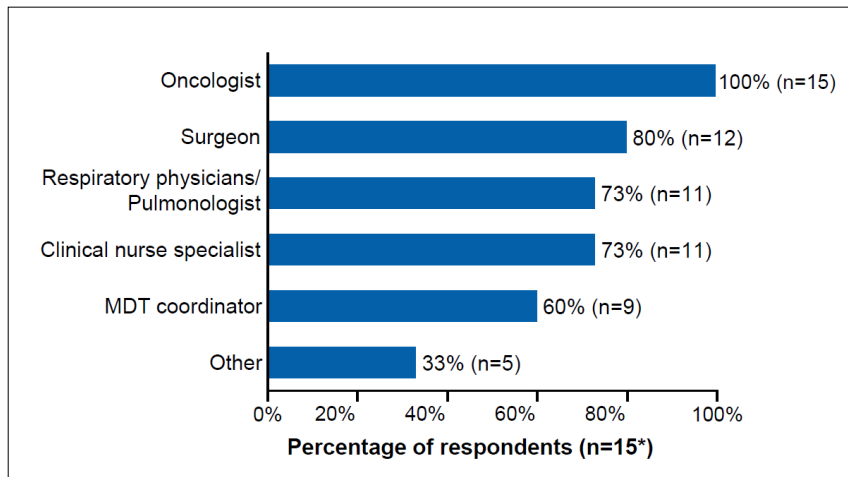
Other included dermatologists (n=3), pathologists (n=1), radiologists (n=1);
*Responses are not mutually exclusive.
n, number of respondents.

Figure S4B. Communication with the clinicians
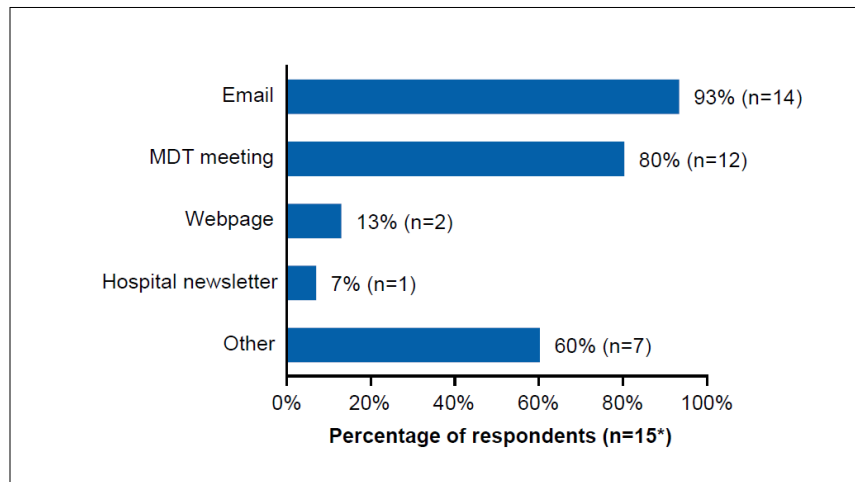
Other included focus groups (n=1), educational webinars (n=1), informal discussions (n=4), conferences (n=1), meetings (n=1) and phone (n=2).
*Responses are not mutually exclusive.
n, number of respondents.

Figure S5. Perceived impact of COVID-19 on the current services
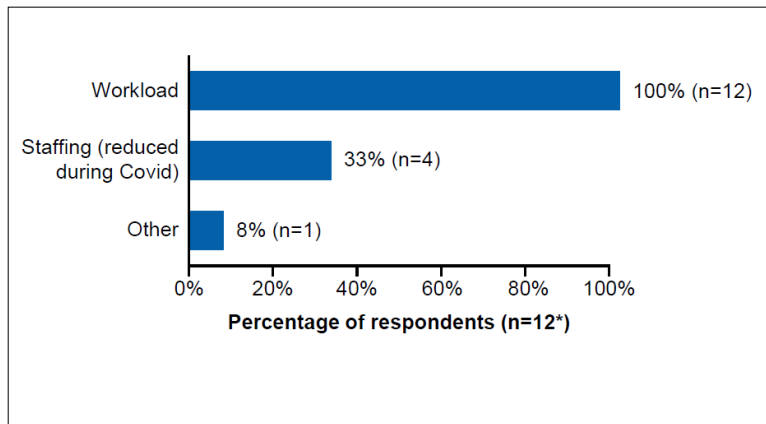
*Responses are not mutually exclusive; 3 respondents were not able to provide responses.
n, number of respondents.

Figure S6. Role of regional pathology centres in the optimal delivery of the GMS
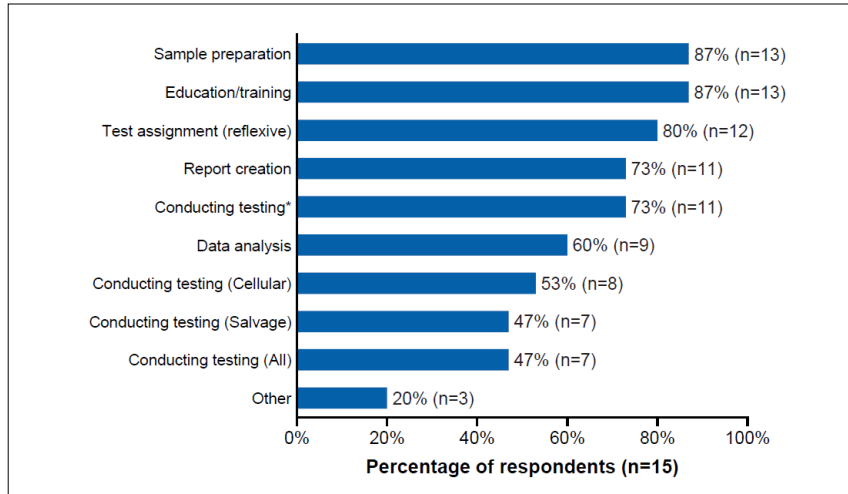
*Urgent or first-line testing.

Responses are not mutually exclusive.

Other included integrate diagnostic information from different sources, provide prognostic and predictive factors on timely basis and unclear role (n=1 each).

GMS, genomic medicine service; n, number of respondents.

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Figure S7. Additional resources required at local pathology to support optimal delivery of the GMS
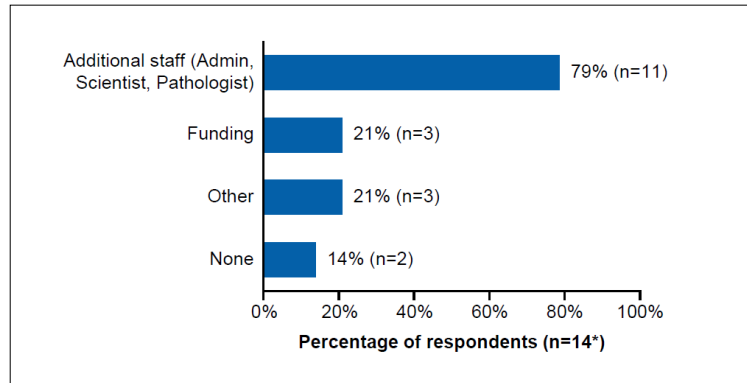
Other included improved IT efficiency (sample tracking and reports), improved communication, educational support.
*Responses are not mutually exclusive; 1 respondent was unable to provide a response.
n, number of respondents.

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Figure S8. Educational support methods preferred by the respondents
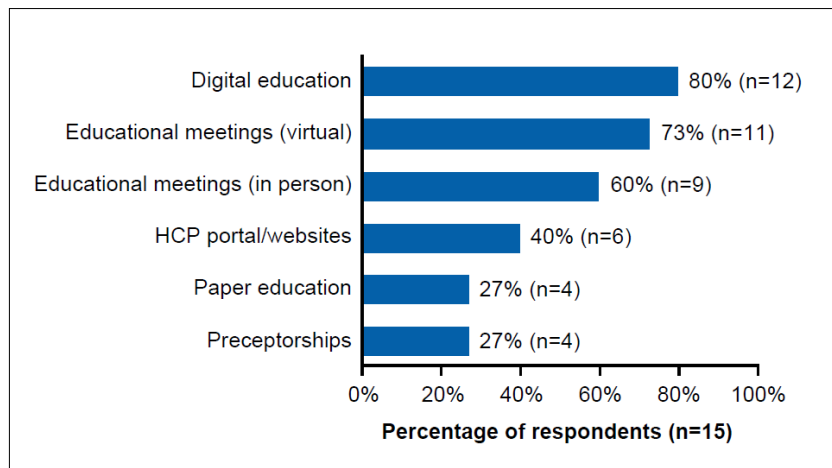
Responses are not mutually exclusive.
HCP, healthcare practitioners; n, number of respondents.

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Abbreviations	
SD	Standard deviation
IQR	Interquartile range (first to third quartile)
NA.	Missing data
N/A	Not applicable

2. Where in the UK is your Lab?

2. Where in the UK is your Lab?	Overall	
	n	% (N = 15)
England	15	100%
NA.	0	-

3. How would you categorise your hospital?

3. How would you categorise your hospital?	Overall	
	n	% (N = 15)
Other	1	7%
Regional Centre	14	93%
NA.	0	-

4. What region does your lab cover for diagnosis and management of cancer samples?

4. What region does your lab cover for diagnosis and management of cancer samples?	Overall	
	n	% (N = 15)
Referal network	15	100%
NA.	0	-

4. Estimated population size (in million)

4. Estimated population size (in million)	Overall
	N = 15
Mean	3.3
SD	2.9
Median	2.5
IQR	1.9 to 3.6
Range	1 to 12
NA.	3

5. Which is your regional GLH or genomics centre?

5. Which is your regional GLH or genomics centre?	Overall	
	n	% (N = 15)
Central and South GLH	3	20%
Central and South GLH + North Thames GLH	1	7%
East GLH	2	13%
North East & Yorkshire GLH	2	13%
North Thames GLH	2	13%
North West GLH	3	20%
South West GLH	2	13%
NA.	0	-

6. IHC

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6. IHC	Overall	
	n	% (N = 15)
Yes	15	100%
NA.	0	-

6. FISH

6. FISH	Overall	
	n	% (N = 15)
No	11	73%
Yes	4	27%
NA.	0	-

6. RT-PCR

6. RT-PCR	Overall	
	n	% (N = 15)
No	6	40%
Yes	9	60%
NA.	0	-

6. Sanger Sequencing

6. Sanger Sequencing	Overall	
	n	% (N = 15)
No	13	87%
Yes	2	13%
NA.	0	-

6. NGS

6. NGS	Overall	
	n	% (N = 15)
No	13	87%
Yes	2	13%
NA.	0	-

6. Other

6. Other	Overall	
	n	% (N = 1)
Pyro sequencing & digital based (AI) assessment of proteins	1	100%
NA.	14	-

7. Breast

7. Breast	Overall
	N = 15

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Mean	234.4
SD	229.8
Median	130
IQR	40 to 425
Range	35 to 600
NA.	7

7. Lung

7. Lung	Overall
	N = 15
Mean	112.9
SD	143.1
Median	65
IQR	30 to 100
Range	20 to 500
NA.	0

7 . Melanoma Skin

7 . Melanoma Skin	Overall
	N = 15
Mean	87.9
SD	96.7
Median	52.5
IQR	20 to 105
Range	18 to 300
NA.	7

7. Other Cancers

7. Other Cancers	Overall
	N = 15
Mean	183.3
SD	104.1
Median	150
IQR	125 to 225
Range	100 to 300
NA.	12

IHC: Reflex at diagnosis - HR

IHC: Reflex at diagnosis - HR	Overall	
	n	% (N = 9)
Yes	9	100%
NA.	0	-

IHC: Reflex at diagnosis - HER2

IHC: Reflex at diagnosis - HER2	Overall	
	n	% (N = 9)
Yes	9	100%
NA.	0	-

IHC: Reflex at diagnosis - PGR

IHC: Reflex at diagnosis - PGR	Overall	
	n	% (N = 9)
On request	1	11%
Yes	8	89%
NA.	0	-

IHC: Reflex at diagnosis - PD-L1

IHC: Reflex at diagnosis - PD-L1	Overall	
	n	% (N = 9)
No	2	22%
On request	4	44%
Yes	3	33%
NA.	0	-

IHC: Reflex at diagnosis - NTRKfus

IHC: Reflex at diagnosis - NTRKfus	Overall	
	n	% (N = 9)
No	5	56%
On request	4	44%
NA.	0	-

IHC: Testing at progression/ relapse/
other post Dx timepoints - HR

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IHC: Testing at progression/ relapse/ other post Dx timepoints - HR	Overall	
	n	% (N = 9)
No	4	44%
On request	1	11%
Yes	4	44%
NA.	0	-

IHC: Testing at progression/ relapse/ other post Dx timepoints - HER2

IHC: Testing at progression/ relapse/ other post Dx timepoints - HER2	Overall	
	n	% (N = 9)
No	4	44%
Yes	5	56%
NA.	0	-

IHC: Testing at progression/ relapse/ other post Dx timepoints - PGR

IHC: Testing at progression/ relapse/ other post Dx timepoints - PGR	Overall	
	n	% (N = 9)
No	4	44%
Yes	5	56%
NA.	0	-

IHC: Testing at progression/ relapse/ other post Dx timepoints - PD-L1

IHC: Testing at progression/ relapse/ other post Dx timepoints - PD-L1	Overall	
	n	% (N = 9)
No	3	33%
On request	3	33%
Yes	3	33%
NA.	0	-

IHC: Testing at progression/ relapse/
other post Dx timepoints - NTRKfus

IHC: Testing at progression/ relapse/ other post Dx timepoints - NTRKfus	Overall	
	n	% (N = 9)
No	5	56%
On request	4	44%
NA.	0	-

IHC: Performed by pathology lab - HR

IHC: Performed by pathology lab - HR	Overall	
	n	% (N = 9)
Yes	9	100%
NA.	0	-

IHC: Performed by pathology lab -
HER2

IHC: Performed by pathology lab - HER2	Overall	
	n	% (N = 9)
Other external lab	2	22%
Yes	7	78%
NA.	0	-

IHC: Performed by pathology lab -
PGR

IHC: Performed by pathology lab - PGR	Overall	
	n	% (N = 9)
Yes	9	100%
NA.	0	-

IHC:Performed by pathology lab - PD-
L1

IHC:Performed by pathology lab - PD-L1	Overall	
	n	% (N = 8)
Other external lab	2	25%

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Yes	6	75%
NA.	1	-

IHC: Performed by pathology lab - NTRKfus

IHC: Performed by pathology lab - NTRKfus	Overall	
	n	% (N = 4)
No	2	50%
Other external lab	1	25%
Yes	1	25%
NA.	5	-

IHC: Moved to GLH/ Genomic centre - HR

IHC: Moved to GLH/ Genomic centre - HR	Overall	
	n	% (N = 9)
No	9	100%
NA.	0	-

IHC: Moved to GLH/ Genomic centre - HER2

IHC: Moved to GLH/ Genomic centre - HER2	Overall	
	n	% (N = 9)
No	9	100%
NA.	0	-

IHC: Moved to GLH/ Genomic centre - PGR

IHC: Moved to GLH/ Genomic centre - PGR	Overall	
	n	% (N = 9)
No	9	100%
NA.	0	-

IHC: Moved to GLH/ Genomic centre - PD-L1

IHC: Moved to GLH/ Genomic centre - PD-L1	Overall	
	n	% (N = 8)
No	8	100%
NA.	1	-

IHC: Moved to GLH/ Genomic centre - NTRKfus

IHC: Moved to GLH/ Genomic centre - NTRKfus	Overall	
	n	% (N = 4)
No	2	50%
Yes	2	50%
NA.	5	-

IHC: Moving to GLH/ Genomic hubs - HR

IHC: Moving to GLH/ Genomic hubs - HR	Overall	
	n	% (N = 9)
No	9	100%
NA.	0	-

IHC: Moving to GLH/ Genomic hubs - HER2

IHC: Moving to GLH/ Genomic hubs - HER2	Overall	
	n	% (N = 9)
No	9	100%
NA.	0	-

IHC: Moving to GLH/ Genomic hubs - PGR

IHC: Moving to GLH/ Genomic hubs - PGR	Overall	
	n	% (N = 9)
No	9	100%
NA.	0	-

IHC: Moving to GLH/ Genomic hubs - PD-L1

IHC: Moving to GLH/ Genomic hubs - PD-L1	Overall	
	n	% (N = 8)
No	8	100%
NA.	1	-

IHC: Moving to GLH/ Genomic hubs - NTRKfus

IHC: Moving to GLH/ Genomic hubs - NTRKfus	Overall	
	n	% (N = 4)
No	4	100%
NA.	5	-

IHC: Current Average Turnaround time - HR

IHC: Current Average Turnaround time - HR	Overall
	N = 9
Mean	2.1
SD	0.6
Median	2
IQR	2 to 2.2
Range	1 to 3
NA.	1

IHC: Current Average Turnaround time - HER2

IHC: Current Average Turnaround time - HER2	Overall
	N = 9
Mean	2.9
SD	1.1
Median	2.8
IQR	2 to 3.2
Range	2 to 5
NA.	1

IHC: Current Average Turnaround time - PGR

IHC: Current Average Turnaround time - PGR	Overall
	N = 9
Mean	2.2

SD	0.7
Median	2
IQR	2 to 2.6
Range	1 to 3
NA.	1

IHC: Current Average Turnaround time - PD-L1

IHC: Current Average Turnaround time - PD-L1	Overall
	N = 9
Mean	8.7
SD	10.6
Median	3
IQR	2.2 to 11.2
Range	1 to 30
NA.	2

IHC: Current Average Turnaround time - NTRKfus

IHC: Current Average Turnaround time - NTRKfus	Overall
	N = 9
Mean	19
SD	10.1
Median	19.2
IQR	12.4 to 25.9
Range	7.5 to 30
NA.	5

