



Genomics
england



The 100,000 Genomes Project Transforming Healthcare

Berlin Institute of Health

Prof Sir Mark Caulfield FMedSci
Chief Scientist

William Harvey Research Institute
Queen Mary University of London

- Genomics England is a Department of Health Company
- Seconded to Genomics England from Queen Mary/Barts who pay my salary
- Multiple industry partnerships e.g. Illumina, iQVIA
- No shares in anything except failed banks in 2008

The 100,000 Genomes Project Milestones



Announced by David Cameron, former Prime Minister in December 2012 –An Olympic Legacy

Genomics England launched by then Secretary of State for Health in speech during NHS 65th Anniversary Celebrations, July 2013



Opening of new Sequencing Centre by Theresa May in 2016



CMO's Generation Genome and the Life Sciences report in 2017



Commissioning of new NHS Genomic Medicine Service October 2018

Reached goal of sequencing 100,000 genomes in December 2018



“aspiration to undertake 5 million genome analyses over the next 5 years”



The 100,000 Genomes Project in numbers



Over **100,000** genomes



Over **97,000** patients and family members

```
110001010101001010100101010000101  
110110111010101010001011101000101  
110101010001001101010001010100010  
001001001110010001000010101010100  
100111101100101010110101111001101
```

21+ Petabytes of data.
1 Petabyte of music would take 2,000 years to play on an MP3 player.



13 Genomic Medicine Centres, and **98** NHS Trusts within them were involved in recruiting participants



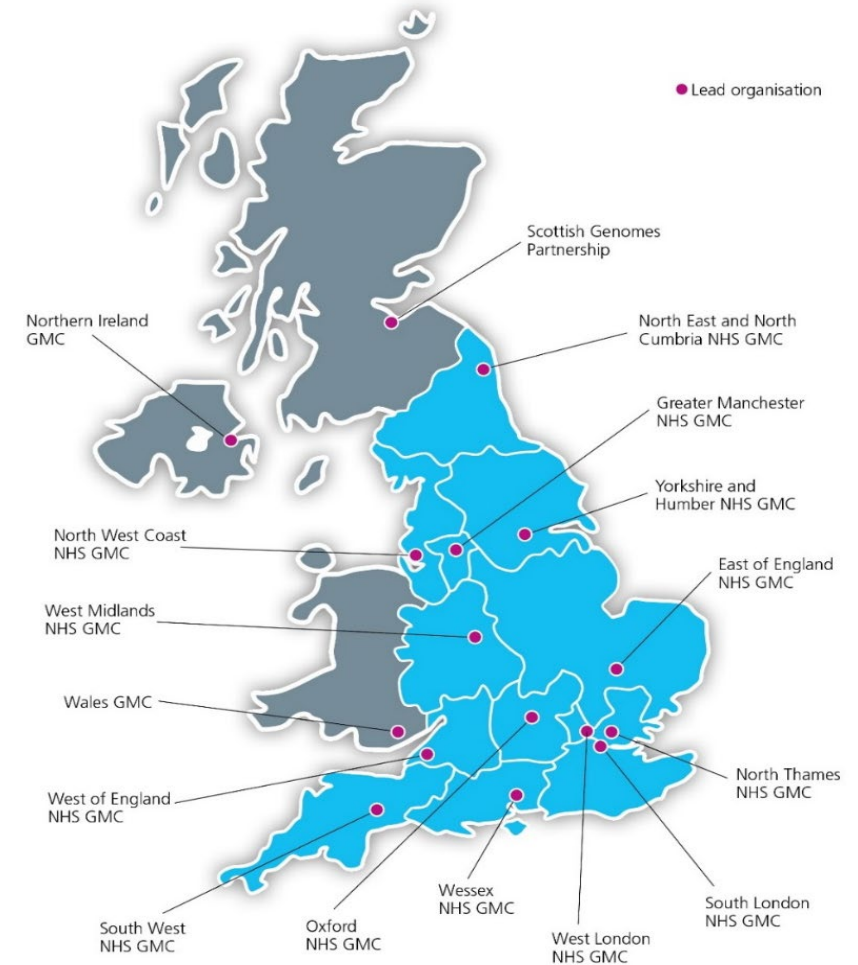
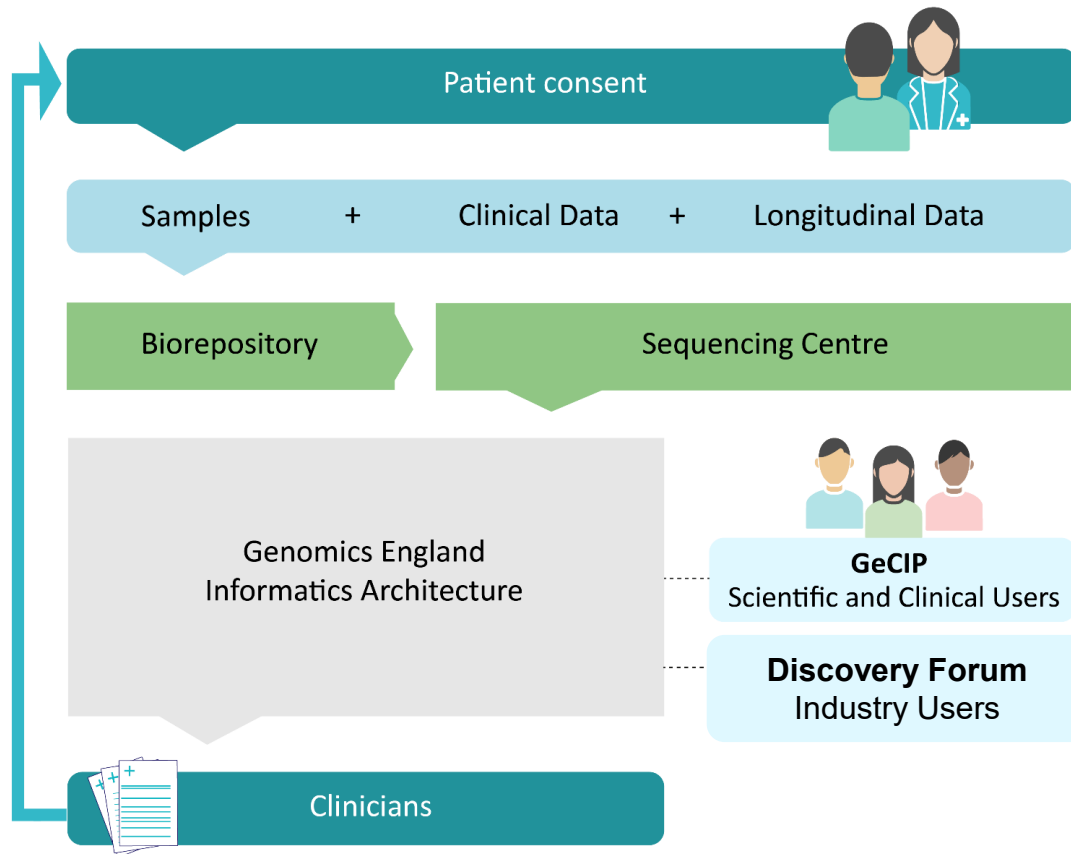
Around **5,000** NHS staff (doctors, nurses, pathologists, laboratory staff, genetic counsellors)