FISH: Reflex at diagnosis - HER2

FISH: Reflex at diagnosis - HER2	Overall	
	n	% (N = 9)
No	1	11%
On request	2	22%
Yes	6	67%
NA.	0	-

FISH: Reflex at diagnosis - NTRKfus

FISH: Reflex at diagnosis - NTRKfus	Overall	
	n	% (N = 9)
No	6	67%
On request	3	33%
NA.	0	-

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FISH:Testing at progression/ relapse/
other post Dx timepoints - HER2

FISH:Testing at progression/ relapse/ other post Dx timepoints - HER2	Overall	
	n	% (N = 9)
No	5	56%
On request	1	11%
Yes	3	33%
NA.	0	-

FISH: Testing at progression/ relapse/
other post Dx timepoints - NTRKfus

FISH: Testing at progression/ relapse/ other post Dx timepoints - NTRKfus	Overall	
	n	% (N = 9)
No	5	56%
On request	3	33%
Yes	1	11%
NA.	0	-

FISH: Performed by pathology lab -
HER2

FISH: Performed by pathology lab - HER2	Overall	
	n	% (N = 8)
No	3	38%
Other external lab	1	12%
Yes	4	50%
NA.	1	-

FISH: Performed by pathology lab -
NTRKfus

FISH: Performed by pathology lab - NTRKfus	Overall	
	n	% (N = 4)
No	3	75%
Other external lab	1	25%
NA.	5	-

FISH: Moved to GLH/ Genomic centre
- HER2

FISH: Moved to GLH/ Genomic centre - HER2	Overall	
	n	% (N = 8)
No	5	62%
Yes	3	38%
NA.	1	-

FISH: Moved to GLH/ Genomic centre
- NTRKfus

FISH: Moved to GLH/ Genomic centre - NTRKfus	Overall	
	n	% (N = 4)
No	1	25%
Yes	3	75%
NA.	5	-

FISH: Moving to GLH/ Genomic hubs -
HER2

FISH: Moving to GLH/ Genomic hubs - HER2	Overall	
	n	% (N = 8)
No	8	100%
NA.	1	-

FISH: Moving to GLH/ Genomic hubs -
NTRKfus

FISH: Moving to GLH/ Genomic hubs - NTRKfus	Overall	
	n	% (N = 4)
No	4	100%
NA.	5	-

FISH: Current Average Turnaround
time - HER2

FISH: Current Average Turnaround time - HER2	Overall
	N = 9

Mean	7.2
SD	4.5
Median	7
IQR	3.5 to 10.2
Range	2 to 14
NA.	2

FISH: Current Average Turnaround
time - NTRKfus

FISH: Current Average Turnaround time - NTRKfus	Overall
	N = 9
Mean	23.2
SD	6.7
Median	24.5
IQR	21.9 to 25.9
Range	14 to 30
NA.	5

RT-PCR: Reflex at diagnosis - PIK3CA

RT-PCR: Reflex at diagnosis - PIK3CA	Overall	
	n	% (N = 9)
No	6	67%
On request	3	33%
NA.	0	-

RT-PCR: Reflex at diagnosis - BRCA
1/2

RT-PCR: Reflex at diagnosis - BRCA 1/2	Overall	
	n	% (N = 9)
No	8	89%
Yes	1	11%
NA.	0	-

RT-PCR: Reflex at diagnosis - NTRKfus

RT-PCR: Reflex at diagnosis - NTRKfus	Overall	
	n	% (N = 9)
No	6	67%
On request	3	33%
NA.	0	-

RT-PCR: Testing at progression/
relapse/ other post Dx timepoints -
PIK3CA

RT-PCR: Testing at progression/ relapse/ other post Dx timepoints - PIK3CA	Overall	
	n	% (N = 9)
No	7	78%
On request	2	22%
NA.	0	-

RT-PCR: Testing at progression/
relapse/ other post Dx timepoints -
BRCA 1/2

RT-PCR: Testing at progression/ relapse/ other post Dx timepoints - BRCA 1/2	Overall	
	n	% (N = 9)
No	8	89%
Yes	1	11%
NA.	0	-

RT-PCR: Testing at progression/
relapse/ other post Dx timepoints -
NTRKfus

RT-PCR: Testing at progression/ relapse/ other post Dx timepoints - NTRKfus	Overall	
	n	% (N = 9)
No	6	67%
On request	3	33%
NA.	0	-

RT-PCR: Performed by pathology lab -
PIK3CA+BE4

RT-PCR: Performed by pathology lab - PIK3CA+BE4	Overall	
	n	% (N = 4)
No	3	75%
Yes	1	25%
NA.	5	-

RT-PCR: Performed by pathology lab -
BRCA 1/2

RT-PCR: Performed by pathology lab - BRCA 1/2	Overall	
	n	% (N = 2)
No	2	100%
NA.	7	-

RT-PCR: Performed by pathology lab -
NTRKfus

RT-PCR: Performed by pathology lab - NTRKfus	Overall	
	n	% (N = 4)
No	3	75%
Yes	1	25%
NA.	5	-

RT-PCR: Moved to GLH/ Genomic
centre - PIK3CA

RT-PCR: Moved to GLH/ Genomic centre - PIK3CA	Overall	
	n	% (N = 4)
No	1	25%
Yes	3	75%
NA.	5	-

RT-PCR: Moved to GLH/ Genomic
centre - BRCA 1/2

RT-PCR: Moved to GLH/ Genomic centre - BRCA 1/2	Overall	
	n	% (N = 2)
Yes	2	100%
NA.	7	-

RT-PCR: Moved to GLH/ Genomic
centre - NTRKfus

RT-PCR: Moved to GLH/ Genomic centre - NTRKfus	Overall	
	n	% (N = 4)
No	1	25%

Yes	3	75%
NA.	5	-

RT-PCR: Moving to GLH/ Genomic
hubs - PIK3CA

RT-PCR: Moving to GLH/ Genomic hubs - PIK3CA	Overall	
	n	% (N = 4)
No	4	100%
NA.	5	-

RT-PCR: Moving to GLH/ Genomic
hubs - BRCA 1/2

RT-PCR: Moving to GLH/ Genomic hubs - BRCA 1/2	Overall	
	n	% (N = 2)
No	2	100%
NA.	7	-

RT-PCR: Moving to GLH/ Genomic
hubs - NTRKfus

RT-PCR: Moving to GLH/ Genomic hubs - NTRKfus	Overall	
	n	% (N = 4)
No	4	100%
NA.	5	-

RT-PCR: Current Average Turnaround
time - PIK3CA

RT-PCR: Current Average Turnaround time - PIK3CA	Overall
	N = 9
Mean	17.2
SD	11.6
Median	14
IQR	10.8 to 22
Range	7.5 to 30
NA.	6

RT-PCR: Current Average Turnaround
time - BRCA 1/2

RT-PCR: Current Average Turnaround time - BRCA 1/2	Overall
	N = 9
Mean	15
SD	
Median	15
IQR	15 to 15
Range	15 to 15
NA.	8

RT-PCR: Current Average Turnaround time - NTRKfus

RT-PCR: Current Average Turnaround time - NTRKfus	Overall
	N = 9
Mean	17.5
SD	11.5
Median	15
IQR	11.2 to 22.5
Range	7.5 to 30
NA.	6

NGS: Reflex at diagnosis - PIK3CA

NGS: Reflex at diagnosis - PIK3CA	Overall	
	n	% (N = 9)
No	7	78%
On request	1	11%
Test Done - Timeline unknown	1	11%
NA.	0	-

NGS: Reflex at diagnosis - HER2

NGS: Reflex at diagnosis - HER2	Overall	
	n	% (N = 9)
No	8	89%
Test Done - Timeline unknown	1	11%
NA.	0	-

NGS: Reflex at diagnosis - NTRKfus

NGS: Reflex at diagnosis - NTRKfus	Overall	
	n	% (N = 9)
No	5	56%

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On request	2	22%
Test Done - Timeline unknown	1	11%
Yes	1	11%
NA.	0	-

NGS: Reflex at diagnosis - BRCA 1/2

NGS: Reflex at diagnosis - BRCA 1/2	Overall	
	n	% (N = 9)
No	6	67%
On request	2	22%
Test Done - Timeline unknown	1	11%
NA.	0	-

NGS: Testing at progression/ relapse/ other post Dx timepoints - PIK3CA

NGS: Testing at progression/ relapse/ other post Dx timepoints - PIK3CA	Overall	
	n	% (N = 9)
No	7	78%
On request	1	11%
Test Done - Timeline unknown	1	11%
NA.	0	-

NGS: Testing at progression/ relapse/ other post Dx timepoints - HER2

NGS: Testing at progression/ relapse/ other post Dx timepoints - HER2	Overall	
	n	% (N = 9)
No	8	89%
Test Done - Timeline unknown	1	11%
NA.	0	-

NGS: Testing at progression/ relapse/ other post Dx timepoints - NTRKfus

NGS: Testing at progression/ relapse/ other post Dx timepoints - NTRKfus	Overall	
	n	% (N = 9)
No	4	44%
On request	2	22%
Test Done - Timeline unknown	1	11%
Yes	2	22%
NA.	0	-

NGS: Testing at progression/ relapse/ other post Dx timepoints - BRCA 1/2

NGS: Testing at progression/ relapse/ other post Dx timepoints - BRCA 1/2	Overall	
	n	% (N = 9)
No	5	56%
On request	2	22%
Test Done - Timeline unknown	1	11%
Yes	1	11%
NA.	0	-

NGS: Performed by pathology lab - PIK3CA

NGS: Performed by pathology lab - PIK3CA	Overall	
	n	% (N = 2)
No	2	100%
NA.	7	-

NGS: Performed by pathology lab - HER2

NGS: Performed by pathology lab - HER2	Overall	
	n	% (N = 1)
No	1	100%
NA.	8	-

NGS: Performed by pathology lab - NTRKfus

NGS: Performed by pathology lab - NTRKfus	Overall	

	n	% (N = 5)
No	4	80%
Yes	1	20%
NA.	4	-

NGS: Performed by pathology lab - BRCA 1/2

NGS: Performed by pathology lab - BRCA 1/2	Overall	
	n	% (N = 4)
No	4	100%
NA.	5	-

NGS: Moved to GLH/ Genomic centre - PIK3CA

NGS: Moved to GLH/ Genomic centre - PIK3CA	Overall	
	n	% (N = 2)
Yes	2	100%
NA.	7	-

NGS: Moved to GLH/ Genomic centre - HER2

NGS: Moved to GLH/ Genomic centre - HER2	Overall	
	n	% (N = 1)
Yes	1	100%
NA.	8	-

NGS: Moved to GLH/ Genomic centre - NTRKfus

NGS: Moved to GLH/ Genomic centre - NTRKfus	Overall	
	n	% (N = 5)
No	1	20%
Yes	4	80%
NA.	4	-

NGS: Moved to GLH/ Genomic centre - BRCA 1/2

NGS: Moved to GLH/ Genomic centre - BRCA 1/2	Overall	
	n	% (N = 4)
Yes	4	100%
NA.	5	-

NGS: Moving to GLH/ Genomic hubs - PIK3CA

NGS: Moving to GLH/ Genomic hubs - PIK3CA	Overall	
	n	% (N = 2)
No	2	100%
NA.	7	-

NGS: Moving to GLH/ Genomic hubs - HER2

NGS: Moving to GLH/ Genomic hubs - HER2	Overall	
	n	% (N = 1)
No	1	100%
NA.	8	-

NGS: Moving to GLH/ Genomic hubs - NTRKfus

NGS: Moving to GLH/ Genomic hubs - NTRKfus	Overall	
	n	% (N = 5)
No	5	100%
NA.	4	-

NGS: Moving to GLH/ Genomic hubs - BRCA 1/2

NGS: Moving to GLH/ Genomic hubs - BRCA 1/2	Overall	
	n	% (N = 4)
No	4	100%
NA	5	

NGS: Current Average Turnaround time - PIK3CA

NGS: Current Average Turnaround time - PIK3CA	Overall
	N = 9
Mean	40
SD	
Median	40
IQR	40 to 40
Range	40 to 40
NA.	8

NGS: Current Average Turnaround time - NTRKfus

NGS: Current Average Turnaround time - NTRKfus	Overall
	N = 9
Mean	26.1
SD	10.2
Median	24.5
IQR	22.2 to 28.4
Range	15.5 to 40
NA.	5

NGS: Current Average Turnaround time - BRCA 1/2

NGS: Current Average Turnaround time - BRCA 1/2	Overall				
	N = 9				
Mean	29.6666667		24.5	24.5	40
SD	8.9				
Median	24.5				
IQR	24.5 to 32.2				
Range	24.5 to 40				
NA.	6				

Others

Others	Overall	
	n	% (N = 9)
ki67 (IHC)	1	11%
N/A	5	56%
ONCOTYPE DX	3	33%
NA.	0	-

Reflex at diagnosis - ONCOTYPE DX

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Reflex at diagnosis - ONCOTYPE DX	Overall	
	n	% (N = 9)
N/A	6	67%
Not specified	2	22%
On request	1	11%
NA.	0	-

Testing at progression/ relapse/ other
post Dx timepoints - ONCOTYPE DX

Testing at progression/ relapse/ other post Dx timepoints - ONCOTYPE DX	Overall	
	n	% (N = 9)
N/A	6	67%
Not specified	2	22%
On request	1	11%
NA.	0	-

Performed by pathology lab -
ONCOTYPE DX

Performed by pathology lab - ONCOTYPE DX	Overall	
	n	% (N = 9)
N/A	6	67%
Other external lab	3	33%
NA.	0	-

Moved to GLH/ Genomic centre -
ONCOTYPE DX

Moved to GLH/ Genomic centre - ONCOTYPE DX	Overall	
	n	% (N = 9)
N/A	6	67%
No	3	33%
NA.	0	-

Moving to GLH/ Genomic hubs -
ONCOTYPE DX

Moving to GLH/ Genomic hubs - ONCOTYPE DX	Overall	
	n	% (N = 9)

N/A	6	67%
No	3	33%
NA.	0	-

Current Average Turnaround time
(calendar days) - ONCOTYPE DX

Current Average Turnaround time (calendar days) - ONCOTYPE DX	Overall	
	n	% (N = 9)
24.5	1	11%
N/A	6	67%
Not specified	2	22%
NA.	0	-

Reflex at diagnosis - ki67 (IHC)

Reflex at diagnosis - ki67 (IHC)	Overall	
	n	% (N = 9)
N/A	8	89%
Yes	1	11%
NA.	0	-

Testing at progression/ relapse/ other
post Dx timepoints - ki67 (IHC)

Testing at progression/ relapse/ other post Dx timepoints - ki67 (IHC)	Overall	
	n	% (N = 9)
N/A	8	89%
No	1	11%
NA.	0	-

Performed by pathology lab - ki67
(IHC)

Performed by pathology lab - ki67 (IHC)	Overall	
	n	% (N = 9)
N/A	8	89%
Yes	1	11%
NA.	0	-

Moved to GLH/ Genomic centre - ki67
(IHC)

Moved to GLH/ Genomic centre - ki67 (IHC)	Overall	
	n	% (N = 9)
N/A	8	89%
No	1	11%
NA.	0	-

Moving to GLH/ Genomic hubs - ki67
(IHC)

Moving to GLH/ Genomic hubs - ki67 (IHC)	Overall	
	n	% (N = 9)
N/A	8	89%
No	1	11%
NA.	0	-

Current Average Turnaround time
(calendar days) - ki67 (IHC)

Current Average Turnaround time (calendar days) - ki67 (IHC)	Overall	
	n	% (N = 9)
N/A	8	89%
Not known	1	11%
NA.	0	-

IHC: Reflex at diagnosis - PD-L1

IHC: Reflex at diagnosis - PD-L1	Overall	
	n	% (N = 15)
Yes	15	100%
NA.	0	-

IHC: Reflex at diagnosis - ROS1fus

IHC: Reflex at diagnosis - ROS1fus	Overall	
	n	% (N = 15)
No	2	13%
Yes	13	87%
NA.	0	-

IHC: Reflex at diagnosis - ALKfus

IHC: Reflex at diagnosis - ALKfus	Overall	
	n	% (N = 15)
On request	1	7%
Yes	14	93%
NA.	0	-

IHC: Reflex at diagnosis - BRAF

IHC: Reflex at diagnosis - BRAF	Overall	
	n	% (N = 15)
No	14	93%
Yes	1	7%
NA.	0	-

IHC: Reflex at diagnosis - NTRKfus

IHC: Reflex at diagnosis - NTRKfus	Overall	
	n	% (N = 15)
No	12	80%
Yes	3	20%
NA.	0	-

IHC: Testing at progression / relapse / other post Dx timepoints - PD-L1

IHC: Testing at progression / relapse / other post Dx timepoints - PD-L1	Overall	
	n	% (N = 15)
No	4	27%
On request	7	47%
Yes	4	27%
NA.	0	-

IHC: Testing at progression / relapse / other post Dx timepoints ROS1fus

IHC: Testing at progression / relapse / other post Dx timepoints ROS1fus	Overall	
	n	% (N = 15)
No	8	53%
On request	5	33%
Yes	2	13%
NA.	0	-

IHC: Testing at progression / relapse / other post Dx timepoints - ALKfus

IHC: Testing at progression / relapse / other post Dx timepoints - ALKfus	Overall	
	n	% (N = 15)
No	7	47%
On request	6	40%
Yes	2	13%
NA.	0	-

IHC: Testing at progression / relapse / other post Dx timepoints - BRAF

IHC: Testing at progression / relapse / other post Dx timepoints - BRAF	Overall	
	n	% (N = 15)
No	14	93%
On request	1	7%
NA.	0	-

IHC: Testing at progression / relapse / other post Dx timepoints - NTRKfus

IHC: Testing at progression / relapse / other post Dx timepoints - NTRKfus	Overall	
	n	% (N = 15)
No	14	93%
On request	1	7%
NA.	0	-

IHC: Performed by pathology lab - PD-L1

IHC: Performed by pathology lab - PD-L1	Overall	
	n	% (N = 15)
Other external lab	1	7%
Yes	14	93%
NA.	0	-

IHC: Performed by pathology lab - ROS1fus

IHC: Performed by pathology lab - ROS1fus	Overall	
	n	% (N = 13)
Other external lab	2	15%
Yes	11	85%
NA.	2	-

IHC: Performed by pathology lab - ALKfus

IHC: Performed by pathology lab - ALKfus	Overall	
	n	% (N = 15)
Other external lab	1	7%
Yes	14	93%
NA.	0	-

IHC: Performed by pathology lab - BRAF

IHC: Performed by pathology lab - BRAF	Overall	
	n	% (N = 1)
Yes	1	100%
NA.	14	-

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IHC: Performed by pathology lab - NTRKfus

IHC: Performed by pathology lab - NTRKfus	Overall	
	n	% (N = 3)
Other external lab	1	33%
Yes	2	67%
NA.	12	-

IHC: Moved to GLH / Genomic Centre - PD-L1

IHC: Moved to GLH / Genomic Centre - PD-L1	Overall	
	n	% (N = 15)
No	15	100%
NA.	0	-

IHC: Moved to GLH / Genomic Centre - ROS1fus

IHC: Moved to GLH / Genomic Centre - ROS1fus	Overall	
	n	% (N = 13)
No	13	100%
NA.	2	-

IHC: Moved to GLH / Genomic Centre - ALKfus

IHC: Moved to GLH / Genomic Centre - ALKfus	Overall	
	n	% (N = 15)
No	15	100%
NA.	0	-

IHC: Moved to GLH / Genomic Centre - BRAF

IHC: Moved to GLH / Genomic Centre - BRAF	Overall	
	n	% (N = 1)
No	1	100%
NA.	14	-

IHC: Moved to GLH / Genomic Centre - NTRKfus

IHC: Moved to GLH / Genomic Centre - NTRKfus	Overall	
	n	% (N = 3)
No	3	100%
NA.	12	-

IHC: Moving to GLH / Genomic hubs - PL-D1

IHC: Moving to GLH / Genomic hubs - PL-D1	Overall	
	n	% (N = 15)
No	15	100%
NA.	0	-

IHC: Moving to GLH / Genomic hubs - ROS1fus

IHC: Moving to GLH / Genomic hubs - ROS1fus	Overall	
	n	% (N = 13)
No	13	100%
NA.	2	-

IHC: Moving to GLH / Genomic hubs - ALKfus

IHC: Moving to GLH / Genomic hubs - ALKfus	Overall	
	n	% (N = 15)
No	15	100%
NA.	0	-

IHC: Moving to GLH / Genomic hubs - BRAF

IHC: Moving to GLH / Genomic hubs - BRAF	Overall	
	n	% (N = 1)
No	1	100%
NA.	14	-

IHC: Moving to GLH / Genomic hubs - NTRKfus

IHC: Moving to GLH / Genomic hubs - NTRKfus	Overall	

	n	% (N = 3)
No	3	100%
NA.	12	-

IHC: Current average turnaround time - PD-L1

IHC: Current average turnaround time - PD-L1	Overall
	N = 15
Mean	4.9
SD	7.5
Median	2.5
IQR	2 to 3
Range	1 to 30
NA.	1

IHC: Current average turnaround time - ROS1fus

IHC: Current average turnaround time - ROS1fus	Overall
	N = 15
Mean	5.8
SD	8
Median	2.8
IQR	2 to 7
Range	1 to 30
NA.	3

IHC: Current average turnaround time - ALKfus

IHC: Current average turnaround time - ALKfus	Overall
	N = 15
Mean	5.1
SD	7.7
Median	2.5
IQR	2 to 3
Range	1 to 30
NA.	2

IHC: Current average turnaround time - BRAF

IHC: Current average turnaround time - BRAF	Overall
	N = 15

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Mean	3
SD	
Median	3
IQR	3 to 3
Range	3 to 3
NA.	14

IHC: Current average turnaround time - NTRKfus

IHC: Current average turnaround time - NTRKfus	Overall
	N = 15
Mean	13.5
SD	14.5
Median	7.5
IQR	5.2 to 18.8
Range	3 to 30
NA.	12

FISH: Reflex at diagnosis - ALKfus

FISH: Reflex at diagnosis - ALKfus	Overall	
	n	% (N = 15)
No	8	53%
On request	2	13%
Yes	5	33%
NA.	0	-

FISH: Reflex at diagnosis - ROS1fus

FISH: Reflex at diagnosis - ROS1fus	Overall	
	n	% (N = 15)
No	8	53%
On request	2	13%
Yes	5	33%
NA.	0	-

FISH: Reflex at diagnosis - METamp

FISH: Reflex at diagnosis - METamp	Overall	
	n	% (N = 15)
No	11	73%
On request	3	20%

Yes	1	7%
NA.	0	-

FISH: Reflex at diagnosis - HER2amp

FISH: Reflex at diagnosis - HER2amp	Overall	
	n	% (N = 15)
No	12	80%
On request	2	13%
Yes	1	7%
NA.	0	-

FISH: Reflex at diagnosis - RETfus

FISH: Reflex at diagnosis - RETfus	Overall	
	n	% (N = 15)
No	10	67%
On request	3	20%
Yes	2	13%
NA.	0	-

FISH: Reflex at diagnosis - NTRKfus

FISH: Reflex at diagnosis - NTRKfus	Overall	
	n	% (N = 15)
No	12	80%
On request	3	20%
NA.	0	-

FISH: Testing at progression / relapse / other post
Dx timepoints - ALKfus

FISH: Testing at progression / relapse / other post Dx timepoints - ALKfus	Overall	
	n	% (N = 15)
No	10	67%
On request	3	20%
Yes	2	13%
NA.	0	-

FISH: Testing at progression / relapse / other post
Dx timepoints ROS1fus

FISH: Testing at progression / relapse / other post Dx timepoints ROS1fus	Overall	
	n	% (N = 15)
No	10	67%
On request	3	20%
Yes	2	13%
NA.	0	-

FISH: Testing at progression / relapse / other post
Dx timepoints - METamp

FISH: Testing at progression / relapse / other post Dx timepoints - METamp	Overall	
	n	% (N = 15)
No	12	80%
On request	3	20%
NA.	0	-

FISH: Testing at progression / relapse / other post
Dx timepoints - HER2amp

FISH: Testing at progression / relapse / other post Dx timepoints - HER2amp	Overall	
	n	% (N = 15)
No	14	93%
On request	1	7%
NA.	0	-

FISH: Testing at progression / relapse / other post
Dx timepoints - RETfus

FISH: Testing at progression / relapse / other post Dx timepoints - RETfus	Overall	
	n	% (N = 15)
No	14	93%
On request	1	7%
NA.	0	-

FISH: Testing at progression / relapse / other post
Dx timepoints - NTRKfus

FISH: Testing at progression / relapse / other post Dx timepoints - NTRKfus	Overall	
	n	% (N = 15)
No	14	93%
On request	1	7%
NA.	0	-

FISH: Performed by pathology lab - ALKfus

FISH: Performed by pathology lab - ALKfus	Overall	
	n	% (N = 8)
No	3	38%
Yes	5	62%
NA.	7	-

FISH: Performed by pathology lab - ROS1fus

FISH: Performed by pathology lab - ROS1fus	Overall	
	n	% (N = 8)
No	3	38%
Yes	5	62%
NA.	7	-

FISH: Performed by pathology lab - METamp

FISH: Performed by pathology lab - METamp	Overall	
	n	% (N = 5)
No	2	40%
Other external lab	1	20%
Yes	2	40%
NA.	10	-

FISH: Performed by pathology lab - HER2amp

FISH: Performed by pathology lab - HER2amp	Overall	
	n	% (N = 4)
No	2	50%
Yes	2	50%
NA.	11	-

FISH: Performed by pathology lab - RETfus

FISH: Performed by pathology lab - RETfus	Overall	
	n	% (N = 6)
No	2	33%
Other external lab	1	17%
Yes	3	50%
NA.	9	-

FISH: Performed by pathology lab - NTRKfus

FISH: Performed by pathology lab - NTRKfus	Overall	
	n	% (N = 4)
No	2	50%
Yes	2	50%
NA.	11	-

FISH: Moved to GLH / Genomic Centre - ALKfus

FISH: Moved to GLH / Genomic Centre - ALKfus	Overall	
	n	% (N = 8)
No	5	62%
Yes	3	38%
NA.	7	-

FISH: Moved to GLH / Genomic Centre - ROS1fus

FISH: Moved to GLH / Genomic Centre - ROS1fus	Overall	
	n	% (N = 8)
No	5	62%
Yes	3	38%
NA.	7	-

FISH: Moved to GLH / Genomic Centre - METamp

FISH: Moved to GLH / Genomic Centre - METamp	Overall	
	n	% (N = 5)
No	3	60%
Yes	2	40%
NA.	10	-

FISH: Moved to GLH / Genomic Centre - HER2amp

FISH: Moved to GLH / Genomic Centre - HER2amp	Overall	
	n	% (N = 4)
No	2	50%
Yes	2	50%
NA.	11	-

FISH: Moved to GLH / Genomic Centre - RETfus

FISH: Moved to GLH / Genomic Centre - RETfus	Overall	
	n	% (N = 6)
No	4	67%
Yes	2	33%
NA.	9	-

FISH: Moved to GLH / Genomic Centre - NTRKfus

FISH: Moved to GLH / Genomic Centre - NTRKfus	Overall	
	n	% (N = 4)
No	2	50%
Yes	2	50%
NA.	11	-

FISH: Moving to GLH / Genomic hubs - ALKfus

FISH: Moving to GLH / Genomic hubs - ALKfus	Overall	
	n	% (N = 8)

No	8	100%
NA.	7	-

FISH: Moving to GLH / Genomic hubs - ROS1fus

FISH: Moving to GLH / Genomic hubs - ROS1fus	Overall	
	n	% (N = 8)
No	8	100%
NA.	7	-

FISH: Moving to GLH / Genomic hubs - METamp

FISH: Moving to GLH / Genomic hubs - METamp	Overall	
	n	% (N = 5)
No	5	100%
NA.	10	-

FISH: Moving to GLH / Genomic hubs - HER2amp

FISH: Moving to GLH / Genomic hubs - HER2amp	Overall	
	n	% (N = 4)
No	4	100%
NA.	11	-

FISH: Moving to GLH / Genomic hubs - RETfus

FISH: Moving to GLH / Genomic hubs - RETfus	Overall	
	n	% (N = 6)
No	6	100%
NA.	9	-

FISH: Moving to GLH / Genomic hubs - NTRKfus

FISH: Moving to GLH / Genomic hubs - NTRKfus	Overall	
	n	% (N = 4)
No	4	100%
NA.	11	-

FISH: Current average turnaround time - ALKfus

FISH: Current average turnaround time - ALKfus	Overall
	N = 15
Mean	8.4
SD	5.8
Median	7.2
IQR	5.5 to 10
Range	2 to 21
NA.	7

FISH: Current average turnaround time - ROS1fus

FISH: Current average turnaround time - ROS1fus	Overall
	N = 15
Mean	8.4
SD	5.8
Median	7.2
IQR	5.5 to 10
Range	2 to 21
NA.	7

FISH: Current average turnaround time - METamp

FISH: Current average turnaround time - METamp	Overall
	N = 15
Mean	14.1
SD	11.3
Median	10
IQR	7.5 to 21
Range	2 to 30
NA.	10

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FISH: Current average turnaround time - HER2amp

FISH: Current average turnaround time - HER2amp	Overall
	N = 15
Mean	10.1
SD	8
Median	8.8
IQR	6.1 to 12.8
Range	2 to 21
NA.	11

FISH: Current average turnaround time - RETfus

FISH: Current average turnaround time - RETfus	Overall
	N = 15
Mean	12.4
SD	10.9
Median	8.8
IQR	4.9 to 18.2
Range	2 to 30
NA.	9

FISH: Current average turnaround time - NTRKfus

FISH: Current average turnaround time - NTRKfus	Overall
	N = 15
Mean	9.2
SD	8.5
Median	7
IQR	3.5 to 12.8
Range	2 to 21
NA.	11

RT-PCR: Reflex at diagnosis - EGFR

RT-PCR: Reflex at diagnosis - EGFR	Overall	
	n	% (N = 15)
No	4	27%
Yes	11	73%
NA.	0	-

RT-PCR: Reflex at diagnosis - ROS1fus

RT-PCR: Reflex at diagnosis - ROS1fus	Overall	
	n	% (N = 15)
No	13	87%
Yes	2	13%
NA.	0	-

RT-PCR: Reflex at diagnosis - ALKfus

RT-PCR: Reflex at diagnosis - ALKfus	Overall	
	n	% (N = 15)
No	13	87%
Yes	2	13%
NA.	0	-

RT-PCR: Reflex at diagnosis - ALK

RT-PCR: Reflex at diagnosis - ALK	Overall	
	n	% (N = 15)
No	13	87%
Yes	2	13%
NA.	0	-

RT-PCR: Reflex at diagnosis - BRAF

RT-PCR: Reflex at diagnosis - BRAF	Overall	
	n	% (N = 15)
No	6	40%
On request	3	20%
Yes	6	40%
NA.	0	-

RT-PCR: Reflex at diagnosis - KRAS

RT-PCR: Reflex at diagnosis - KRAS	Overall	
	n	% (N = 15)
No	8	53%
On request	3	20%
Yes	4	27%

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NA.	0	-

RT-PCR: Reflex at diagnosis - METex14

RT-PCR: Reflex at diagnosis - METex14	Overall	
	n	% (N = 15)
No	9	60%
On request	3	20%
Yes	3	20%
NA.	0	-

RT-PCR: Reflex at diagnosis - HER2

RT-PCR: Reflex at diagnosis - HER2	Overall	
	n	% (N = 15)
No	12	80%
On request	2	13%
Yes	1	7%
NA.	0	-

RT-PCR: Reflex at diagnosis - RETfus

RT-PCR: Reflex at diagnosis - RETfus	Overall	
	n	% (N = 15)
No	10	67%
On request	2	13%
Yes	3	20%
NA.	0	-

RT-PCR: Reflex at diagnosis - NTRKfus

RT-PCR: Reflex at diagnosis - NTRKfus	Overall	
	n	% (N = 15)
No	9	60%
On request	4	27%
Yes	2	13%
NA.	0	-

RT-PCR: Testing at progression / relapse / other
post Dx timepoints - EGFR

RT-PCR: Testing at progression / relapse / other post Dx timepoints - EGFR	Overall	
	n	% (N = 15)
No	7	47%
On request	5	33%
Yes	3	20%
NA.	0	-

RT-PCR: Testing at progression / relapse / other post Dx timepoints - ROS1fus

RT-PCR: Testing at progression / relapse / other post Dx timepoints - ROS1fus	Overall	
	n	% (N = 15)
No	14	93%
On request	1	7%
NA.	0	-

RT-PCR: Testing at progression / relapse / other post Dx timepointss - ALKfus

RT-PCR: Testing at progression / relapse / other post Dx timepointss - ALKfus	Overall	
	n	% (N = 15)
No	14	93%
On request	1	7%
NA.	0	-

RT-PCR: Testing at progression / relapse / other post Dx timepoints - ALK

RT-PCR: Testing at progression / relapse / other post Dx timepoints - ALK	Overall	
	n	% (N = 15)
No	14	93%
On request	1	7%
NA.	0	-

RT-PCR: Testing at progression / relapse / other post Dx timepointss - BRAF

RT-PCR: Testing at progression / relapse / other post Dx timepointss - BRAF	Overall	
	n	% (N = 15)
No	9	60%
On request	5	33%
Yes	1	7%
NA.	0	-

RT-PCR: Testing at progression / relapse / other
post Dx timepoints - KRAS

RT-PCR: Testing at progression / relapse / other post Dx timepoints - KRAS	Overall	
	n	% (N = 15)
No	11	73%
On request	4	27%
NA.	0	-

RT-PCR: Testing at progression / relapse / other
post Dx timepoints - METex14

RT-PCR: Testing at progression / relapse / other post Dx timepoints - METex14	Overall	
	n	% (N = 15)
No	12	80%
On request	3	20%
NA.	0	-

RT-PCR: Testing at progression / relapse / other
post Dx timepoints - HER2

RT-PCR: Testing at progression / relapse / other post Dx timepoints - HER2	Overall	
	n	% (N = 15)
No	14	93%
On request	1	7%
NA.	0	-

RT-PCR: Testing at progression / relapse / other
post Dx timepointss - RETfus

RT-PCR: Testing at progression / relapse / other post Dx timepointss - RETfus	Overall	
	n	% (N = 15)
No	14	93%
On request	1	7%
NA.	0	-

RT-PCR: Testing at progression / relapse / other post Dx timepoints - NTRKfus

RT-PCR: Testing at progression / relapse / other post Dx timepoints - NTRKfus	Overall	
	n	% (N = 15)
No	12	80%
On request	3	20%
NA.	0	-

RT-PCR: Performed by pathology lab - EGFR

RT-PCR: Performed by pathology lab - EGFR	Overall	
	n	% (N = 11)
No	1	9%
Other external lab	1	9%
Yes	9	82%
NA.	4	-

RT-PCR: Performed by pathology lab - ROS1fus

RT-PCR: Performed by pathology lab - ROS1fus	Overall	
	n	% (N = 2)
Yes	2	100%
NA.	13	-

RT-PCR: Performed by pathology lab - ALKfus

RT-PCR: Performed by pathology lab - ALKfus	Overall	
	n	% (N = 2)
Yes	2	100%
NA.	13	-

RT-PCR: Performed by pathology lab - ALK

RT-PCR: Performed by pathology lab - ALK	Overall	
	n	% (N = 2)
Yes	2	100%
NA.	13	-