Over **3,000** researchers and trainees

How did the 100,000 Genomes Project work

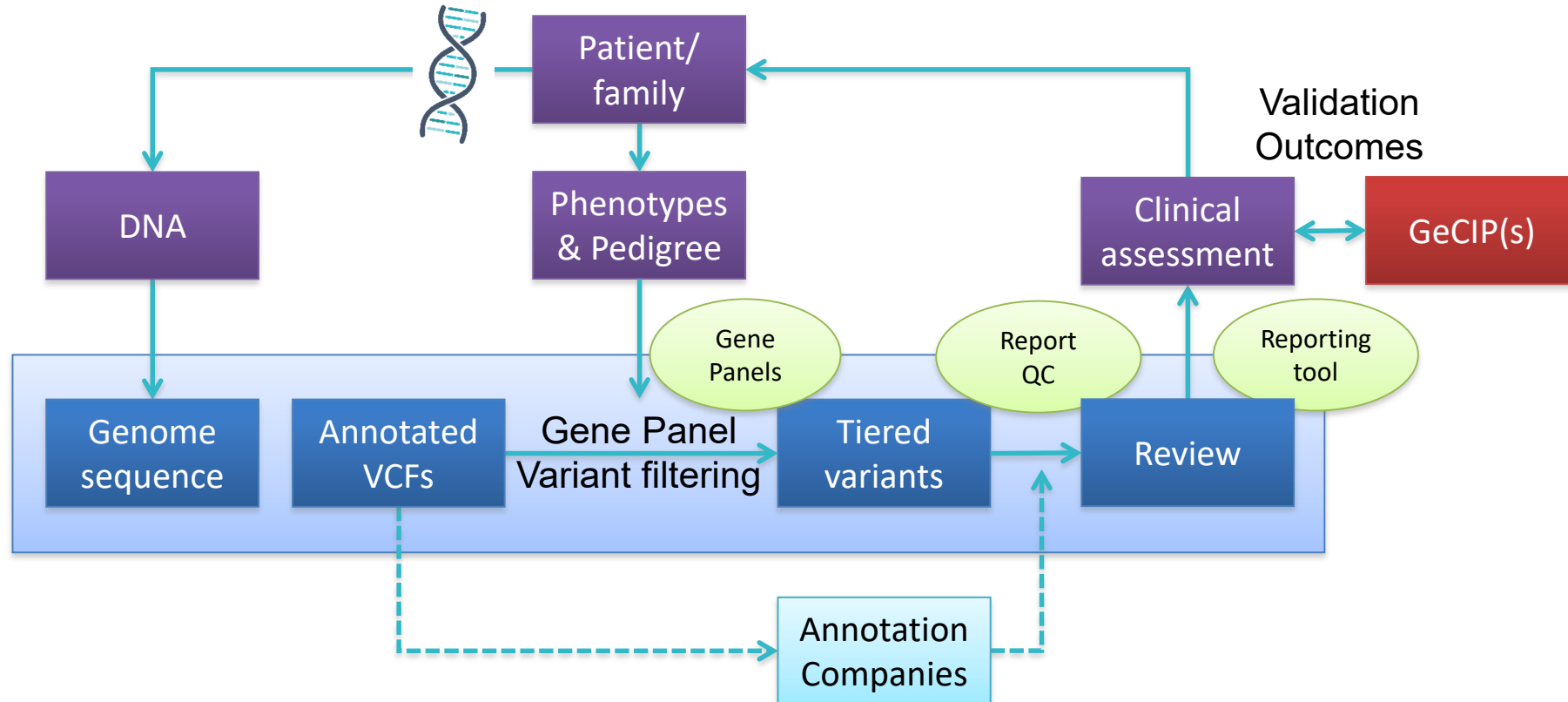
- 13 NHS Genomic Medicine Centres covering England, over 98 hospitals
- Responsible for identifying and recruiting participants and for clinical care following results
- Northern Ireland, Scotland and Wales joined



Scalable disease diagnostics

Sequence depth germline 36x to 40x

Somatic 82x to 100x



Rare diseases



Rare Inherited diseases

- <6% of the UK population
- 1200 disorders unmet need
- Standardised eligibility & phenotyping
- Human Phenotyping Ontology
- Automated analytics
- NHS confirm gene panels & close cases

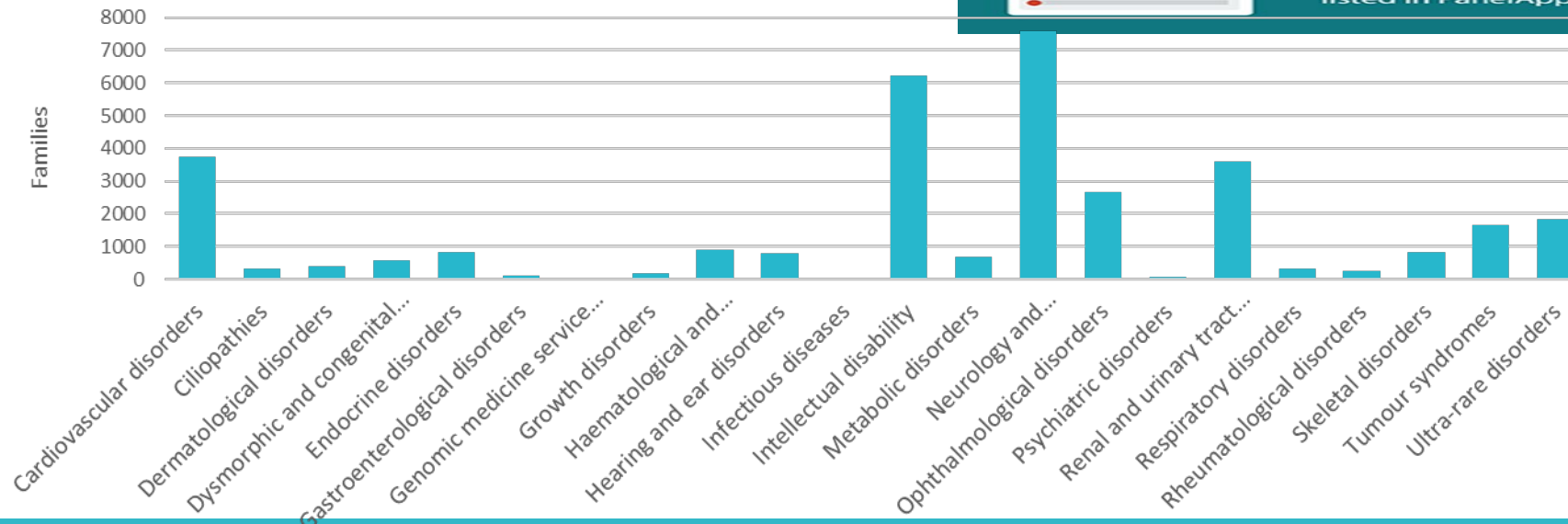
6,414,934 variants in Jessica's genome

677,556 are rare

2,826 predicted to cause change in a protein

67 different to her parents

1 was in a gene listed in PanelApp



Application in the NHS

4 month old fluctuating neurology, repeated infections in NICU

- Died with no diagnosis, immune testing negative, enrolled in the project by parents.
- Mother unexpectedly pregnant didn't want to know diagnosis
- We found a pathogenic Transcobalamin 2 mutation
- Brother born and tested – sadly affected BUT high dose B12 given
- *J Paediatrics* 1974