RT-PCR: Performed by pathology lab - BRAF...94

RT-PCR: Performed by pathology lab - BRAF...94	Overall	
	n	% (N = 9)
No	1	11%
Other external lab	2	22%
Yes	6	67%
NA.	6	-

RT-PCR: Performed by pathology lab - KRAS

RT-PCR: Performed by pathology lab - KRAS	Overall	
	n	% (N = 7)
No	1	14%
Other external lab	2	29%
Yes	4	57%
NA.	8	-

RT-PCR: Performed by pathology lab - METex14

RT-PCR: Performed by pathology lab - METex14	Overall	
	n	% (N = 6)
No	1	17%
Other external lab	2	33%
Yes	3	50%
NA.	9	-

RT-PCR: Performed by pathology lab - HER2

RT-PCR: Performed by pathology lab - HER2	Overall	
	n	% (N = 3)
Other external lab	1	33%
Yes	2	67%
NA.	12	-

RT-PCR: Performed by pathology lab - RETfus

RT-PCR: Performed by pathology lab - RETfus	Overall	
	n	% (N = 5)
No	1	20%
Other external lab	1	20%
Yes	3	60%
NA.	10	-

RT-PCR: Performed by pathology lab - NTRKfus

RT-PCR: Performed by pathology lab - NTRKfus	Overall	
	n	% (N = 6)
No	1	17%
Other external lab	2	33%
Yes	3	50%
NA.	9	-

RT-PCR: Moved to GLH / Genomic Centre - EGFR

RT-PCR: Moved to GLH / Genomic Centre - EGFR	Overall	
	n	% (N = 11)
No	10	91%
Yes	1	9%
NA.	4	-

RT-PCR: Moved to GLH / Genomic Centre - ROS1fus

RT-PCR: Moved to GLH / Genomic Centre - ROS1fus	Overall	
	n	% (N = 2)

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No	2	100%
NA.	13	-

RT-PCR: Moved to GLH / Genomic Centre - ALKfus

RT-PCR: Moved to GLH / Genomic Centre - ALKfus	Overall	
	n	% (N = 2)
No	2	100%
NA.	13	-

RT-PCR: Moved to GLH / Genomic Centre - ALK

RT-PCR: Moved to GLH / Genomic Centre - ALK	Overall	
	n	% (N = 2)
No	2	100%
NA.	13	-

RT-PCR: Moved to GLH / Genomic Centre - BRAF

RT-PCR: Moved to GLH / Genomic Centre - BRAF	Overall	
	n	% (N = 9)
No	8	89%
Yes	1	11%
NA.	6	-

RT-PCR: Moved to GLH / Genomic Centre - KRAS

RT-PCR: Moved to GLH / Genomic Centre - KRAS	Overall	
	n	% (N = 7)
No	6	86%
Yes	1	14%
NA.	8	-

RT-PCR: Moved to GLH / Genomic Centre - METex14

RT-PCR: Moved to GLH / Genomic Centre - METex14	Overall	
	n	% (N = 6)
No	5	83%
Yes	1	17%
NA.	9	-

RT-PCR: Moved to GLH / Genomic Centre - HER2

RT-PCR: Moved to GLH / Genomic Centre - HER2	Overall	
	n	% (N = 3)
No	3	100%
NA.	12	-

RT-PCR: Moved to GLH / Genomic Centre - RETfus

RT-PCR: Moved to GLH / Genomic Centre - RETfus	Overall	
	n	% (N = 5)
No	4	80%
Yes	1	20%
NA.	10	-

RT-PCR: Moved to GLH / Genomic Centre - NTRKfus

RT-PCR: Moved to GLH / Genomic Centre - NTRKfus	Overall	
	n	% (N = 6)
No	5	83%
Yes	1	17%
NA.	9	-

RT-PCR: Moving to GLH / Genomic hubs - EGFR

RT-PCR: Moving to GLH / Genomic hubs - EGFR	Overall	
	n	% (N = 11)
No	11	100%
NA.	4	-

RT-PCR: Moving to GLH / Genomic hubs - ROS1fus

RT-PCR: Moving to GLH / Genomic hubs - ROS1fus	Overall	
	n	% (N = 2)
No	2	100%
NA.	13	-

RT-PCR: Moving to GLH / Genomic hubs - ALKfus

RT-PCR: Moving to GLH / Genomic hubs - ALKfus	Overall	
	n	% (N = 2)
No	2	100%
NA.	13	-

RT-PCR: Moving to GLH / Genomic hubs - ALK

RT-PCR: Moving to GLH / Genomic hubs - ALK	Overall	
	n	% (N = 2)
No	2	100%
NA.	13	-

RT-PCR: Moving to GLH / Genomic hubs - BRAF

RT-PCR: Moving to GLH / Genomic hubs - BRAF	Overall	
	n	% (N = 9)
No	9	100%
NA.	6	-

RT-PCR: Moving to GLH / Genomic hubs - KRAS

RT-PCR: Moving to GLH / Genomic hubs - KRAS	Overall	
	n	% (N = 7)
No	7	100%
NA.	8	-

RT-PCR: Moving to GLH / Genomic hubs - METex14

RT-PCR: Moving to GLH / Genomic hubs - METex14	Overall	
	n	% (N = 6)
No	6	100%
NA.	9	-

RT-PCR: Moving to GLH / Genomic hubs - HER2

RT-PCR: Moving to GLH / Genomic hubs - HER2	Overall	
	n	% (N = 3)
No	3	100%
NA.	12	-

RT-PCR: Moving to GLH / Genomic hubs - RETfus

RT-PCR: Moving to GLH / Genomic hubs - RETfus	Overall	
	n	% (N = 5)
No	5	100%
NA.	10	-

RT-PCR: Moving to GLH / Genomic hubs - NTRKfus

RT-PCR: Moving to GLH / Genomic hubs - NTRKfus	Overall	

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	n	% (N = 6)
No	6	100%
NA.	9	-

RT-PCR: Current average turnaround time - EGFR

RT-PCR: Current average turnaround time - EGFR	Overall
	N = 15
Mean	7.5
SD	8.4
Median	6
IQR	2 to 7.2
Range	1 to 30
NA.	4

RT-PCR: Current average turnaround times - ROS1fus

RT-PCR: Current average turnaround times - ROS1fus	Overall
	N = 15
Mean	4.8
SD	3.9
Median	4.8
IQR	3.4 to 6.1
Range	2 to 7.5
NA.	13

RT-PCR: Current average turnaround time - ALKfus

RT-PCR: Current average turnaround time - ALKfus	Overall
	N = 15
Mean	4.8
SD	3.9
Median	4.8
IQR	3.4 to 6.1
Range	2 to 7.5
NA.	13

RT-PCR: Current average turnaround time - ALK

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RT-PCR: Current average turnaround time - ALK	Overall
	N = 15
Mean	4.8
SD	3.9
Median	4.8
IQR	3.4 to 6.1
Range	2 to 7.5
NA.	13

RT-PCR: Current average turnaround time - BRAF

RT-PCR: Current average turnaround time - BRAF	Overall
	N = 15
Mean	10.6
SD	11.2
Median	7
IQR	2 to 14
Range	1 to 30
NA.	6

RT-PCR: Current average turnaround time - KRAS

RT-PCR: Current average turnaround time - KRAS	Overall
	N = 15
Mean	12.4
SD	12.2
Median	7.5
IQR	3 to 21
Range	1 to 30
NA.	8

RT-PCR: Current average turnaround time - METex14

RT-PCR: Current average turnaround time - METex14	Overall
	N = 15
Mean	14.2
SD	12.1
Median	10.8
IQR	4.9 to 24.5

Range	2 to 30
NA.	9

RT-PCR: Current average turnaround time - HER2

RT-PCR: Current average turnaround time - HER2	Overall
	N = 15
Mean	13.8
SD	14.1
Median	7.5
IQR	5.8 to 18.8
Range	4 to 30
NA.	12

RT-PCR: Current average turnaround time - RETfus

RT-PCR: Current average turnaround time - RETfus	Overall
	N = 15
Mean	11.1
SD	10.5
Median	7.5
IQR	4 to 14
Range	2 to 28
NA.	10

RT-PCR: Current average turnaround time - NTRKfus

RT-PCR: Current average turnaround time - NTRKfus	Overall
	N = 15
Mean	11.1
SD	10.5
Median	7.5
IQR	4 to 14
Range	2 to 28
NA.	10

NGS: Reflex at diagnosis - EGFR

NGS: Reflex at diagnosis - EGFR	Overall	
	n	% (N = 15)

No	3	20%
On request	3	20%
Yes	9	60%
NA.	0	-

NGS: Reflex at diagnosis - ROS1fus

NGS: Reflex at diagnosis - ROS1fus	Overall	
	n	% (N = 15)
No	5	33%
On request	3	20%
Yes	7	47%
NA.	0	-

NGS: Reflex at diagnosis - ALKfus

NGS: Reflex at diagnosis - ALKfus	Overall	
	n	% (N = 15)
No	4	27%
On request	3	20%
Yes	8	53%
NA.	0	-

NGS: Reflex at diagnosis - BRAF

NGS: Reflex at diagnosis - BRAF	Overall	
	n	% (N = 15)
No	3	20%
On request	3	20%
Yes	9	60%
NA.	0	-

NGS: Reflex at diagnosis - KRAS

NGS: Reflex at diagnosis - KRAS	Overall	
	n	% (N = 15)
No	3	20%
On request	3	20%
Yes	9	60%
NA.	0	-

NGS: Reflex at diagnosis - METex14

NGS: Reflex at diagnosis - METex14	Overall	
	n	% (N = 15)
No	4	27%
On request	3	20%
Yes	8	53%
NA.	0	-

NGS: Reflex at diagnosis - HER2

NGS: Reflex at diagnosis - HER2	Overall	
	n	% (N = 15)
No	7	47%
On request	3	20%
Yes	5	33%
NA.	0	-

NGS: Reflex at diagnosis - RETfus

NGS: Reflex at diagnosis - RETfus	Overall	
	n	% (N = 15)
No	4	27%
On request	3	20%
Yes	8	53%
NA.	0	-

NGS: Reflex at diagnosis - NTRKfus

NGS: Reflex at diagnosis - NTRKfus	Overall	
	n	% (N = 15)
No	5	33%
On request	3	20%
Yes	7	47%
NA.	0	-

NGS: Testing at progression / relapse / other post
Dx timepoints - EGFR

NGS: Testing at progression / relapse / other post Dx timepoints - EGFR	Overall	

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	n	% (N = 15)
No	7	47%
On request	8	53%
NA.	0	-

NGS: Testing at progression / relapse / other post Dx timepoints - ROS1fus

NGS: Testing at progression / relapse / other post Dx timepoints - ROS1fus	Overall	
	n	% (N = 15)
No	8	53%
On request	7	47%
NA.	0	-

NGS: Testing at progression / relapse / other post Dx timepointss - ALKfus

NGS: Testing at progression / relapse / other post Dx timepointss - ALKfus	Overall	
	n	% (N = 15)
No	8	53%
On request	7	47%
NA.	0	-

NGS: Testing at progression / relapse / other post Dx timepointss - BRAF

NGS: Testing at progression / relapse / other post Dx timepointss - BRAF	Overall	
	n	% (N = 15)
No	8	53%
On request	7	47%
NA.	0	-

NGS: Testing at progression / relapse / other post Dx timepoints - KRAS

NGS: Testing at progression / relapse / other post Dx timepoints - KRAS	Overall	
	n	% (N = 15)
No	8	53%

On request	7	47%
NA.	0	-

NGS: Testing at progression / relapse / other post Dx timepoints - METex14

NGS: Testing at progression / relapse / other post Dx timepoints - METex14	Overall	
	n	% (N = 15)
No	8	53%
On request	7	47%
NA.	0	-

NGS: Testing at progression / relapse / other post Dx timepoints - HER2

NGS: Testing at progression / relapse / other post Dx timepoints - HER2	Overall	
	n	% (N = 15)
No	9	60%
On request	6	40%
NA.	0	-

NGS: Testing at progression / relapse / other post Dx timepointss - RETfus

NGS: Testing at progression / relapse / other post Dx timepointss - RETfus	Overall	
	n	% (N = 15)
No	8	53%
On request	7	47%
NA.	0	-

NGS: Testing at progression / relapse / other post Dx timepoints - NTRKfus

NGS: Testing at progression / relapse / other post Dx timepoints - NTRKfus	Overall	
	n	% (N = 15)
No	8	53%
On request	7	47%
NA.	0	-

NGS: Performed by pathology lab - EGFR

NGS: Performed by pathology lab - EGFR	Overall	
	n	% (N = 12)
No	10	83%
Yes	2	17%
NA.	3	-

NGS: Performed by pathology lab - ROS1fus

NGS: Performed by pathology lab - ROS1fus	Overall	
	n	% (N = 10)
No	10	100%
NA.	5	-

NGS: Performed by pathology lab - ALKfus

NGS: Performed by pathology lab - ALKfus	Overall	
	n	% (N = 11)
No	11	100%
NA.	4	-

RT-PCR: Performed by pathology lab - BRAF...151

RT-PCR: Performed by pathology lab - BRAF...151	Overall	
	n	% (N = 12)
No	11	92%
Yes	1	8%
NA.	3	-

NGS: Performed by pathology lab - KRAS

NGS: Performed by pathology lab - KRAS	Overall	
	n	% (N = 12)
No	11	92%
Yes	1	8%
NA.	3	-

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NGS: Performed by pathology lab - METex14

NGS: Performed by pathology lab - METex14	Overall	
	n	% (N = 11)
No	10	91%
Yes	1	9%
NA.	4	-

NGS: Performed by pathology lab - HER2

NGS: Performed by pathology lab - HER2	Overall	
	n	% (N = 8)
No	8	100%
NA.	7	-

NGS: Performed by pathology lab - RETfus

NGS: Performed by pathology lab - RETfus	Overall	
	n	% (N = 11)
No	11	100%
NA.	4	-

NGS: Performed by pathology lab - NTRKfus

NGS: Performed by pathology lab - NTRKfus	Overall	
	n	% (N = 10)
No	10	100%
NA.	5	-

NGS: Moved to GLH / Genomic Centre - EGFR

NGS: Moved to GLH / Genomic Centre - EGFR	Overall	
	n	% (N = 12)
No	2	17%
Yes	10	83%
NA.	3	-

NGS: Moved to GLH / Genomic Centre - ROS1fus

NGS: Moved to GLH / Genomic Centre - ROS1fus	Overall	
	n	% (N = 10)
Yes	10	100%
NA.	5	-

NGS: Moved to GLH / Genomic Centre - ALKfus

NGS: Moved to GLH / Genomic Centre - ALKfus	Overall	
	n	% (N = 11)
Yes	11	100%
NA.	4	-

NGS: Moved to GLH / Genomic Centre - BRAF

NGS: Moved to GLH / Genomic Centre - BRAF	Overall	
	n	% (N = 12)
No	1	8%
Yes	11	92%
NA.	3	-

NGS: Moved to GLH / Genomic Centre - KRAS

NGS: Moved to GLH / Genomic Centre - KRAS	Overall	
	n	% (N = 12)
No	1	8%
Yes	11	92%
NA.	3	-

NGS: Moved to GLH / Genomic Centre - METex14

NGS: Moved to GLH / Genomic Centre - METex14	Overall	
	n	% (N = 11)
No	1	9%
Yes	10	91%

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NA.	4	-

NGS: Moved to GLH / Genomic Centre - HER2

NGS: Moved to GLH / Genomic Centre - HER2	Overall	
	n	% (N = 8)
Yes	8	100%
NA.	7	-

NGS: Moved to GLH / Genomic Centre - RETfus

NGS: Moved to GLH / Genomic Centre - RETfus	Overall	
	n	% (N = 11)
Yes	11	100%
NA.	4	-

NGS: Moved to GLH / Genomic Centre - NTRKfus

NGS: Moved to GLH / Genomic Centre - NTRKfus	Overall	
	n	% (N = 10)
Yes	10	100%
NA.	5	-

NGS: Moving to GLH / Genomic hubs - EGFR

NGS: Moving to GLH / Genomic hubs - EGFR	Overall	
	n	% (N = 12)
No	12	100%
NA.	3	-

NGS: Moving to GLH / Genomic hubs - ROS1fus

NGS: Moving to GLH / Genomic hubs - ROS1fus	Overall	
	n	% (N = 10)

No	10	100%
NA.	5	-

NGS: Moving to GLH / Genomic hubs - ALKfus

NGS: Moving to GLH / Genomic hubs - ALKfus	Overall	
	n	% (N = 11)
No	11	100%
NA.	4	-

NGS: Moving to GLH / Genomic hubs - BRAF

NGS: Moving to GLH / Genomic hubs - BRAF	Overall	
	n	% (N = 12)
No	12	100%
NA.	3	-

NGS: Moving to GLH / Genomic hubs - KRAS

NGS: Moving to GLH / Genomic hubs - KRAS	Overall	
	n	% (N = 12)
No	12	100%
NA.	3	-

NGS: Moving to GLH / Genomic hubs - METex14

NGS: Moving to GLH / Genomic hubs - METex14	Overall	
	n	% (N = 11)
No	11	100%
NA.	4	-

NGS: Moving to GLH / Genomic hubs - HER2

NGS: Moving to GLH / Genomic hubs - HER2	Overall	
	n	% (N = 8)
No	8	100%
NA.	7	-

NGS: Moving to GLH / Genomic hubs - RETfus

NGS: Moving to GLH / Genomic hubs - RETfus	Overall	
	n	% (N = 11)
No	11	100%
NA.	4	-

NGS: Moving to GLH / Genomic hubs - NTRKfus

NGS: Moving to GLH / Genomic hubs - NTRKfus	Overall	
	n	% (N = 10)
No	10	100%
NA.	5	-