10 year old girl admitted to ITU with life threatening chicken pox

- Prior unusual severe infections. Detailed immune testing no diagnosis.
- Mutations in *CTP synthase 1* gene affects B and T lymphocyte responses to infection of both capsulated bacterial infection and viruses
- Curative bone marrow transplant- Siblings tested and not at risk of these infections
- *J Allergy Clin Immunol* 2016 Vol: 138: 6

5 year old boy unexplained anaemia, developmental delay, short stature and constipation

- ?Diamond-Blackfan anaemia, may have limited lifespan due to cancer risk
- 100,000 Genomes Project Intellectual Disability Panel via Panel app
- Tier 1 *de novo* variant identified in *Thyroid Hormone Receptor Alpha*
- Now receiving high dose thyroid hormone replacement
- *Nature Reviews Endocrinology* volume 10, 582–591(2014)

5 year old with a rare disease

From Mum:

- “Thanks to the 100,000 Genomes Project my 5 yr old has been diagnosed with GAMT deficiency which is a treatable metabolic disorder.
- Before diagnosis it was thought she had a degenerative neurological disorder and I was waiting for her end up in a wheelchair. She had uncontrollable epilepsy, the developmental age of a 12 month old and couldn't retain any skills, she was very much locked inside her mind and unable to communicate in any way.
- After 6 months of treatment later with creatine, ornithine and arginine she is a new child, the light is back in her eyes, she's learning new skills every day and she is free of epilepsy finally.
- It has been nothing short of a miracle, I've spent so long waiting for her to get even worse or even die from her epilepsy, it doesn't feel real that she is improving and thriving.”



<https://mamaunexpected.com/2018/02/12/1904-days-d-is-for-diagnosis/>

PanelApp

<https://panelapp.genomicsengland.co.uk/>

PanelApp Panels Genes and Entities Activity Log in Register

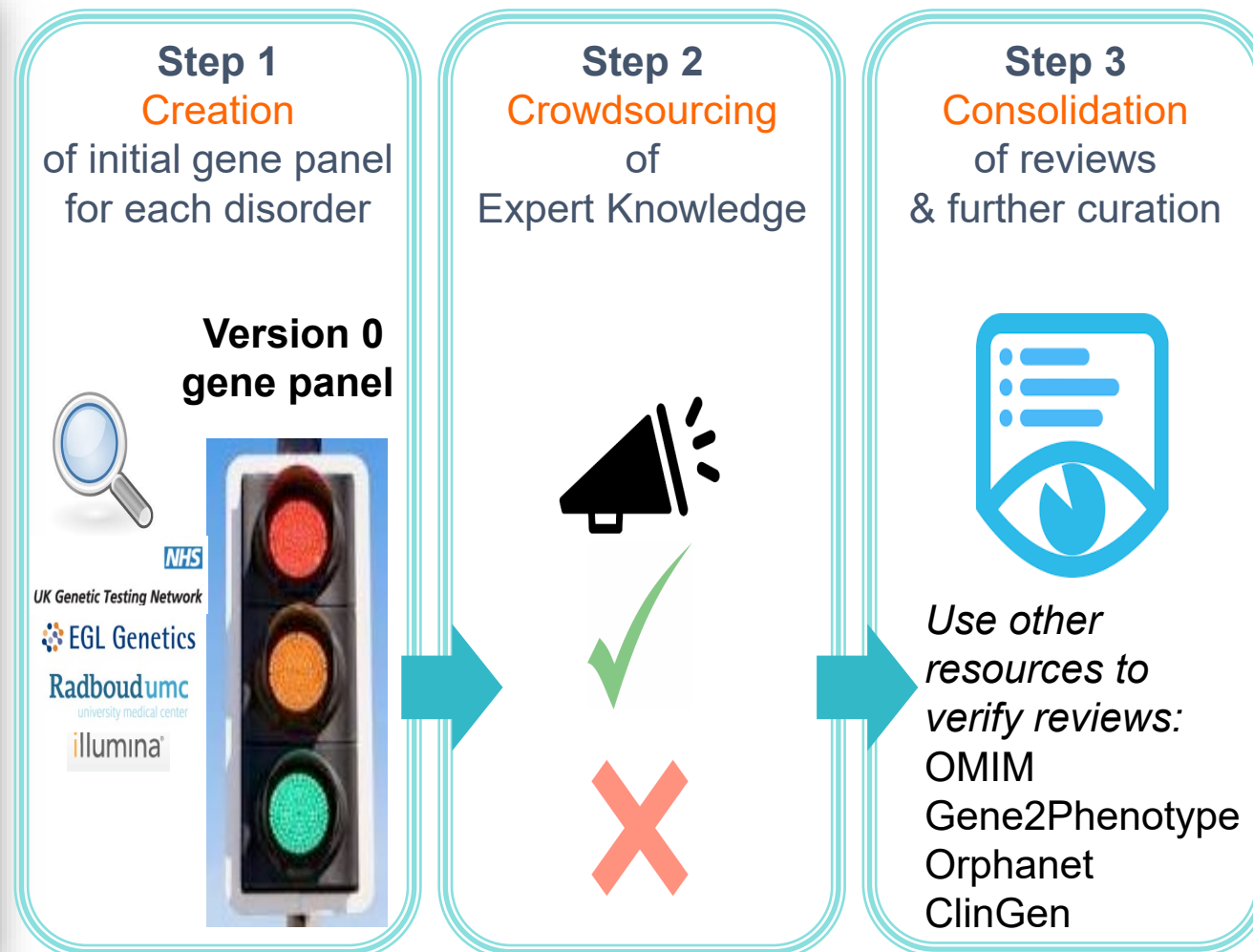
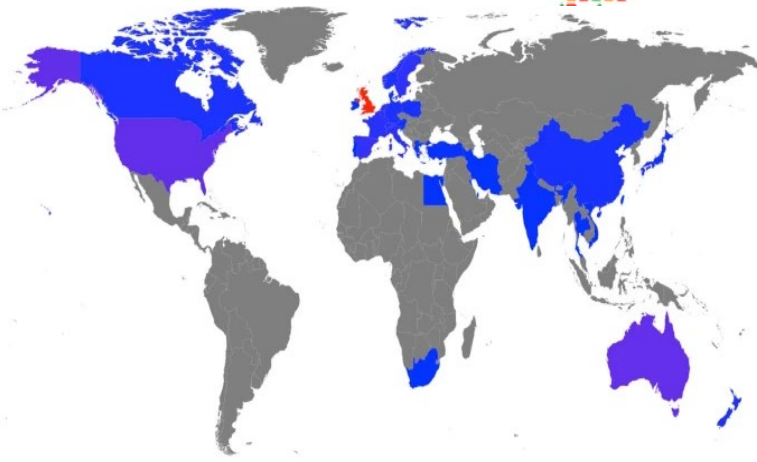
Genomics England PanelApp

A crowdsourcing tool to allow gene panels to be shared, downloaded, viewed and evaluated by the Scientific Community

Home

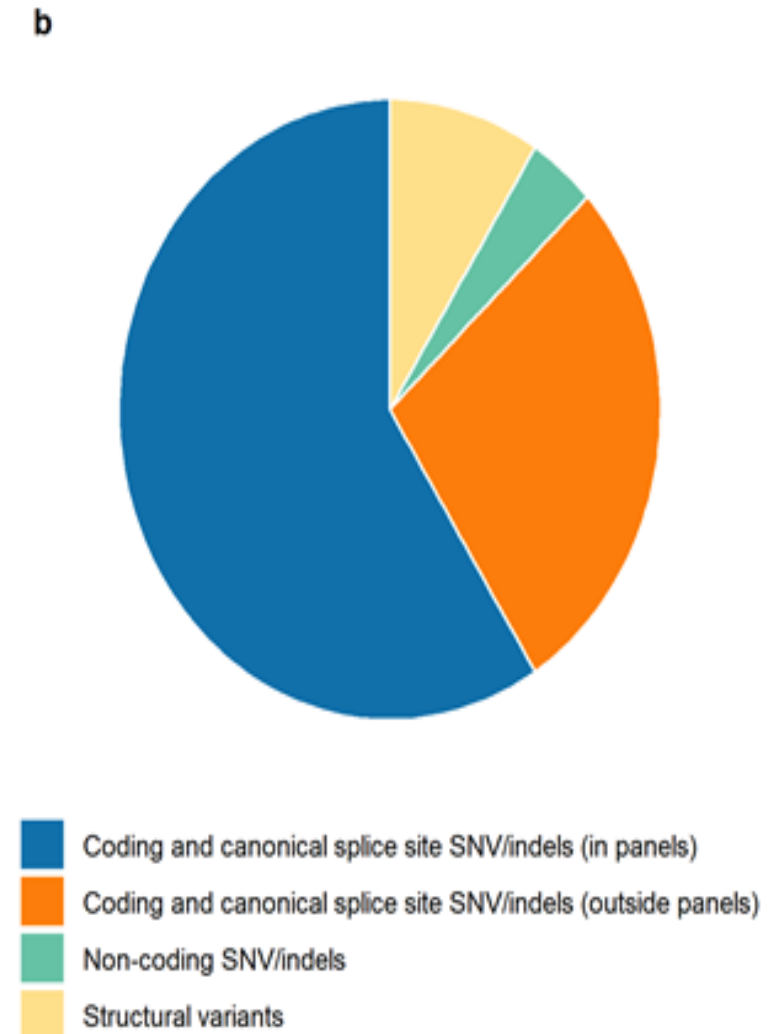
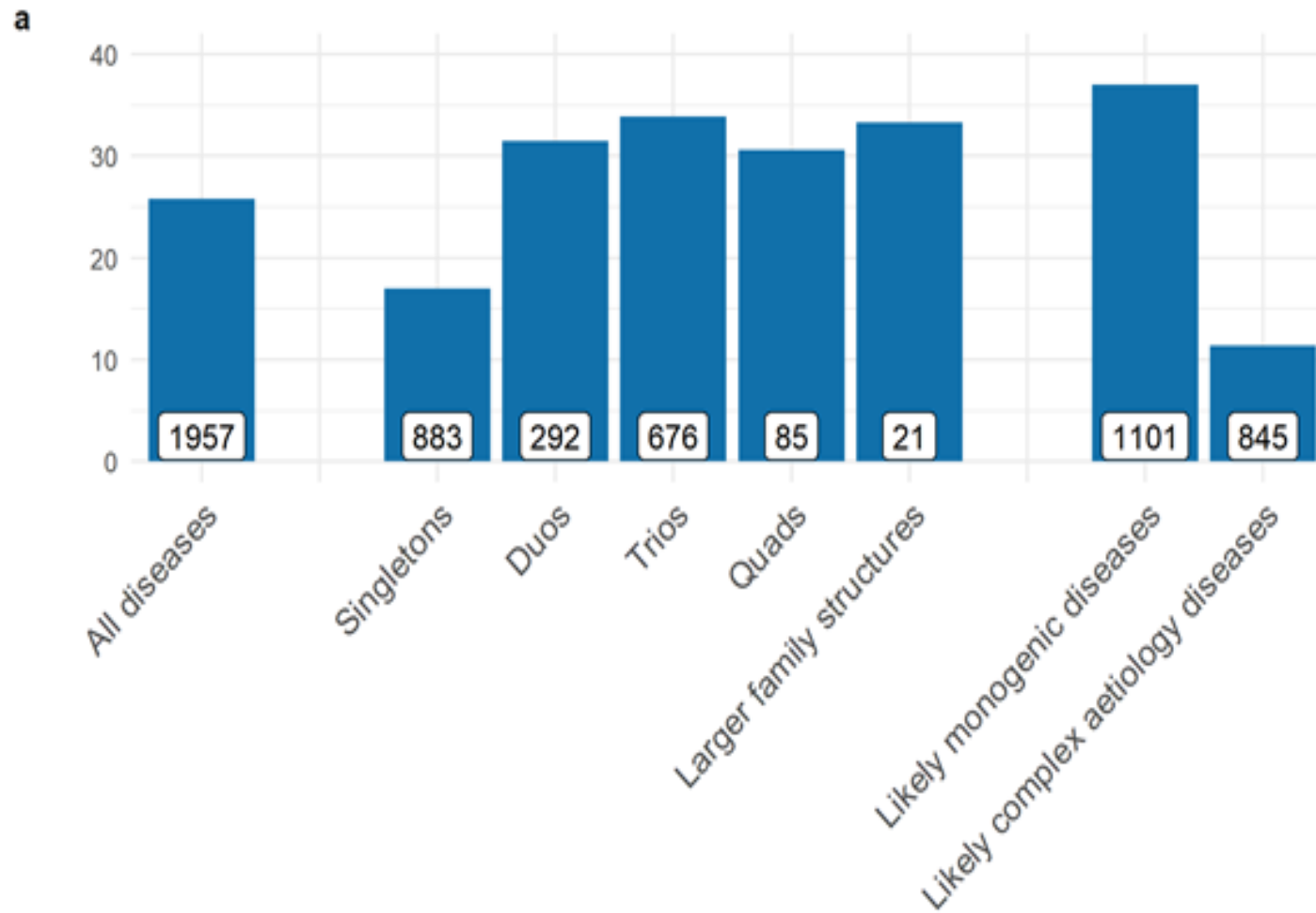
- News
- Navigate & Explore
- Reviewers
- Guidelines
- Webservices
- FAQs
- Contact, Content & Glossary

In the last week, we have had **572,503 requests** to the PanelApp website & API, and **3,930 unique visitors** from around the world:

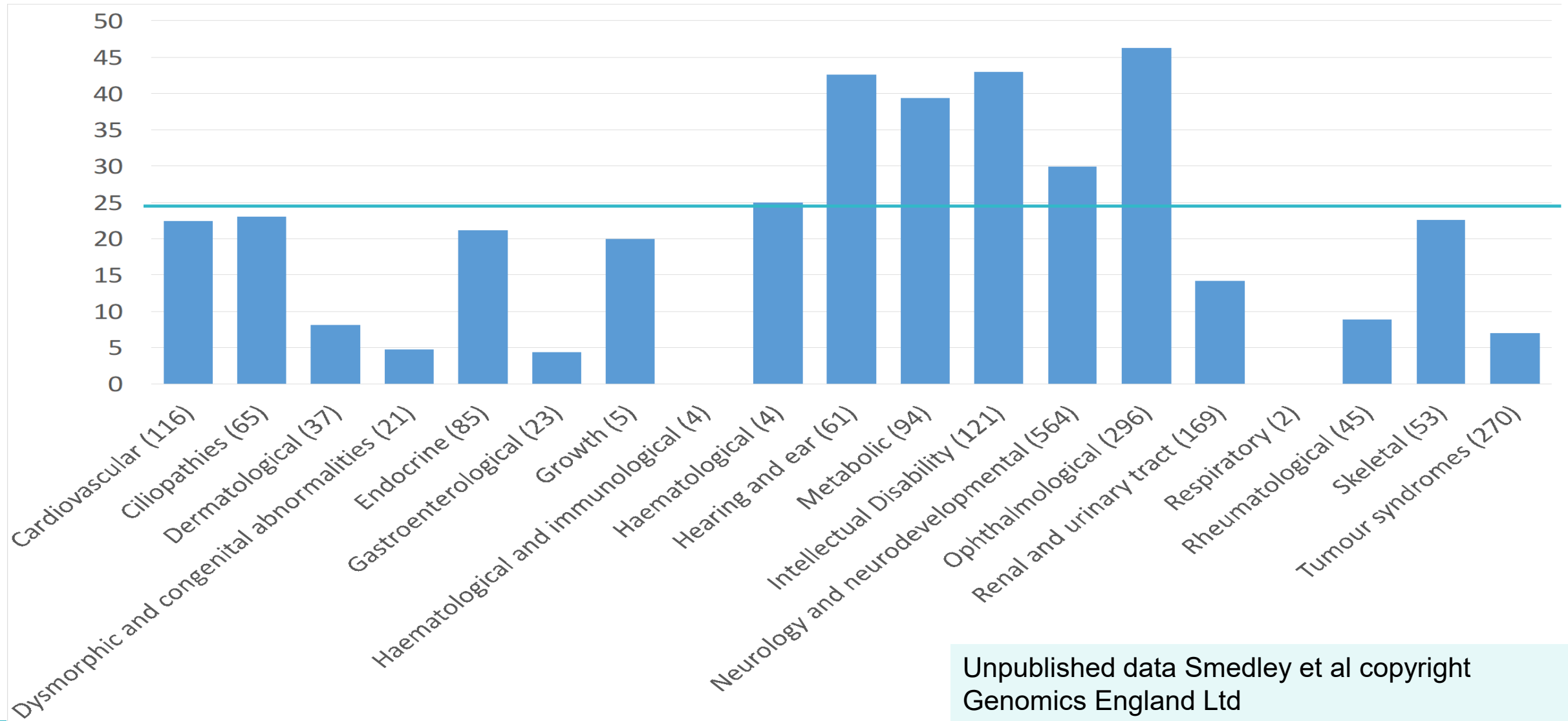


Rare Disease Diagnoses and Family Size

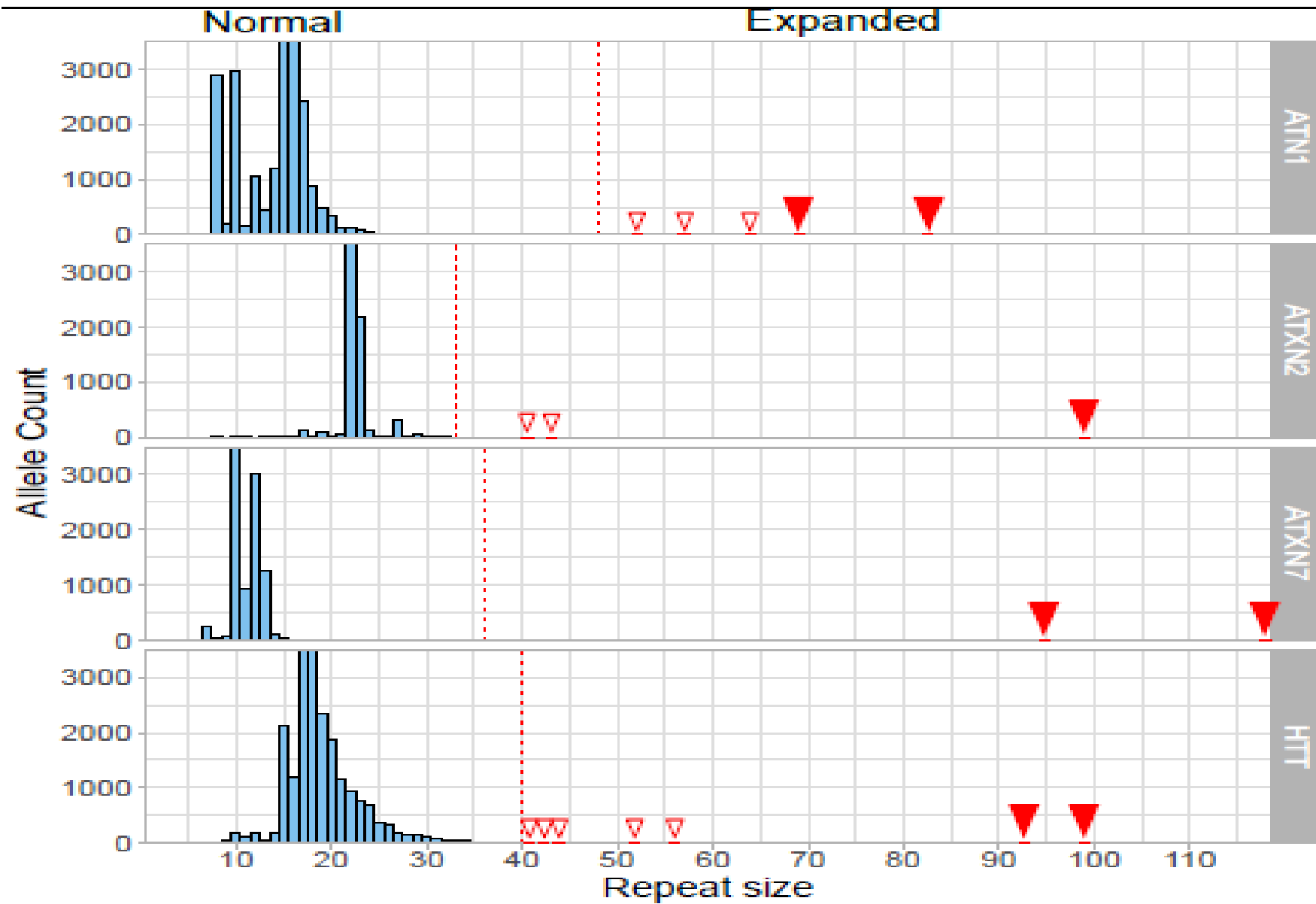
2183 families from 160 rare disease categories in 4660 people