NGS: Current average turnaround time - EGFR

NGS: Current average turnaround time - EGFR	Overall
	N = 15
Mean	16.9
SD	6
Median	17.5
IQR	13 to 21.8
Range	7.5 to 24.5
NA.	4

NGS: Current average turnaround times - ROS1fus

NGS: Current average turnaround times - ROS1fus	Overall
	N = 15
Mean	19.2
SD	5.6
Median	19
IQR	14 to 24.5
Range	10 to 24.5
NA.	6

NGS: Current average turnaround time - ALKfus

NGS: Current average turnaround time - ALKfus	Overall
	N = 15
Mean	18.5
SD	5.8
Median	18.5
IQR	14 to 24.5
Range	10 to 24.5
NA.	5

NGS: Current average turnaround time - BRAF

NGS: Current average turnaround time - BRAF	Overall
	N = 15
Mean	16.9
SD	6
Median	17.5
IQR	13 to 21.8
Range	7.5 to 24.5
NA.	4

NGS: Current average turnaround time - KRAS

NGS: Current average turnaround time - KRAS	Overall
	N = 15
Mean	16.9
SD	6
Median	17.5
IQR	13 to 21.8
Range	7.5 to 24.5
NA.	4

NGS: Current average turnaround time - METex14

NGS: Current average turnaround time - METex14	Overall
	N = 15
Mean	17.4
SD	6.1
Median	17.8
IQR	14 to 23.1
Range	7.5 to 24.5
NA.	5

NGS: Current average turnaround time - HER2

NGS: Current average turnaround time - HER2	Overall
	N = 15
Mean	17.5
SD	5.5
Median	17.5
IQR	14 to 21.2
Range	10 to 24.5
NA.	8

NGS: Current average turnaround time - RETfus

NGS: Current average turnaround time - RETfus	Overall
	N = 15
Mean	18.5
SD	5.8
Median	18.5
IQR	14 to 24.5
Range	10 to 24.5
NA.	5

NGS: Current average turnaround time - NTRKfus

NGS: Current average turnaround time - NTRKfus	Overall
	N = 15
Mean	19.2
SD	5.6
Median	19
IQR	14 to 24.5
Range	10 to 24.5
NA.	6

Others

Others	Overall	
	n	% (N = 15)
N/A	14	93%
PIK3CA, TP53	1	7%
NA.	0	-

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Reflex at diagnosis : Others - PIK3CA

Reflex at diagnosis : Others - PIK3CA	Overall	
	n	% (N = 15)
N/A	14	93%
Yes	1	7%
NA.	0	-

Testing at progression/ relapse/ other post Dx timepoints: Others - PIK3CA

Testing at progression/ relapse/ other post Dx timepoints: Others - PIK3CA	Overall	
	n	% (N = 15)
N/A	14	93%
No	1	7%
NA.	0	-

Performed by pathology lab: Others - PIK3CA

Performed by pathology lab: Others - PIK3CA	Overall	
	n	% (N = 15)
N/A	14	93%
No	1	7%
NA.	0	-

Moved to GLH/ Genomic centre: Others - PIK3CA

Moved to GLH/ Genomic centre: Others - PIK3CA	Overall	
	n	% (N = 15)
N/A	14	93%
Yes	1	7%
NA.	0	-

Moving to GLH/ Genomic hub: Others - PIK3CA

Moving to GLH/ Genomic hub: Others - PIK3CA	Overall	
	n	% (N = 15)

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N/A	14	93%
No	1	7%
NA.	0	-

Current Average Turnaround time - PIK3CA

Current Average Turnaround time - PIK3CA	Overall	
	n	% (N = 15)
10 to 14	1	7%
N/A	14	93%
NA.	0	-

Reflex at diagnosis : Others - TP53

Reflex at diagnosis : Others - TP53	Overall	
	n	% (N = 15)
N/A	14	93%
Yes	1	7%
NA.	0	-

Testing at progression/ relapse/ other post Dx timepoints: Others - TP53

Testing at progression/ relapse/ other post Dx timepoints: Others - TP53	Overall	
	n	% (N = 15)
N/A	14	93%
No	1	7%
NA.	0	-

Performed by pathology lab: Others - TP53

Performed by pathology lab: Others - TP53	Overall	
	n	% (N = 15)
N/A	14	93%
No	1	7%
NA.	0	-

Moved to GLH/ Genomic centre: Others - TP53

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Moved to GLH/ Genomic centre: Others - TP53	Overall	
	n	% (N = 15)
N/A	14	93%
Yes	1	7%
NA.	0	-

Moving to GLH/ Genomic hub: Others - TP53

Moving to GLH/ Genomic hub: Others - TP53	Overall	
	n	% (N = 15)
N/A	14	93%
No	1	7%
NA.	0	-

Current Average Turnaround time - TP53

Current Average Turnaround time - TP53	Overall	
	n	% (N = 15)
10 to 14	1	7%
N/A	14	93%
NA.	0	-

IHC: Reflex at diagnosis - BRAF

IHC: Reflex at diagnosis - BRAF	Overall	
	n	% (N = 11)
No	8	73%
On request	3	27%
NA.	0	-

IHC: Reflex at diagnosis - PD-L1

IHC: Reflex at diagnosis - PD-L1	Overall	
	n	% (N = 11)
No	9	82%
On request	2	18%
NA.	0	-

IHC: Testing at progression / relapse / other post Dx timepoints - BRAF

IHC: Testing at progression / relapse / other post Dx timepoints - BRAF	Overall	
	n	% (N = 11)
No	9	82%
On request	2	18%
NA.	0	-

IHC: Testing at progression / relapse / other post Dx timepoints - PD-L1

IHC: Testing at progression / relapse / other post Dx timepoints - PD-L1	Overall	
	n	% (N = 11)
No	9	82%
On request	2	18%
NA.	0	-

IHC: Performed by pathology lab - BRAF

IHC: Performed by pathology lab - BRAF	Overall	
	n	% (N = 3)
Other external lab	2	67%

Yes	1	33%
NA.	8	-

IHC: Performed by pathology lab - PD-L1

IHC: Performed by pathology lab - PD-L1	Overall	
	n	% (N = 2)
Other external lab	1	50%
Yes	1	50%
NA.	9	-

IHC: Moved to GLH / Genomic Centre - BRAF

IHC: Moved to GLH / Genomic Centre - BRAF	Overall	
	n	% (N = 3)
No	3	100%
NA.	8	-

IHC: Moved to GLH / Genomic Centre - PD-L1

IHC: Moved to GLH / Genomic Centre - PD-L1	Overall	
	n	% (N = 2)
No	2	100%
NA.	9	-

IHC: Moving to GLH / Genomic hubs - BRAF

IHC: Moving to GLH / Genomic hubs - BRAF	Overall	
	n	% (N = 3)
No	3	100%
NA.	8	-

IHC: Moving to GLH / Genomic hubs - PD-L1

IHC: Moving to GLH / Genomic hubs - PD-L1	Overall	
	n	% (N = 2)
No	2	100%
NA.	9	-

IHC: Current average turnaround time - BRAF

IHC: Current average turnaround time - BRAF	Overall
	N = 11
Mean	13
SD	14.9
Median	7
IQR	4.5 to 18.5
Range	2 to 30
NA.	8

IHC: Current average turnaround time - PD-L1

IHC: Current average turnaround time - PD-L1	Overall
	N = 11
Mean	17
SD	18.4
Median	17
IQR	10.5 to 23.5
Range	4 to 30
NA.	9

Sanger Sequencing: Reflex at diagnosis - BRAF

Sanger Sequencing: Reflex at diagnosis - BRAF	Overall	
	n	% (N = 11)
No	10	91%
On request	1	9%
NA.	0	-

Sanger Sequencing: Reflex at diagnosis - NRAS

Sanger Sequencing: Reflex at diagnosis - NRAS	Overall	
	n	% (N = 11)
No	11	100%
NA.	0	-

Sanger Sequencing: Testing at progression / relapse /
other post Dx timepoints - BRAF

Sanger Sequencing: Testing at progression / relapse / other post Dx timepoints - BRAF	Overall	
	n	% (N = 11)

No	10	91%
On request	1	9%
NA.	0	-

Sanger Sequencing: Testing at progression / relapse / other post Dx timepoints - NRAS

Sanger Sequencing: Testing at progression / relapse / other post Dx timepoints - NRAS	Overall	
	n	% (N = 11)
No	11	100%
NA.	0	-

Sanger Sequencing: Performed by pathology lab - BRAF

Sanger Sequencing: Performed by pathology lab - BRAF	Overall	
	n	% (N = 1)
Other external lab	1	100%
NA.	10	-

Sanger Sequencing: Moved to GLH / Genomic Centre - BRAF

Sanger Sequencing: Moved to GLH / Genomic Centre - BRAF	Overall	
	n	% (N = 1)
No	1	100%
NA.	10	-

Sanger Sequencing: Moving to GLH / Genomic hubs - BRAF

Sanger Sequencing: Moving to GLH / Genomic hubs - BRAF	Overall	
	n	% (N = 1)
No	1	100%
NA.	10	-

Sanger Sequencing: Current average turnaround time - BRAF

Sanger Sequencing: Current average turnaround time - BRAF	Overall	
	n	% (N = 1)
7	1	100%
NA.	10	-

Pyrosequencing: Reflex at diagnosis - BRAF

Pyrosequencing: Reflex at diagnosis - BRAF	Overall	
	n	% (N = 11)
No	11	100%
NA.	0	-

Pyrosequencing: Testing at progression / relapse / other post Dx timepoints - BRAF

Pyrosequencing: Testing at progression / relapse / other post Dx timepoints - BRAF	Overall	
	n	% (N = 11)
No	11	100%
NA.	0	-

RT-PCR: Reflex at diagnosis - BRAF

RT-PCR: Reflex at diagnosis - BRAF	Overall	
	n	% (N = 11)
No	2	18%
On request	1	9%
Yes	8	73%
NA.	0	-

RT-PCR: Reflex at diagnosis - NRAS

RT-PCR: Reflex at diagnosis - NRAS	Overall	
	n	% (N = 11)
No	8	73%
On request	2	18%
Yes	1	9%
NA.	0	-

RT-PCR: Reflex at diagnosis - KIT

RT-PCR: Reflex at diagnosis - KIT	Overall	
	n	% (N = 11)
No	9	82%
On request	2	18%
NA.	0	-

RT-PCR: Testing at progression / relapse / other post Dx timepointss - BRAF

RT-PCR: Testing at progression / relapse / other post Dx timepointss - BRAF	Overall	
	n	% (N = 11)
No	7	64%
On request	2	18%
Yes	2	18%
NA.	0	-

RT-PCR: Testing at progression / relapse / other post Dx timepointss - NRAS

RT-PCR: Testing at progression / relapse / other post Dx timepointss - NRAS	Overall	
	n	% (N = 11)
No	9	82%
On request	1	9%
Yes	1	9%
NA.	0	-

RT-PCR: Testing at progression / relapse / other post Dx timepointss - KIT

RT-PCR: Testing at progression / relapse / other post Dx timepointss - KIT	Overall	
	n	% (N = 11)
No	10	91%
On request	1	9%
NA.	0	-

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RT-PCR: Performed by pathology lab - BRAF

RT-PCR: Performed by pathology lab - BRAF	Overall	
	n	% (N = 9)
No	1	11%
Other external lab	2	22%
Yes	6	67%
NA.	2	-

RT-PCR: Performed by pathology lab - NRAS

RT-PCR: Performed by pathology lab - NRAS	Overall	
	n	% (N = 2)
Other external lab	1	50%
Yes	1	50%
NA.	9	-

RT-PCR: Performed by pathology lab - KIT

RT-PCR: Performed by pathology lab - KIT	Overall	
	n	% (N = 1)
Other external lab	1	100%
NA.	10	-

RT-PCR: Moved to GLH / Genomic Centre - BRAF

RT-PCR: Moved to GLH / Genomic Centre - BRAF	Overall	
	n	% (N = 9)
No	8	89%
Yes	1	11%
NA.	2	-

RT-PCR: Moved to GLH / Genomic Centre - NRAS

RT-PCR: Moved to GLH / Genomic Centre - NRAS	Overall	
	n	% (N = 3)
No	3	100%
NA.	8	-

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RT-PCR: Moved to GLH / Genomic Centre - KIT

RT-PCR: Moved to GLH / Genomic Centre - KIT	Overall	
	n	% (N = 2)
No	2	100%
NA.	9	-

RT-PCR: Moving to GLH / Genomic hubs - BRAF

RT-PCR: Moving to GLH / Genomic hubs - BRAF	Overall	
	n	% (N = 9)
No	9	100%
NA.	2	-

RT-PCR: Moving to GLH / Genomic hubs - NRAS

RT-PCR: Moving to GLH / Genomic hubs - NRAS	Overall	
	n	% (N = 3)
No	3	100%
NA.	8	-

RT-PCR: Moving to GLH / Genomic hubs - KIT

RT-PCR: Moving to GLH / Genomic hubs - KIT	Overall	
	n	% (N = 2)
No	2	100%
NA.	9	-

RT-PCR: Current average turnaround time - BRAF

RT-PCR: Current average turnaround time - BRAF	Overall
	N = 11
Mean	7.5
SD	8.9
Median	6
IQR	2.5 to 7.5
Range	1 to 30
NA.	2

RT-PCR: Current average turnaround time - NRAS

RT-PCR: Current average turnaround time - NRAS	Overall
	N = 11
Mean	17.8
SD	21
Median	7.5
IQR	5.8 to 24.8
Range	4 to 42
NA.	8

RT-PCR: Current average turnaround time - KIT

RT-PCR: Current average turnaround time - KIT	Overall
	N = 11
Mean	23
SD	26.9
Median	23
IQR	13.5 to 32.5
Range	4 to 42
NA.	9

NGS: Reflex at diagnosis - BRAF

NGS: Reflex at diagnosis - BRAF	Overall	
	n	% (N = 11)
No	4	36%
On request	5	45%
Yes	2	18%
NA.	0	-

NGS: Reflex at diagnosis - NRAS

NGS: Reflex at diagnosis - NRAS	Overall	
	n	% (N = 11)
No	3	27%
On request	6	55%
Yes	2	18%
NA.	0	-

NGS: Reflex at diagnosis - KIT

NGS: Reflex at diagnosis - KIT	Overall	
	n	% (N = 11)
No	3	27%
On request	6	55%

Yes	2	18%
NA.	0	-

NGS: Testing at progression / relapse / other post Dx timepointss - BRAF

NGS: Testing at progression / relapse / other post Dx timepointss - BRAF	Overall	
	n	% (N = 11)
No	9	82%
On request	2	18%
NA.	0	-

NGS: Testing at progression / relapse / other post Dx timepointss - NRAS

NGS: Testing at progression / relapse / other post Dx timepointss - NRAS	Overall	
	n	% (N = 11)
No	9	82%
On request	2	18%
NA.	0	-

NGS: Testing at progression / relapse / other post Dx timepointss - KIT

NGS: Testing at progression / relapse / other post Dx timepointss - KIT	Overall	
	n	% (N = 11)
No	9	82%
On request	2	18%
NA.	0	-

NGS: Performed by pathology lab - BRAF

NGS: Performed by pathology lab - BRAF	Overall	
	n	% (N = 7)
No	6	86%
Yes	1	14%
NA.	4	-

NGS: Performed by pathology lab - NRAS

NGS: Performed by pathology lab - NRAS	Overall	
	n	% (N = 8)
No	6	75%
Other external lab	1	12%
Yes	1	12%
NA.	3	-

NGS: Performed by pathology lab - KIT

NGS: Performed by pathology lab - KIT	Overall	
	n	% (N = 8)
No	6	75%
Other external lab	1	12%
Yes	1	12%
NA.	3	-

NGS: Moved to GLH / Genomic Centre - BRAF

NGS: Moved to GLH / Genomic Centre - BRAF	Overall	
	n	% (N = 7)
No	2	29%
Yes	5	71%
NA.	4	-

NGS: Moved to GLH / Genomic Centre - NRAS

NGS: Moved to GLH / Genomic Centre - NRAS	Overall	
	n	% (N = 8)
No	3	38%
Yes	5	62%
NA.	3	-

NGS: Moved to GLH / Genomic Centre - KIT

NGS: Moved to GLH / Genomic Centre - KIT	Overall	
	n	% (N = 8)
No	3	38%
Yes	5	62%
NA.	3	-

NGS: Moving to GLH / Genomic hubs - BRAF

NGS: Moving to GLH / Genomic hubs - BRAF	Overall	
	n	% (N = 7)
No	6	86%
Yes	1	14%
NA.	4	-

NGS: Moving to GLH / Genomic hubs - NRAS

NGS: Moving to GLH / Genomic hubs - NRAS	Overall	
	n	% (N = 8)
No	7	88%
Yes	1	12%
NA.	3	-

NGS: Moving to GLH / Genomic hubs - KIT

NGS: Moving to GLH / Genomic hubs - KIT	Overall	
	n	% (N = 8)
No	7	88%
Yes	1	12%
NA.	3	-

NGS: Current average turnaround time - BRAF

NGS: Current average turnaround time - BRAF	Overall
	N = 11
Mean	23.2
SD	11.1
Median	21.5
IQR	15.8 to 26.2
Range	12 to 45
NA.	4

NGS: Current average turnaround time - NRAS

NGS: Current average turnaround time - NRAS	Overall
	N = 11
Mean	23.2

SD	11.1
Median	21.5
IQR	15.8 to 26.2
Range	12 to 45
NA.	4

NGS: Current average turnaround time - KIT

NGS: Current average turnaround time - KIT	Overall
	N = 11
Mean	23.2
SD	11.1
Median	21.5
IQR	15.8 to 26.2
Range	12 to 45
NA.	4

Others

Others	Overall	
	n	% (N = 11)
BRAF FISH	1	9%
KIT pyrosequencing	1	9%
N/A	8	73%
NTRK1-3	1	9%
NA.	0	-