Confirmed Diagnostic Yield by Category

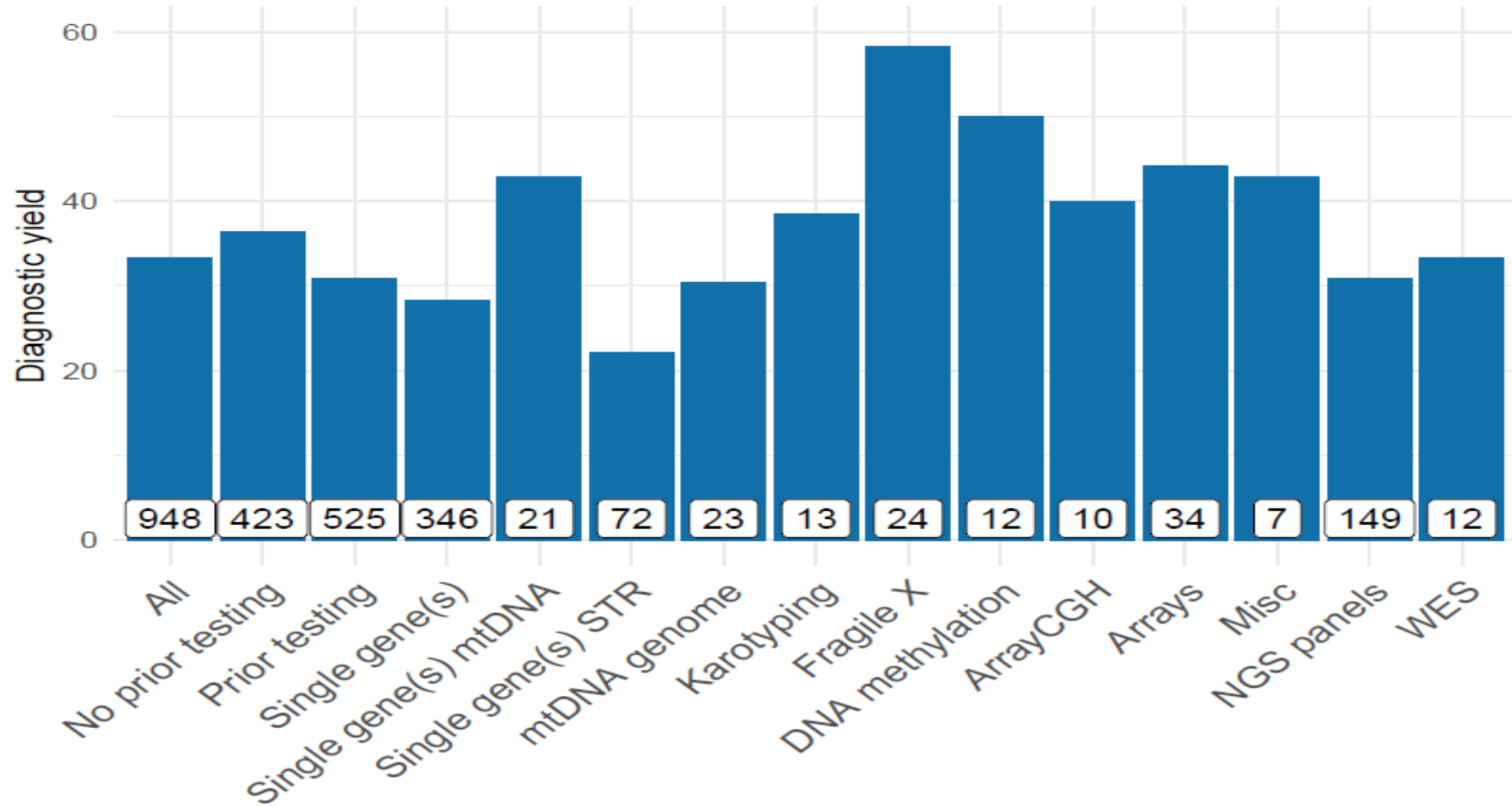


Unpublished data Smedley et al copyright
Genomics England Ltd



Diagnostic uplift from whole genomes over usual care

c



NHS Reporting portal

Genome Interpretation Portal

PROBAND VIEW

Pedigree

Click to go and check this family pedigree using [panogram](#)

Files

List of files ready for download (notice the link only works within the GMC portal)

Actions

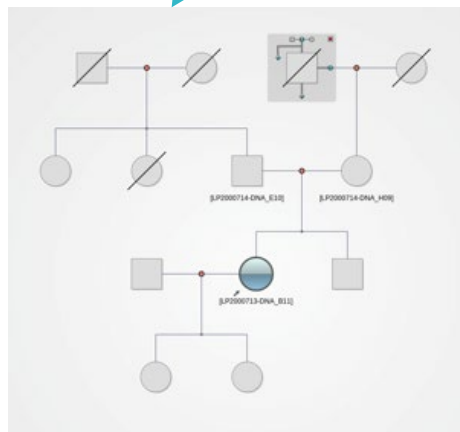
Select an action from the list, (notice it will only work within the embassy environment)

VIEW PEDIGREE DOWNLOAD DO IT!

View family pedigree

Download the report

Review variants and close case



Report ID: OPA154-1 Report date: Not approved Proband GEL Participant ID: S0003761

Whole Genome Sequencing Rare Disease Primary Findings

Genomics England, Queen Mary University of London, Division H41, Charterhouse Square, EC1M 6BQ
Email: GenomicsEngland@reportingteam@nhs.uk

NHS Genomic Medicine Centre, South London, Intergration Request ID: OPA154-1
Intergration Request date: 05/06/2025

Participant Information

Participant ID	Year of Birth	Gender	Relationship to Proband	Affection Status
S0003761	2006	Female	Proband	Affected
S0004430	1977	Female	Mother	Unaffected
S0004248	1978	Male	Father	Unaffected
S0008859	2008	Female	Sibling II	Unaffected

Report context
Genomics England Primary Findings include variants classified as tier 1 or 2, i.e. variants in the variant gene panel(s) that are likely or possibly pathogenic. It may also contain additional prioritised variant calls of clinical relevance to the patient's phenotype. It does not include additional look-up for findings unrelated to the patient's phenotype. If any variants have been included as primary findings, we are currently unable to identify an etiological cause for the patient's condition.

Primary finding

Gene	Variant	Effect	Yzygosity	Mother	Father	Yzygosity	Quality	IKG AF	ExAC AF	Omic	Evidence	Class	VAAS	Phevor	Inheritance	Scoring	Confirmation	
DEPC5	chr22:32227351 rs371377906	C + T splice region	0	0	0	1091/99	0.777	0.00039	155-22-13	0.00150	HS04	EPILEPSY, FAMILIAL, FOCAL, WITH VARIABLE FOCI			Recessive	2	Scoring	Omic
ERCC5	chr10:50678884 rs139007661	T + G missense	0	0	0	1277/99	0.00100	0.00154	29-19-20	0.00163	HS04							No Stat
ERCC5	chr10:50909096 rs61760163	G + A missense	0	0	0	1234/99	0.00100	0.00154	38-18-20	0.00163	HS04							No Stat
Score Variant	0:50722085 rs371546606	C + A missense splice site impact	0	0	0	904/99	0.0347	0.00002	27-16-11	0.00002	HS04							No Stat
CFHR2	chr1:196918738 rs144096230	C + T missense	0	0	0	2401/90	0.00140	0.00591	31-1-30	0.00397	HS04							No Stat

Table 1. Candidate variant(s)

Gene	Variant	Effect	Yzygosity	Mother	Father	Yzygosity	Quality	IKG AF	ExAC AF	Omic	Evidence	Class	VAAS	Phevor	Inheritance	Scoring	Confirmation	
PTN13	chr1:196918738 rs144096230	C + T missense	0	0	0	2401/90	0.00140	0.00591	31-1-30	0.00397	HS04							No Stat

Table 2. This table describes the candidate variant(s) from the perspective of the participant's variant interpretation.
The patient is heterozygous for variant p.L382Val in the PTN13 gene. This patient is heterozygous for p.L382Val variant in PTN13 gene. This gene has been associated with Neurocan and LEOPARD syndrome. This variant has been reported previously in ClinVar multiple times (RCV000833503.0, RCV000837965.0, and RCV001244602.0) and there are multiple lines of computational evidence support the pathogenicity of this variant. There are no overlapping features with these two syndromes, and clinical history and evidence which of the syndromes is more likely relevant for this patient.
The protein encoded by this gene is a member of the protein tyrosine phosphatase (PTP) family. PTPs are known to be

Review	Priority	Gene	Position	Change	Effect	Zygosity	Mother	Father	Zygosity	Quality	IKG AF	ExAC AF	Omic	Evidence	Class	VAAS	Phevor	Inheritance	Scoring	Confirmation	
	0	DEPC5	chr22:32227351 rs371377906	C + T c.3228-3C>T	splice region	0	0	0	0	1091/99	0.777	0.00039	155-22-13	0.00150	HS04					Scoring	Omic
	0	ERCC5	chr10:50678884 rs139007661	T + G p.Gln1041Pro	missense	0	0	0	0	1277/99	0.00100	0.00154	29-19-20	0.00163	HS04						No Stat
	0	ERCC5	chr10:50909096 rs61760163	G + A p.Arg666Cys	missense	0	0	0	0	1234/99	0.00100	0.00154	38-18-20	0.00163	HS04						No Stat
	0	Score Variant	0:50722085 rs371546606	C + A c.1391G>T p.Arg454Leu	missense splice site impact	0	0	0	0	904/99	0.0347	0.00002	27-16-11	0.00002	HS04						No Stat
	0	CFHR2	chr1:196918738 rs144096230	C + T c.212C>T p.Trp71Met	missense	0	0	0	0	2401/90	0.00140	0.00591	31-1-30	0.00397	HS04						No Stat

Healthcare Benefits – NHS feedback & druggability tests

- 24% of diagnoses had immediate clinical utility
- 0.2% no current benefit
- The remainder had unknown utility at this early stage.

Headline clinical utility

- 3 probands changed medication
- 20 diagnoses leading to additional surveillance for the proband or relatives,
- 13 eligible for clinical trials,
- 52 - the diagnosis could inform future reproductive choices
- 32 - other benefits e.g. dietary change or vitamins

Druggability assessments

- 33% of the diagnoses have an existing approved drug that targets the protein

Cohort-wide burden tests

- 500 genomewide significant signals – potential diagnoses

Diagnostic odyssey of children born 2003 onward

- **Families spent 6 years** (median 75 months) attended a median of 68 hospital appointments prior to diagnosis
- Unaffected relatives attended a median of 18 appointments over 120 months from birth.
- Post-diagnosis over 18 months, fewer focused clinical episodes
- **Affected participants used 183,273** episodes of hospital care via the emergency department, outpatients, inpatients and critical care,
- **Cost £87 million** (median cost of £15,310 per participant)
- **Compared to 53,706 episodes at a cost of £21 million** (median cost of £4,285/participant) for the unaffected participants
- Not including visits to the family physician, or disease treatment costs.

Rare Disease Pilot – 240,000 Hospital Episodes

Total Cost of Hospital Episodes 1CD10 coded since 2007

Dataset	Number of episodes	Total cost
Critical care	347	£387,085
Accident and Emergency care	16,696	£2,530,399
Inpatient care	43,714	£77,276,982
Outpatient care	177,125	£26,243,354
TOTAL	237,882	£106,437,820

\$138,189,286

Unpublished – Buchanan and Wordsworth
Copyright Genomics England and Oxford

Clinical Variant Ark

CVA in Numbers

3,156,215

Variants

36,278

Cases

6,613

Phenotypes

Overall diagnosis

20.14 %
Current diagnostic yield*

5,921 cases
Positive primary findings

23,482 cases
Negative primary findings

1,814 cases
Inconclusive findings

*number of positive primary findings against total number of non inconclusive cases

Pathogenicity of variants

3,969
Pathogenic

2,926
Likely pathogenic

4,458
VUS

495
Likely benign

225
Benign

Cancer



Making Whole Genomes Work for Cancer

Cancer is a disease of disordered genomes

Tested Vacuum packaging and refrigeration

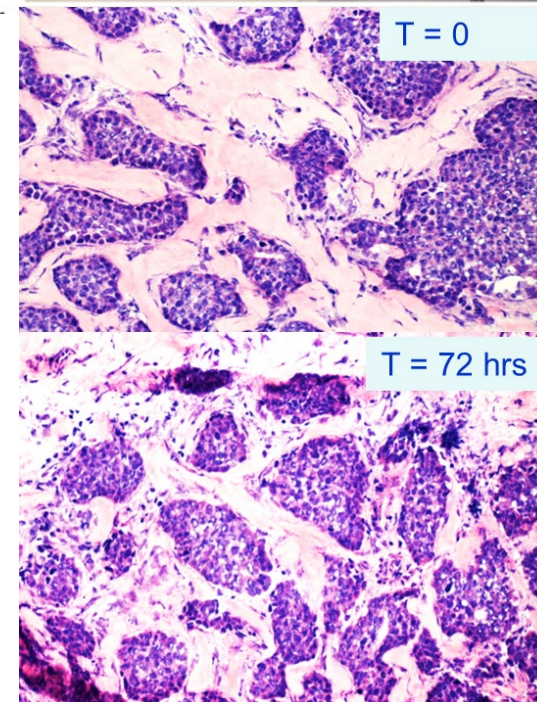
- Conclusion: Histomorphology maintained out to 72 Hrs Out of hours storage as fresh tissue perfectly possible