Reflex at diagnosis - NTRK1-3

Reflex at diagnosis - NTRK1-3	Overall	
	n	% (N = 11)
N/A	10	91%
On request	1	9%
NA.	0	-

Testing at progression/ relapse/ other post Dx timepoints
- NTRK1-3

Testing at progression/ relapse/ other post Dx timepoints - NTRK1-3	Overall	
	n	% (N = 11)
N/A	10	91%
On request	1	9%
NA.	0	-

Performed by pathology lab - NTRK1-3

Performed by pathology lab - NTRK1-3	Overall	
	n	% (N = 11)
N/A	10	91%
No	1	9%
NA.	0	-

Moved to GLH/ Genomic centre - NTRK1-3

Moved to GLH/ Genomic centre - NTRK1-3	Overall	
	n	% (N = 11)
N/A	10	91%
Yes	1	9%
NA.	0	-

Moving to GLH/ Genomic hubs - NTRK1-3

Moving to GLH/ Genomic hubs - NTRK1-3	Overall	
	n	% (N = 11)
N/A	10	91%
No	1	9%
NA.	0	-

Current Average Turnaround time (calendar days) - NTRK1-3

Current Average Turnaround time (calendar days) - NTRK1-3	Overall	
	n	% (N = 11)
21 to 28	1	9%
N/A	10	91%
NA.	0	-

Reflex at diagnosis - KIT pyrosequencing

Reflex at diagnosis - KIT pyrosequencing	Overall	
	n	% (N = 11)
N/A	10	91%

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No	1	9%
NA.	0	-

Testing at progression/ relapse/ other post Dx timepoints
- KIT pyrosequencing

Testing at progression/ relapse/ other post Dx timepoints - KIT pyrosequencing	Overall	
	n	% (N = 11)
N/A	10	91%
No	1	9%
NA.	0	-

Performed by pathology lab - KIT pyrosequencing

Performed by pathology lab - KIT pyrosequencing	Overall	
	n	% (N = 11)
N/A	10	91%
Yes	1	9%
NA.	0	-

Moved to GLH/ Genomic centre - KIT pyrosequencing

Moved to GLH/ Genomic centre - KIT pyrosequencing	Overall	
	n	% (N = 11)
N/A	10	91%
No	1	9%
NA.	0	-

Moving to GLH/ Genomic hubs - KIT pyrosequencing

Moving to GLH/ Genomic hubs - KIT pyrosequencing	Overall	
	n	% (N = 11)
N/A	10	91%
No	1	9%
NA.	0	-

Current Average Turnaround time (calendar days) - KIT
pyrosequencing

Current Average Turnaround time (calendar days) - KIT pyrosequencing	Overall	
	n	% (N = 10)
N/A	10	100%
NA.	1	-

Reflex at diagnosis - BRAF FISH

Reflex at diagnosis - BRAF FISH	Overall	
	n	% (N = 11)
N/A	10	91%
Yes	1	9%
NA.	0	-

Testing at progression/ relapse/ other post Dx timepoints
- BRAF FISH

Testing at progression/ relapse/ other post Dx timepoints - BRAF FISH	Overall	
	n	% (N = 11)
N/A	10	91%
No	1	9%
NA.	0	-

Performed by pathology lab - BRAF FISH

Performed by pathology lab - BRAF FISH	Overall	
	n	% (N = 11)
N/A	10	91%
Other lab	1	9%
NA.	0	-

Moved to GLH/ Genomic centre - BRAF FISH

Moved to GLH/ Genomic centre - BRAF FISH	Overall	
	n	% (N = 11)
N/A	10	91%
No	1	9%

NA.	0	-

Moving to GLH/ Genomic hubs - BRAF FISH

Moving to GLH/ Genomic hubs - BRAF FISH	Overall	
	n	% (N = 11)
N/A	10	91%
No	1	9%
NA.	0	-

Current Average Turnaround time (calendar days) - BRAF FISH

Current Average Turnaround time (calendar days) - BRAF FISH	Overall	
	n	% (N = 11)
N/A	10	91%
Not known	1	9%
NA.	0	-

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Numerical Data   **Grouped data - if applicable**

11.a.i. Breast cancer: HR

11.a.i. Breast cancer: HR	Overall	
	n	% (N = 9)
No	4	44%
Yes	5	56%
NA.	0	-

11.a.i. Breast cancer: PGR

11.a.i. Breast cancer: PGR	Overall	
	n	% (N = 9)
No	3	33%
Yes	6	67%
NA.	0	-

11.a.i. Breast cancer: HER2

11.a.i. Breast cancer: HER2	Overall	
	n	% (N = 9)
No	3	33%
Yes	6	67%
NA.	0	-

11.a.i. Other

11.a.i. Other	Overall	
	n	% (N = 9)
N/A	8	89%
PDL1 for Triple neagtive BC on request	1	11%
NA.	0	-

11.a.i. NA

11.a.i. NA	Overall	
	n	% (N = 9)
No	6	67%
Yes	3	33%
NA.	0	-

11.a.ii. Lung Cancer: PD-L1

11.a.ii. Lung Cancer: PD-L1	Overall	
	n	% (N = 15)
No	2	13%
Yes	13	87%
NA.	0	-

11.a.ii. Lung Cancer: EGFR

11.a.ii. Lung Cancer: EGFR	Overall	
	n	% (N = 15)
No	2	13%
Yes	13	87%
NA.	0	-

11.a.ii. Lung Cancer: ALK

11.a.ii. Lung Cancer: ALK	Overall	
	n	% (N = 15)
No	2	13%
Yes	13	87%
NA.	0	-

11.a.ii. Lung Cancer: BRAF

11.a.ii. Lung Cancer: BRAF	Overall	
	n	% (N = 15)
No	7	47%
Yes	8	53%
NA.	0	-

11.a.ii. Lung Cancer: ROS1

11.a.ii. Lung Cancer: ROS1	Overall	
	n	% (N = 15)
No	3	20%
Yes	12	80%
NA.	0	-

11.a.ii. Lung Cancer: RET

11.a.ii. Lung Cancer: RET	Overall	
	n	% (N = 15)
No	9	60%
Yes	6	40%
NA.	0	-

11aii Other

11aii Other	Overall	
	n	% (N = 15)
KRAS	2	13%

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KRAS, NTRK	1	7%
N/A	11	73%
T790M	1	7%
NA.	0	-

11.a.ii. NA

11.a.ii. NA	Overall	
	n	% (N = 15)
No	13	87%
Yes	2	13%
NA.	0	-

11.a.iii Melanoma: BRAF

11.a.iii Melanoma: BRAF	Overall	
	n	% (N = 11)
No	1	9%
Yes	10	91%
NA.	0	-

11.a.iii Other

11.a.iii Other	Overall	
	n	% (N = 11)
N/A	11	100%
NA.	0	-

11.a.iii NA

11.a.iii NA	Overall	
	n	% (N = 11)
No	10	91%
Yes	1	9%
NA.	0	-

11.b.

11.b.	Overall	
	n	% (N = 15)
No	7	47%
Yes	8	53%
NA.	0	-

11.b. Specify

11.b. Specify	Overall	
	n	% (N = 7)
Mix, Pathology lab + GLH	4	57%
Mix, Pathology lab + GLH + Other external lab	1	14%
Mix, Pathology lab + Other external lab	1	14%
Other external lab	1	14%
NA.	8	-

11.c.

11.c.	Overall	
	n	% (N = 15)
Both depending on target + NGS locally would be preferred	1	7%
Both IHC and RT-PCR depending on target	9	60%
IHC	2	13%
IHC + NGS	1	7%
IHC + Other not specified	1	7%
RT-PCR	1	7%
NA.	0	-

11.d.

11.d.	Overall	
	n	% (N = 15)
GLH	2	13%
N/A	1	7%
NHS Trust	9	60%
NHS Trust + GLH	3	20%
NA.	0	-

11.e

11.e	Overall	
	n	% (N = 15)
N/A	2	13%
No	3	20%
Yes	10	67%
NA.	0	-

12. Breast

12. Breast	Overall
	N = 15
Mean	85
SD	36.7
Median	100
IQR	100 to 100
Range	10 to 100
NA.	9

12. Melanoma

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12. Melanoma	Overall
	N = 15
Mean	37.2
SD	38.1
Median	20
IQR	5 to 80
Range	5 to 100
NA.	6

12. Lung

12. Lung	Overall
	N = 15
Mean	69.1
SD	33.4
Median	75
IQR	50 to 100
Range	5 to 100
NA.	1

13.a. Please describe the process for request of archival tissue:

13.a. Please describe the process for request of archival tissue:	Overall	
	n	% (N = 15)
Complete request form, retrieval from off-site storage for older tissues (over 2 years). Onsite if more recent	1	7%
Need to request samples (book in/out)	1	7%
Online request for retrieval (storage site not specified)	1	7%
Request from pathology team storage site not specified	1	7%
Request to audit team, retrieval from offsite storage	1	7%
Request to pathology team, selection and request of the block, can be onsite or offsite (older samples)	1	7%
Requested from archival team, Retrieval from off-site storage for older tissues (over 4 years). Onsite if more recent	1	7%
Requested, Retrieval from onsite or offsite, often tissue blocks	1	7%
Requested, Retrieval from onsite storage	1	7%
Retrieval from off-site storage for older tissues, Onsite if more recent	1	7%
Retrieval from onsite storage	1	7%
Selection and request of tissue, Retrieval from off-site storage	1	7%
System based request, retrieval from off-site storage for older tissues (over 5 years). Onsite if more recent	1	7%
Up to 2 years request from onsite, after 2 years, Request from offsite storage.	1	7%
Up to 2 years Request from onsite, after 2 years, request from offsite storage.	1	7%
NA.	0	-

13.a. Please describe the process for request of archival tissue:

13.a. Please describe the process for request of archival tissue:	Overall	
	n	% (N = 15)
Request	/	/
Form	1	7%
Online	1	7%
System based	1	7%
To archival team	1	7%
To pathology team	2	13%
To audit team	1	7%
Not specified	8	53%
Retrieval	/	/
From onsite storage (only)	2	13%
From offsite storage (only)	2	13%
Onsite (recent) - Offsite (after 2 years)	3	20%
Onsite (recent) - Offsite (after 4 years)	1	7%
Onsite (recent) - Offsite (after 5 years)	1	7%
Onsite (recent) - Offsite (older - unspecified)	3	20%
Not specified	3	20%
NA.	0	-

* Request and Retrieval not mutually exclusive (but respectively mutually exclusive within)

13.b. Describe the specific challenges with archival tissue that may exists for Lung, Breast or Melanoma?

13.b. Describe the specific challenges with archival tissue that may exists for Lung, Breast or Melanoma?	Overall	
	n	% (N = 15)
Additional administration, Unpredictable sample quality, Frequent failure of lung cancer tissue	1	7%
Difficulties with sample retrieval, Hard to access or lost samples	1	7%
DNA degradation, Overfixed tissue	1	7%
Loss of tissue sample, Sample quality for lung and melanoma	1	7%
None	1	7%
Sample quality for lung, Small sample size, Loss of tissue sample	1	7%
Sample size with lung cancer	2	13%
Small sample (for lung cancer)	1	7%
Small sample (for lung cancer), Logistics issues with offsite storage	1	7%
Small sample size	1	7%
Small sample size, Cost and resources	1	7%
Small samples, Insufficient sample available, TAT for retrival of offsite stored samples, Cost	1	7%
Time to retrieve from offsite	2	13%
NA.	0	-

13.b. Describe the specific challenges with archival tissue that may exists for Lung, Breast or Melanoma?	Overall	
	n	% (N = 15)
Technical (sample quality, sample quantity, failure rates)	11	
Logistics (additional admin, loss of sample, difficulty with retrieval, cost, turnaround time)	9	
None	1	

13.c.i. Breast

13.c.i. Breast	Overall
	N = 15
Mean	5.2
SD	6.7
Median	2.2
IQR	1.1 to 6.5
Range	0 to 17.5
NA.	7

13.c.ii. Lung

13.c.ii. Lung	Overall
	N = 15
Mean	2.5
SD	3.4
Median	1.5
IQR	1.2 to 2.5
Range	0 to 14
NA.	0

13.c.iii. Melanoma

13.c.iii. Melanoma	Overall
	N = 15
Mean	4.5

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SD	5.8
Median	2
IQR	1.5 to 4.2
Range	0 to 17.5
NA.	4

13.d. Sample quality

13.d. Sample quality	Overall	
	n	% (N = 15)
No	8	53%
Yes	7	47%
NA.	0	-

13.d. Additional resource requirements

13.d. Additional resource requirements	Overall	
	n	% (N = 15)
No	9	60%
Yes	6	40%
NA.	0	-

13.d. Processing issues

13.d. Processing issues	Overall	
	n	% (N = 15)
No	14	93%
Yes	1	7%
NA.	0	-

13.d. Transport

13.d. Transport	Overall	
	n	% (N = 15)
No	11	73%
Yes	4	27%
NA.	0	-

13.d. Other What are the challenges with archival tissue for genomics at GLH?

13.d. Other What are the challenges with archival tissue for genomics at GLH?	Overall	
	n	% (N = 5)
Administration burden	2	40%
Retrieval	1	20%
Small sample size	2	40%
NA.	10	-

14.a. Do you currently offer molecular testing of liquid biopsies at your lab?
EGFR only ☐ No ☐

14.a.	Overall	
	n	% (N = 15)
EGFR only	2	13%
EGFR, BRAF, RET, MET	1	7%
EGFR, KIT, BRAF, KRAS, RAS - VERY FEW REQUESTS. NGS VALIDATED BY PLASMA	1	7%
No	11	73%
NA.	0	-

14.b. Are there any other molecular liquid biopsies performed at your lab? If so, which one(s) and for which cancer types?
No ☐
Yes ☐_____

14.b.	Overall	
	n	% (N = 15)
EGFR only	2	13%
EGFR, BRAF, RET, MET	1	7%
EGFR, KIT, BRAF, KRAS, RAS - VERY FEW REQUESTS. NGS VALIDATED BY PLASMA	1	7%
No	11	73%
NA.	0	-

14.c. What do you foresee will be the use of liquid biopsy within the diagnostic pathway?
14.c. For all testing

14.c. For all testing	Overall	
	n	% (N = 15)
No	14	93%
Yes	1	7%
NA.	0	-

14.c. In addition to tissue testing (same targets)

14.c. In addition to tissue testing (same targets)	Overall	
	n	% (N = 15)
No	2	13%
Yes	13	87%
NA.	0	-

14.c. If a suitable tissue sample is not available

14.c. If a suitable tissue sample is not available	Overall	
	n	% (N = 15)
No	6	40%
Yes	9	60%
NA.	0	-

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14.c. Upon progression only

14.c. Upon progression only	Overall	
	n	% (N = 15)
No	12	80%
Yes	3	20%
NA.	0	-

14.c. For specific tests only i.e.

14.c. For specific tests only i.e.	Overall	
	n	% (N = 15)
Yes (not specified)	1	7%
As clinically relevant	2	13%
No	12	80%
NA.	0	-

14.c. For panel testing

14.c. For panel testing	Overall	
	n	% (N = 15)
No	7	47%
Yes	8	53%
NA.	0	-

14.c. Not used

14.c. Not used	Overall	
	n	% (N = 15)
No	15	100%
NA.	0	-

14.d. What are the challenges with liquid biopsies?

14.d. What are the challenges with liquid biopsies?	Overall	
	n	% (N = 14)
Administrative burden, Pathway integration	1	7%
Report preparation, Pathway integration	1	7%
Sensitivity and Specificity	1	7%
Sensitivity, Funding	1	7%
Sensitivity, Limited range of testing methods	2	14%
Sensitivity, Pathway integration	1	7%
Sensitivity, Sample preparation, Interpretation of results	1	7%
Sensitivity, Variable levels of ctDNA in blood	3	21%
Sensitivity, Variable levels of ctDNA in blood, Interpretation of results	1	7%
Sensitivity, Variable levels of ctDNA in blood, Limited range of testing methods	1	7%
Technology, Validation, Interpretation of results (eg MRD)	1	7%
NA.	1	-

14.d. What are the challenges with liquid biopsies?	Overall	
	n	% (N = 14)
Technical issues (Poor sensitivity, variable levels of ctDNA in sample, limited technology/testing options)	12	
Logistical issues (additional admin, pathway integration, funding, results interpretation)	7	
NA	1	

15. Are you currently developing any other molecular tests for Lung, Breast or Melanoma?

15. Are you currently developing any other molecular tests for Lung, Breast or Melanoma?	Overall	
	n	% (N = 15)
Acquiring Genexus platform	2	13%
Acquiring Genexus platform, NGS for Lung Cancer genomics, IHC for BRAF in melanoma	1	7%
Acquiring Genexus platform, NGS locally for urgent Lung cancer, FISH	1	7%
BAP 1 - Immuno stain for Meso and melanomas	1	7%
IHC for BRAF in melanoma	1	7%
NGS locally	2	13%
No	7	47%
NA.	0	-

15. Are you currently developing any other molecular tests for Lung, Breast or Melanoma?	Overall	
	n	% (N = 15)
IHC	3	
NGS technologies	6	
Other	1	
None	7	

16. Timelines for implementation

16. Timelines for implementation	Overall	
	n	% (N = 15)
No	7	47%
Yes	8	53%
NA.	0	-

16. Test development

16. Test development	Overall	
	n	% (N = 15)
No	11	73%
Yes	4	27%
NA.	0	-

16. Test validation

16. Test validation	Overall	
	n	% (N = 15)
No	3	20%
Yes	12	80%
NA.	0	-

16. Administration

16. Administration	Overall	
	n	% (N = 15)
No	6	40%
Yes	9	60%
NA.	0	-

16. Funding / Resource allocation

16. Funding / Resource allocation	Overall	
	n	% (N = 15)
No	2	13%
Yes	13	87%
NA.	0	-

16. Communication

16. Communication	Overall	
	n	% (N = 15)
No	11	73%
Yes	4	27%
NA.	0	-

17. Respiratory physicians / Pulmonologists

17. Respiratory physicians / Pulmonologists	Overall	
	n	% (N = 15)
No	4	27%
Yes	11	73%
NA.	0	-

17. Surgeon

17. Surgeon	Overall	
	n	% (N = 15)
No	3	20%
Yes	12	80%
NA.	0	-

17. Oncologist

17. Oncologist	Overall	
	n	% (N = 15)
Yes	15	100%
NA.	0	-

17. MDT Coordinator

17. MDT Coordinator	Overall	
	n	% (N = 15)
No	6	40%
Yes	9	60%
NA.	0	-

17. Clinical nurse specialist

17. Clinical nurse specialist	Overall	
	n	% (N = 15)
No	4	27%
Yes	11	73%
NA.	0	-

17. Other

17. Other	Overall	
	n	% (N = 5)
Dermatologists	3	60%
Pathologists	1	20%
Radiologists	1	20%
NA.	10	-

18. Do you regularly attend MDT?

18. Do you regularly attend MDT?	Overall	
	n	% (N = 15)
No	1	7%
Yes	14	93%
NA.	0	-

19. Do you discuss results at standard MDTs?

19. Do you discuss results at standard MDTs?	Overall	
	n	% (N = 15)
Yes	15	100%
NA.	0	-

20. Do you have a molecular specific MDTs?

20. Do you have a molecular specific MDTs?	Overall	
	n	% (N = 15)
No	12	80%
Yes	3	20%
NA.	0	-

21. Respiratory physicians / Pulmonologists

21. Respiratory physicians / Pulmonologists	Overall	
	n	% (N = 15)
No	10	67%

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Yes	5	33%
NA.	0	-

21. Surgeon

21. Surgeon	Overall	
	n	% (N = 15)
No	11	73%
Yes	4	27%
NA.	0	-

21. Administrator

21. Administrator	Overall	
	n	% (N = 15)
No	12	80%
Yes	3	20%
NA.	0	-

21. Pathologists

21. Pathologists	Overall	
	n	% (N = 15)
Yes	15	100%
NA.	0	-

21. Clinical scientist (genomics)

21. Clinical scientist (genomics)	Overall	
	n	% (N = 15)
No	12	80%
Yes	3	20%
NA.	0	-

21. Oncologist

21. Oncologist	Overall	
	n	% (N = 15)
No	5	33%
Yes	10	67%
NA.	0	-

21. Other

21. Other	Overall	
	n	% (N = 2)
CNS	1	50%
CNS, Dermatologist	1	50%
NA.	13	-

22. Email

22. Email	Overall	
	n	% (N = 15)
No	1	7%
Yes	14	93%
NA.	0	-

22. Webpage

22. Webpage	Overall	
	n	% (N = 15)
No	13	87%
Yes	2	13%
NA.	0	-

22. Hospital Newsletter

22. Hospital Newsletter	Overall	
	n	% (N = 15)
No	14	93%
Yes	1	7%
NA.	0	-

22. MDT meeting

22. MDT meeting	Overall	
	n	% (N = 15)
No	3	20%
Yes	12	80%
NA.	0	-

22. Other

22. Other	Overall	
	n	% (N = 7)
Focus groups, Educational webinars	1	14%
Informal discussions	2	29%
Informal discussions, Conferences	1	14%
Informal discussions, Meetings	1	14%
Phone	2	29%
NA.	8	-

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23. No

23. No	Overall	
	n	% (N = 15)
No	1	7%
Reference to available targeted therapies only	2	13%
Reference to published therapy area guidelines only	3	20%
Yes	9	60%
NA.	0	-

23. Other specify

23. Other specify	Overall	
	n	% (N = 6)
Cross-reference literature for less known alterations	1	17%
Drug classes only - no specified named treatments	1	17%
Drug classes only - no specified named treatments, Not for melanoma	1	17%
Less for melanoma	1	17%
Notes on whether sentizing mutation or not (i.e. EGFR)	1	17%
Variant classification would be a good to include but not done at the moment	1	17%
NA.	9	-

24. What impact has COVID-19 had on your current services?

24. What impact has COVID-19 had on your current services?	Overall	
	n	% (N = 15)
High impact	6	40%
Medium impact	5	33%
Minimal or no impact	4	27%
NA.	0	-

24. Please describe if medium or high impact

24. Please describe if medium or high impact	Overall	
	n	% (N = 12)
Backlog (Breast + Melanoma), Increased workload (Breast + Melanoma)	1	8%
Backlog of patient presenting with later diagnosis	1	8%
Delays in getting specimens	1	8%
Impact on referal services	1	8%
Increase in workload	1	8%
Increase workload from backlog	1	8%
Less staff, Increase in workload	2	17%
Less staff, Increase in workload, Backlog, Reallocation of consumables	1	8%
Number of specimens dicreased early on, Normal numbers now	1	8%
Reduced capacity early pandemic, Backlog on current testing service	1	8%
Slight increase in current workload particularly for urgent services	1	8%
NA.	3	-

24. Please describe if medium or high impact of COVID	Overall	
	n	% (N = 12)
Staffing (reduced during COVID)	4	
Workloads (lower presentation, delays in referral, backlogs)	12	
Other	1	
NA	3	

25. What impact has the roll out of the GMS and GLH had on your current services (positiveand/or negative)?

25. What impact has the roll out of the GMS and GLH had on your current services (positiveand/or negative)?	Overall	
	n	% (N = 15)
High impact	8	53%
Medium impact	4	27%
Minimal or no impact	1	7%
N/A	2	13%
NA.	0	-

25. Please describe

25. Please describe	Overall	
	n	% (N = 15)
N/A	1	7%
Negative - Cost, Funding issues / Positive - GLH improved TAT (due to salvage pathway using Genexus), more GLH usage leading to less wait for batching	1	7%
Negative - Extra workload	1	7%
Negative - GLH not running, No local funding, Incomplete testing, Poor TAT, pathway not streamlined, Roles unclear, Higher staff turnover, Increased resource requirements	1	7%
Negative - Increased administrative burden, Increase resource, Poor compatibility of IT system	1	7%
Negative - Loss of local genomic lab, Service moving further from patient, Pathway not streamlined	1	7%
Negative - No pathology input into new service	1	7%
Negative - Poor TAT, Higher sample quality requirements for NGS, High failure rate, Poor compatibility of IT system	1	7%
Negative - Poor TAT, Inefficient results reporting, Hinderance of local research projects	1	7%
Negative - Poor TAT, Logistical burden / Positive - Improved failure rate	1	7%
Negative - Service moving further from patient, Pathway not streamlined, Funding, Lack of pathology acknowledgement, Lack of collaboration	1	7%
Negative - TAT, Sample quantity requirement is higher, Pathway not streamlined, Inefficient results reporting (too complicated)	1	7%
Positive - Funding, Efficient test delivery, Higher sequence coverage	1	7%
Positive - Lung streamlined pathway (reflex), Good communication / Negative - Melanoma + Breast not streamlined, Poor TAT, Higher tissue quality requirements, Administrative burden, Lack of collaboration, Poor IT integration	1	7%
Positive - No extra workload	1	7%
NA.	0	-

24. Please describe if medium or high impact of GLH/GMS	Overall	
	n	% (N = 15)
Negative	/	/
Technical (Higher tissue quality requirements, High failure rates, incomplete testing)	3	
Logistics (Funding issues, TAT, increase resource requirements, increased admin, poor compatibility with IT, pathway not streamlined and further from patient, lack of collaboration)	12	
NA		
Positive	/	/
Technical (Improved TAT due to new NGS locally, Improved failure rates, Higher sequence coverage)	2	
Logistics (Funding, efficiency/streamlined pathway, communication)	5	
NA		

26. What impact will the roll out of the GMS and GLH had on your future services (positive and/ornegative)?

26. What impact will the roll out of the GMS and GLH had on your future services (positive and/ornegative)?	Overall	
	n	% (N = 12)
High impact	8	67%
Minimal or no impact	3	25%
N/A	1	8%

NA.	3	-

26. Please describe

26. Please describe	Overall	
	n	% (N = 15)
Negative - Administrative burden, Inefficient reporting	1	7%
Negative - Division of pathology and genomics, Longer TAT, Higher tissue quality requirements, Administrative burden	1	7%
Negative - Longer TAT	1	7%
Negative - Longer TAT (Lung + Melanoma)	1	7%
Negative - Longer TAT, Lack of guidance, May need to find alternatives to GLH / Positive - In melanoma could improve dianosis and prognosis	1	7%
Negative - Service not streamlined, Funding concerns	1	7%
N/A	1	7%
Positive - Increased use of GLH, More capacity locally for urgent samples	1	7%
Positive - Reduced workload, More capacity for urgent samples, Complex cases being handled by GLH	1	7%
Positive - Will overcome sample quanitity constraints / Negative - Logistical burden	1	7%
Unsure	4	27%
Unsure / Positive - Save money, Standardise results	1	7%
NA.	0	-

24. Please describe if medium or high impact of GLH/GMS	Overall	
	n	% (N = 15)
Negative	/	/
Technical (higher tissue requirements)	1	
Logistics (additional admin, inefficient reporting, devision of pathway, longer turnaround times, lack of guidance, funding concerns)	7	
Positive	/	/
Technical	0	
Logistics (more capacity locally for urgent samples, reduced workload)	4	
Other	1	
Unsure	5	33%
N/A	1	7%

27. Sample Preparation

27. Sample Preparation	Overall	
	n	% (N = 15)
No	2	13%
Yes	13	87%
NA.	0	-

27. Test assignment (reflexive)

27. Test assignment (reflexive)	Overall	
	n	% (N = 15)
No	3	20%
Yes	12	80%
NA.	0	-

27. Conducting testing: All

27. Conducting testing: All	Overall	
	n	% (N = 15)
No	8	53%
Yes	7	47%
NA.	0	-

27. Conducting testing: Cellular

27. Conducting testing: Cellular	Overall	
	n	% (N = 15)
No	7	47%
Yes	8	53%
NA.	0	-

27. Conducting testing: Salvage

27. Conducting testing: Salvage	Overall	
	n	% (N = 15)
No	8	53%
Yes	7	47%
NA.	0	-

27. Conducting testing: Urgent or first line testing

27. Conducting testing: Urgent or first line testing	Overall	
	n	% (N = 15)
No	4	27%
Yes	11	73%
NA.	0	-

27. Data analysis

27. Data analysis	Overall	
	n	% (N = 15)
No	6	40%
Yes	9	60%
NA.	0	-

27. Report creation

27. Report creation	Overall	
	n	% (N = 15)
No	4	27%
Yes	11	73%
NA.	0	-

27. Education Training

27. Education Training	Overall	
	n	% (N = 15)
No	2	13%

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Yes	13	87%
NA.	0	-

27. Where do you see the role of regional pathology centres in the optimal delivery of the GMS?

Other

27. Where do you see the role of regional pathology centres in the optimal delivery of the GMS? Other	Overall	
	n	% (N = 3)
Intergrate diagnostic information from different sources	1	33%
Providing prognostic and predictive factors on a timely basis	1	33%
Role unclear	1	33%
NA.	12	-

28. How do you currently work with your GLH? i.e. access to tissue, sample preparation, salvage/urgent testing, preparation of reports, etc.

28. How do you currently work with your GLH? i.e. access to tissue, sample preparation, salvage/urgent testing, preparation of reports, etc.	Overall	
	n	% (N = 13)
Collaborate on issues	1	8%
Collaboration on region wide issues, Testing, Test development / provide validation set for new indications, Report generation and integration	1	8%
None	1	8%
Pathology integrates GLH report into their local reporting system	1	8%
Prepare tissue sections / samples for GLH, GLH provides molecular report	2	15%
Prepare tissue sections / samples for GLH, GLH provides molecular report, Pathology to input report on local system	2	15%
Prepare tissue sections / samples for GLH, Urgent testing 1L, Training GLH scientists	1	8%
Request test, Prepare tissue sections / samples for GLH, GLH provides molecular report	1	8%
Request test, prepare tissue sections / samples for GLH, GLH provides molecular report, Collaborate on issues	1	8%
Request test, Prepare tissue sections / samples for GLH, GLH provides molecular report, Pathology authorise the final report	1	8%
Request testing, Prepare tissue sections / samples for GLH, GLH provides molecular report	1	8%
NA.	2	-

28. How do you currently work with your GLH? i.e. access to tissue, sample preparation, salvage/urgent testing, preparation of reports, etc.

28. How do you currently work with your GLH? i.e. access to tissue, sample preparation, salvage/urgent testing, preparation of reports, etc.	Overall	
	n	% (N = 13)
Collaborate on issues	3	23%
Test development / provide validation set for new indications	1	8%
Report generation and integration	1	8%
Pathology integrates GLH report into their local reporting system	1	8%
Prepare tissue sections / samples for GLH	9	69%
GLH provides molecular report	8	62%
Pathology to input report on local system	1	8%
Urgent testing 1L	1	8%
Training GLH scientists	1	8%
Request test	4	31%
Pathology authorise the final report	1	8%
Testing	1	8%
None	1	8%
NA.	2	-

* Categories not mutually exclusive

29. Sample Quality

29. Sample Quality	Overall	
	n	% (N = 15)
High impact	7	47%
Medium impact	5	33%
Minimal or no impact	3	20%
NA.	0	-

29. Transportation

29. Transportation	Overall	
	n	% (N = 15)
High impact	5	33%
Medium impact	3	20%
Minimal or no impact	7	47%
NA.	0	-

29. Ordering GLH tests

29. Ordering GLH tests	Overall	
	n	% (N = 15)
High impact	1	7%
Medium impact	4	27%
Minimal or no impact	9	60%
Not applicable	1	7%
NA.	0	-

29. Admin

29. Admin	Overall	
	n	% (N = 15)
High impact	6	40%
Medium impact	5	33%
Minimal or no impact	4	27%
NA.	0	-

29. Testing options/capabilities

29. Testing options/capabilities	Overall	
	n	% (N = 15)
High impact	6	40%
Medium impact	2	13%
Minimal or no impact	5	33%
Not applicable	2	13%
NA.	0	-

29. Data analysis/ bioinformatics

29. Data analysis/ bioinformatics	Overall	
	n	% (N = 14)
High impact	2	14%
Medium impact	2	14%

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Minimal or no impact	7	50%
Not applicable	3	21%
NA.	1	-

29. IT requirements/ compatibility

29. IT requirements/ compatibility	Overall	
	n	% (N = 15)
High impact	5	33%
Medium impact	6	40%
Minimal or no impact	3	20%
Not applicable	1	7%
NA.	0	-

29. Reporting

29. Reporting	Overall	
	n	% (N = 14)
High impact	1	7%
Medium impact	5	36%
Minimal or no impact	8	57%
NA.	1	-

29. Education/training

29. Education/training	Overall	
	n	% (N = 15)
High impact	2	13%
Medium impact	6	40%
Minimal or no impact	6	40%
Not applicable	1	7%
NA.	0	-

29.Resource/Capacity

29.Resource/Capacity	Overall	
	n	% (N = 15)
High impact	7	47%
Medium impact	7	47%
Minimal or no impact	1	7%
NA.	0	-

29. Funding

29. Funding	Overall	
	n	% (N = 15)
High impact	7	47%
Medium impact	4	27%
Minimal or no impact	3	20%
Not applicable	1	7%
NA.	0	-

29. What do you see as the current barriers for optimal delivery of the GMS?

Other

29. What do you see as the current barriers for optimal delivery of the GMS? Other	Overall	
	n	% (N = 5)
Communication	1	20%
Pathology having control/ pathway integration - high impact	1	20%
Poor service (no access)	1	20%
Recognition	1	20%
TATs - High impact	1	20%
NA.	10	-

30. Do you have other concerns regarding the delivery of this service?

30. Do you have other concerns regarding the delivery of this service?	Overall	
	n	% (N = 15)
No	5	33%
Yes	10	67%
NA.	0	-

30. Do you have other concerns regarding the delivery of this service?

30. Do you have other concerns regarding the delivery of this service?	Overall	
	n	% (N = 11)
Funding, TAT	1	9%
Insufficient training on GLH, New technology implementation	1	9%
Outdated technology, Inefficient service	1	9%
Poor communication, Service not flexible	1	9%
Resource, Capacity, Collaboration	1	9%
Service moving further from patient, Pathway not streamlined, More collabotration and flexibility required	1	9%
Service moving further from patient, TAT, Sample flow not streamlined, Pathway not streamlined, Service not flexible	1	9%
TAT, Pathway not streamlined	1	9%
TAT, Pathway not streamlined, Poor communication, Poor collaboration, Need for clear procedures, Need for clear interpretable reports	1	9%
TAT, Workload, Heterogeneity across GLHs	1	9%
Uneven experience and expertise across network, Failure rates	1	9%
NA.	4	-

24. Please describe if medium or high impact of GLH/GMS	Overall	
	n	% (N = 11)
Technical (implementation of new technology, outdated technology, failure rates)	3	
Logistics (Funding, TAT, insufficient training, poor communication, capacity, lack of collaboration, pathway not streamlined, lack of clarity of pathway and roles, heterogeneity in experience and expertise across network)	10	
Other	4	
NA	4	

31. What additional resources are required at local pathology labs to support optimal delivery of this service?

31. What additional resources are required at local pathology labs to support optimal delivery of this service?	Overall	
	n	% (N = 14)
Additional staff (Admin)	1	7%
Additional staff (Admin, Scientist), Additional sample prep resource	1	7%
Additional staff (Admin, Scientist), Improved IT efficiency (for sample tracking and reports), Improved communication with MDT	1	7%
Additional staff (Pathologists, Scientist)	1	7%
Additional staff (Pathologists, Admin, Scientist)	1	7%
Additional staff (Pathologists, Scientist)	1	7%
Additional staff (Pathologists, Scientist), Improve communication and collaboration with GLH	1	7%
Additional staff, Additional admin resource	1	7%
Educational support on sample suitability	1	7%
Funding for local testing, Additional staff (Pathologists)	1	7%
Funding, Additional staff (Admin)	1	7%
More facilities	1	7%
None	2	14%
NA.	1	-

24. Please describe if medium or high impact of GLH/GMS	Overall	
	n	% (N = 14)
Staffing	11	
Funding	2	
Other		
None	2	
NA	1	

Regional pathology centre - New treatment trial results

Regional pathology centre - New treatment trial results	Overall	
	n	% (N = 15)
No	4	27%
Yes	11	73%
NA.	0	-

Regional pathology centre - Optimal reporting

Regional pathology centre - Optimal reporting	Overall	
	n	% (N = 15)
No	4	27%
Yes	11	73%
NA.	0	-

Regional pathology centre - Guideline reviews/updates

Regional pathology centre - Guideline reviews/updates	Overall	
	n	% (N = 15)
No	3	20%
Yes	12	80%
NA.	0	-

Regional pathology centre - Understanding the new molecular testing pathway

Regional pathology centre - Understanding the new molecular testing pathway	Overall	
	n	% (N = 15)
No	1	7%
Yes	14	93%
NA.	0	-

Regional pathology centre - Best practice sharing across lab

Regional pathology centre - Best practice sharing across lab	Overall	
	n	% (N = 15)
No	1	7%
Yes	14	93%
NA.	0	-

Regional pathology centre - Cross-functional education with clinicians

Regional pathology centre - Cross-functional education with clinicians	Overall	
	n	% (N = 15)
No	3	20%
Yes	12	80%
NA.	0	-

Regional pathology centre - Other

Regional pathology centre - Other	Overall	
	n	% (N = 15)
Development and support of molecular MDTs	1	7%
New molecular markers	1	7%
No	13	87%
NA.	0	-

DGH pathology labs - New treatment trial results

DGH pathology labs - New treatment trial results	Overall	
	n	% (N = 15)
No	7	47%
Yes	8	53%
NA.	0	-

DGH pathology labs - Optimal reporting

DGH pathology labs - Optimal reporting	Overall	
	n	% (N = 15)
No	7	47%

Yes	8	53%
NA.	0	-

DGH pathology labs - Guideline reviews/updates

DGH pathology labs - Guideline reviews/updates	Overall	
	n	% (N = 15)
No	7	47%
Yes	8	53%
NA.	0	-

DGH pathology labs - Understanding the new molecular testing pathway

DGH pathology labs - Understanding the new molecular testing pathway	Overall	
	n	% (N = 15)
No	5	33%
Yes	10	67%
NA.	0	-

DGH pathology labs - Best practice sharing across lab

DGH pathology labs - Best practice sharing across lab	Overall	
	n	% (N = 15)
No	5	33%
Yes	10	67%
NA.	0	-

DGH pathology labs - Cross-functional education with clinicians

DGH pathology labs - Cross-functional education with clinicians	Overall	
	n	% (N = 15)
No	7	47%
Yes	8	53%
NA.	0	-

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DGH pathology labs - Other

DGH pathology labs - Other	Overall	
	n	% (N = 15)
Development and support of molecular MDTs	1	7%
importance of tissue stewardship	1	7%
No	13	87%
NA.	0	-

Surgeons - Interpreting reports/results

Surgeons - Interpreting reports/results	Overall	
	n	% (N = 15)
No	9	60%
Yes	6	40%
NA.	0	-

Surgeons - Overview of different types of tests

Surgeons - Overview of different types of tests	Overall	
	n	% (N = 15)
No	7	47%
Yes	8	53%
NA.	0	-

Surgeons - Tissue requirements

Surgeons - Tissue requirements	Overall	
	n	% (N = 15)
No	5	33%
Yes	10	67%
NA.	0	-

Surgeons - Patient information – testing and
results

Surgeons - Patient information – testing and results	Overall	
	n	% (N = 15)
No	4	27%
Yes	11	73%
NA.	0	-

Surgeons - Other

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Surgeons - Other	Overall	
	n	% (N = 15)
new tests for neo/adjuvant	1	7%
No	14	93%
NA.	0	-

CNS - Interpreting reports/results

CNS - Interpreting reports/results	Overall	
	n	% (N = 15)
No	5	33%
Yes	10	67%
NA.	0	-

CNS - Overview of different types of tests

CNS - Overview of different types of tests	Overall	
	n	% (N = 15)
No	5	33%
Yes	10	67%
NA.	0	-

CNS - Tissue requirements

CNS - Tissue requirements	Overall	
	n	% (N = 15)
No	6	40%
Yes	9	60%
NA.	0	-

CNS - Patient information – testing and results

CNS - Patient information – testing and results	Overall	
	n	% (N = 15)
No	3	20%
Yes	12	80%

NA.	0	-

CNS - Other

CNS - Other	Overall	
	n	% (N = 15)
No	15	100%
NA.	0	-

Clinicians - Interpreting reports/results

Clinicians - Interpreting reports/results	Overall	
	n	% (N = 15)
No	4	27%
Yes	11	73%
NA.	0	-

Clinicians - Overview of different types of tests

Clinicians - Overview of different types of tests	Overall	
	n	% (N = 15)
No	4	27%
Yes	11	73%
NA.	0	-

Clinicians - Tissue requirements

Clinicians - Tissue requirements	Overall	
	n	% (N = 15)
No	4	27%
Yes	11	73%
NA.	0	-

Clinicians - Patient information – testing and results

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Clinicians - Patient information – testing and results	Overall	
	n	% (N = 15)
No	2	13%
Yes	13	87%
NA.	0	-

Clinicians - Other

Clinicians - Other	Overall	
	n	% (N = 15)
Lab tours: Understanding of how pathology works, requirements for planning the service	1	7%
No	13	87%
Understanding of what is being ordered	1	7%
NA.	0	-

34. Digital education

34. Digital education	Overall	
	n	% (N = 15)
No	3	20%
Yes	12	80%
NA.	0	-

34. Paper education

34. Paper education	Overall	
	n	% (N = 15)
No	11	73%
Yes	4	27%
NA.	0	-

34. HCP Portal/Websites

34. HCP Portal/Websites	Overall	
	n	% (N = 15)
No	9	60%
Yes	6	40%
NA.	0	-

34. Educational Meetings: virtual

34. Educational Meetings: virtual	Overall	
	n	% (N = 15)
No	4	27%
Yes	11	73%
NA.	0	-

34. Educational Meetings: in person

34. Educational Meetings: in person	Overall	
	n	% (N = 15)
No	6	40%
Yes	9	60%
NA.	0	-

34. Preceptorships

34. Preceptorships	Overall	
	n	% (N = 15)
No	11	73%
Yes	4	27%
NA.	0	-

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NOVARTIS

PATHways UK 2021

Understanding Current Challenges in Oncology Molecular Pathways in the UK

This market research study is organised and funded by Novartis Pharmaceuticals UK Ltd

Introduction

The purpose of this nationwide survey is to gain a better understanding of the current services and challenges for cancer diagnostics in UK pathology laboratories.

With recent events impacting the patient oncology diagnostic pathway, including impact of COVID-19 and the centralisation of molecular services to Genomic Laboratory Hubs, this study is designed to capture key points on current and evolving molecular pathology services and pathways with a specific focus on molecular testing in Melanoma, Breast and Lung Cancer.

In particular, we aim to highlight the barriers and challenges that may exist for pathology laboratories in providing, and areas requiring further support that may help enable, a diagnostic infrastructure supporting optimal patient management.

Please note, the results are anonymised and will be aggregated together with the responses of other participants. Your responses will therefore not be attributable to you as an individual or center and you will not be identifiable.

Respondent Profile

1. **Responder ID (to be completed by Novartis Associate)** ....

2. **Where in the UK is your Lab?**

England ☐   Scotland ☐   Wales ☐   Northern Ireland ☐

3. **How would you categorise your hospital?**

District General ☐   Regional Centre ☐   Other ☐

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4. **What region does your lab cover for diagnosis and management of cancer samples?**

Local only ☐   Referral network ☐

Estimated populations size: ....

5. **Which is your regional GLH or genomics centre?**

Central & South GLH ☐   East GLH ☐   North West GLH ☐   North Thames GLH ☐   South East GLH ☐   South West GLH ☐   North East & Yorkshire GLH ☐

Scottish Genetics Consortium: Glasgow ☐   Edinburgh ☐   Aberdeen ☐   Dundee ☐

All Wales Medical Genomics Service (Cardiff) ☐

Precision Medicine Centre (Belfast) ☐

6. **Which technologies do you currently use at your lab?**

IHC ☐   FISH ☐   RT-PCR ☐   Sanger Sequencing ☐   NGS ☐

Other ....

Testing for Specific Cancers of Interest

7. **Can you provide an estimate of the number of samples you receive per month for each of the following:**

Breast ☐   Lung ☐   Melanoma Skin ☐   Other Cancers ☐

8. **For breast cancer, what is the current status of the following tests within your lab?**

Test	Reflex at diagnosis Y/N/On request	Testing at progression/ relapse/ other post Dx timepoints Reflex/On request/No	Performed by pathology lab Y/N	Moved to GLH/ Genomic centre Y/N	Moving to GLH/ Genomic hubs Y*/N *include timeframe if known	Current Average Turnaround time (calendar days)	Additional Notes
IHC							
HR							
HER2							
PGR							
PD-L1							
NTRKfus							
FISH							
HER2							
NTRKfus							
RT-PCR							
PIK3CA							

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BRCA1/2						
NTRKfus						
NGS						
PIK3CA						
HER2						
NTRKfus						
BRCA1/2						
Others						

9. For lung cancer, what is the current status of the following tests within your lab?

Test	Reflex at diagnosis Y/N/On request	Testing at progression/ relapse/ other post Dx timepoints Reflex/On request/No	Performed by pathology lab Y/N	Moved to GLH/ Genomic centre Y/N	Moving to GLH/ Genomic hubs Y*/N *include timeframe if known	Current Average Turnaround time (calendar days)	Additional Notes
IHC							
PD-L1							
ROS1fus							
ALKfus							
BRAF							
NTRKfus							
FISH							
ALKfus							
ROS1fus							
METamp							
HER2amp							
RETfus							
NTRKfus							
RT-PCR							
EGFR							
ROS1fus							
ALKfus							
ALK							
BRAF							
KRAS							
METex14							
HER2							
RETfus							
NTRKfus							
NGS							
EGFR							
ROS1fus							
ALKfus							
BRAF							

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KRAS							
METex14							
HER2							
RETfus							
NTRKfus							
Others							

10. For melanoma, what is the current status of the following tests within your lab?

Test	Reflex at diagnosis Y/N/On request	Testing at progression/ relapse/ other post Dx timepoints Reflex/On request/No	Performed by pathology lab Y/N	Moved to GLH/ Genomic centre Y/N	Moving to GLH/ Genomic hubs Y*/N *include timeframe if known	Current Average Turnaround time (receipt of sample to results reported - calendar days)	Additional Notes
IHC							
BRAF							
PD-L1							
Sanger sequencing							
BRAF							
NRAS							
Pyrosequencing							
BRAF							
RT-PCR							
BRAF							
NRAS							
KIT							
NGS							
BRAF							
NRAS							
KIT							
Others							

11. Please answer the following questions regarding your process for managing urgent samples?

    a. What is the selection of tests used for the following types of cancer:

        i. Breast Cancer: HR ☐ PGR ☐ HER2 ☐ Other .... N/A ☐

        ii. Lung Cancer: PD-L1 ☐ EGFR ☐ ALK ☐ BRAF ☐ ROS1 ☐ RET ☐ Other.................................... N/A ☐

        iii. Melanoma: BRAF ☐ Other.. N/A ☐

    b. Are these all performed in house? i.e. at your regional pathology centre. If not, where are they performed?
        Yes ☐ No ☐ :..

    c. For molecular testing, which technology is preferred? (Select one)
        IHC ☐ RT-PCR ☐ Other..

    d.   Who is funding this testing?
        NHS Trust ☐ GLH ☐ N/A ☐

    e.   Are samples also sent to GLH for NGS?
        Yes ☐ No ☐ N/A ☐

12. What percentage of samples you receive for the following cancers are urgent?

Breast.......................................

Melanoma.................................

Lung.....................................

13. Please answer the following questions regarding the use of archival tissue:
    a.   Please describe the process for request of archival tissue: .
        ....
        ....

    b.   Describe the specific challenges with archival tissue that may exists for Lung, Breast or
        Melanoma?..
        ....
        ....

    c.   What is the turnaround times from request to receipt of the tissue? (calendar days)
          i.   Breast ....
         ii.   Lung ....
        iii.   Melanoma ....

    d.   What are the challenges with archival tissue for genomics at GLH?
        Sample quality ☐
        Additional resource requirements ☐
        Processing issues ☐
        Transport ☐
        Other ....

14. Please answer the following questions regarding liquid biopsies:
    a.   Do you currently offer molecular testing of liquid biopsies at your lab?
        EGFR only ☐ No ☐

    b.   Are there any other molecular liquid biopsies performed at your lab? If so, which one(s)
        and for which cancer types?
        No ☐
        Yes ☐:..

    c.   What do you foresee will be the use of liquid biopsy within the diagnostic pathway?
        For all testing ☐
        In addition to tissue testing (same targets) ☐
        If a suitable tissue sample is not available ☐

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Upon progression only ☐

For specific tests only ☐ i.e. ....

For panel testing ☐

Not used ☐

    d. What are the challenges with liquid biopsies? ....
....
....
....

15. Are you currently developing any other molecular tests for Lung, Breast or Melanoma?

    Please describe ....

Pathway and Logistics

16. What are the biggest difficulties with implementing a new test?

Timelines for implementation ☐

Test development ☐

Test validation ☐

Administration ☐

Funding/Resource allocation ☐

Communication ☐

Other ....

17. Who is your point of contact within clinic?

Respiratory physicians/ Pulmonologists ☐

Surgeon ☐

Oncologist ☐

MDT coordinator ☐

Clinical nurse specialist ☐

Other ....

18. Do you regularly attend MDT?

Yes ☐ No ☐

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19. Do you discuss results at standard MDTs?

Yes ☐ No ☐

20. Do you have a molecular specific MDTs?

Yes ☐ No ☐

21. Who initiates the testing process?

Respiratory physicians/ Pulmonologists ☐

Surgeon ☐

Administrator ☐

Pathologist ☐

Clinical Scientist (genomics) ☐

Oncologist ☐

Other ....

22. How do you communicate with clinicians? i.e. regarding how to access testing or to inform them of the availability of a new test?

Email ☐

Webpage ☐

Hospital Newsletter ☐

MDT meeting ☐

Other ....

23. On your reports, is clinical interpretation of the molecular results provided with reference to published disease area management recommendations, and available targeted therapies?

No ☐

Yes ☐

Reference to published therapy area guidelines only ☐

Reference to available targeted therapies only ☐

Other ....

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Recent Changes

24. What impact has COVID-19 had on your <u>current</u> services?

Minimal or no impact ☐   Medium impact ☐   High impact ☐

Please describe if medium or high impact……...…………………..

25. What impact has the roll out of the GMS and GLH had on your <u>current</u> services (positive and/or negative)?

Minimal or no impact ☐   Medium impact ☐   High impact ☐   N/A ☐

Please describe ....…………………………..

26. What impact will the roll out of the GMS and GLH had on your <u>future</u> services (positive and/or negative)??

Minimal or no impact ☐   Medium impact ☐   High impact ☐   N/A ☐

Please describe …..………………………..

27. Where do you see the role of regional pathology centres in the optimal delivery of the GMS?

Sample preparation ☐

Test assignment (reflexive) ☐

Conducting testing: all ☐   cellular ☐   salvage ☐   urgent or first line testing ☐

Data analysis ☐

Report creation ☐

Education/training ☐

Other ....

28. How do you currently work with your GLH? i.e. access to tissue, sample preparation, salvage/urgent testing, preparation of reports, etc.

Please describe ……………………...
....

N/A ☐

Barriers and Support

29. What do you see as the current barriers for optimal delivery of the GMS? Tick the relevant boxes.

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Barrier	Minimal or no impact	Medium Impact	High Impact	Not applicable
Sample Quality	☐	☐	☐	☐
Transportation	☐	☐	☐	☐
Ordering GLH tests	☐	☐	☐	☐
Admin	☐	☐	☐	☐
Testing options/capabilities	☐	☐	☐	☐
Data analysis/ bioinformatics	☐	☐	☐	☐
IT requirements/ compatibility	☐	☐	☐	☐
Reporting	☐	☐	☐	☐
Education/training	☐	☐	☐	☐
Resource/Capacity	☐	☐	☐	☐
Funding				
Other.....................................				

30. Do you have other concerns regarding the delivery of this service?

Yes ☐   No ☐

If yes please describe ....……………………………..
....

31. What additional resources are required at local pathology labs to support optimal delivery of this service?

Please describe ....……………………...
....

32. What educational support is needed for pathologists from different sites?

Topics	Regional pathology centres	DGH pathology labs
New treatment trial results		
Optimal reporting		
Guideline reviews/updates		
Understanding the new molecular testing pathway		
Best practice sharing across lab		
Cross-functional education with clinicians		
Other...		

33. What educational support is needed for HCPs?

Topics	Surgeons	CNS	Clinicians
Interpreting reports/results			
Overview of different types of tests			
Tissue requirements			
Patient information – testing and results			
Other...			

34. What type of education is preferred?

Digital education ☐

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Paper education ☐

HCP Portal/websites ☐

Educational Meetings: virtual ☐   in person ☐

Preceptorships ☐

Other ....

Thank you for taking the time to complete the survey

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