Compared same cancer/same patient handled differently

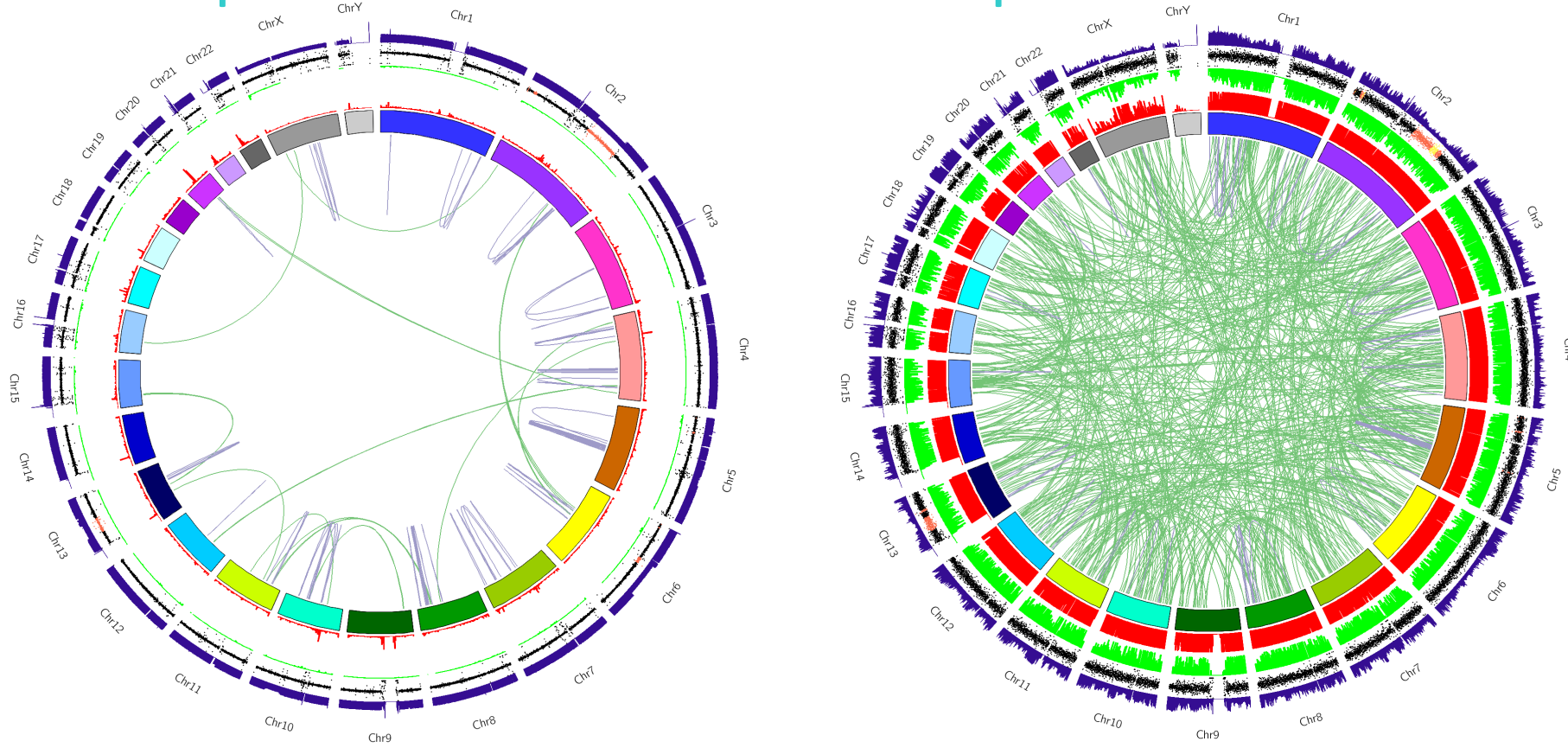
- Even optimised FFPE still worse than fresh tissue for WGS

Tested and mobilised 400 molecular pathology pathways

- Mainstream supply of fresh frozen tissue
- PCR free genomes with 750 ng input DNA
- Alternative fixatives e.g. Paxgene
- Shaken biopsy for EBUS
- Genomic and a Pathology biopsy

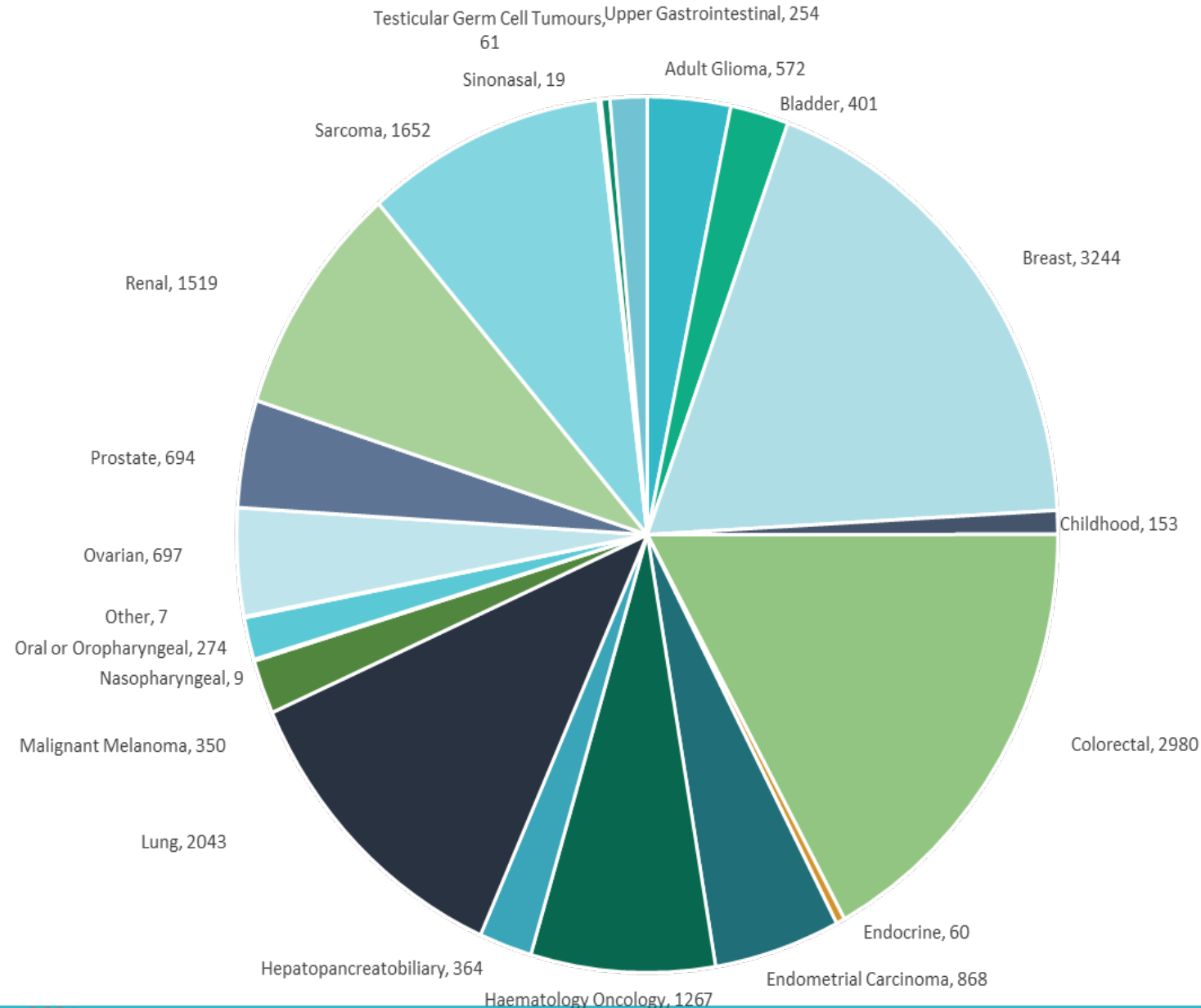


An overview of somatic changes in FF and FFPE samples taken from the same prostate tumour



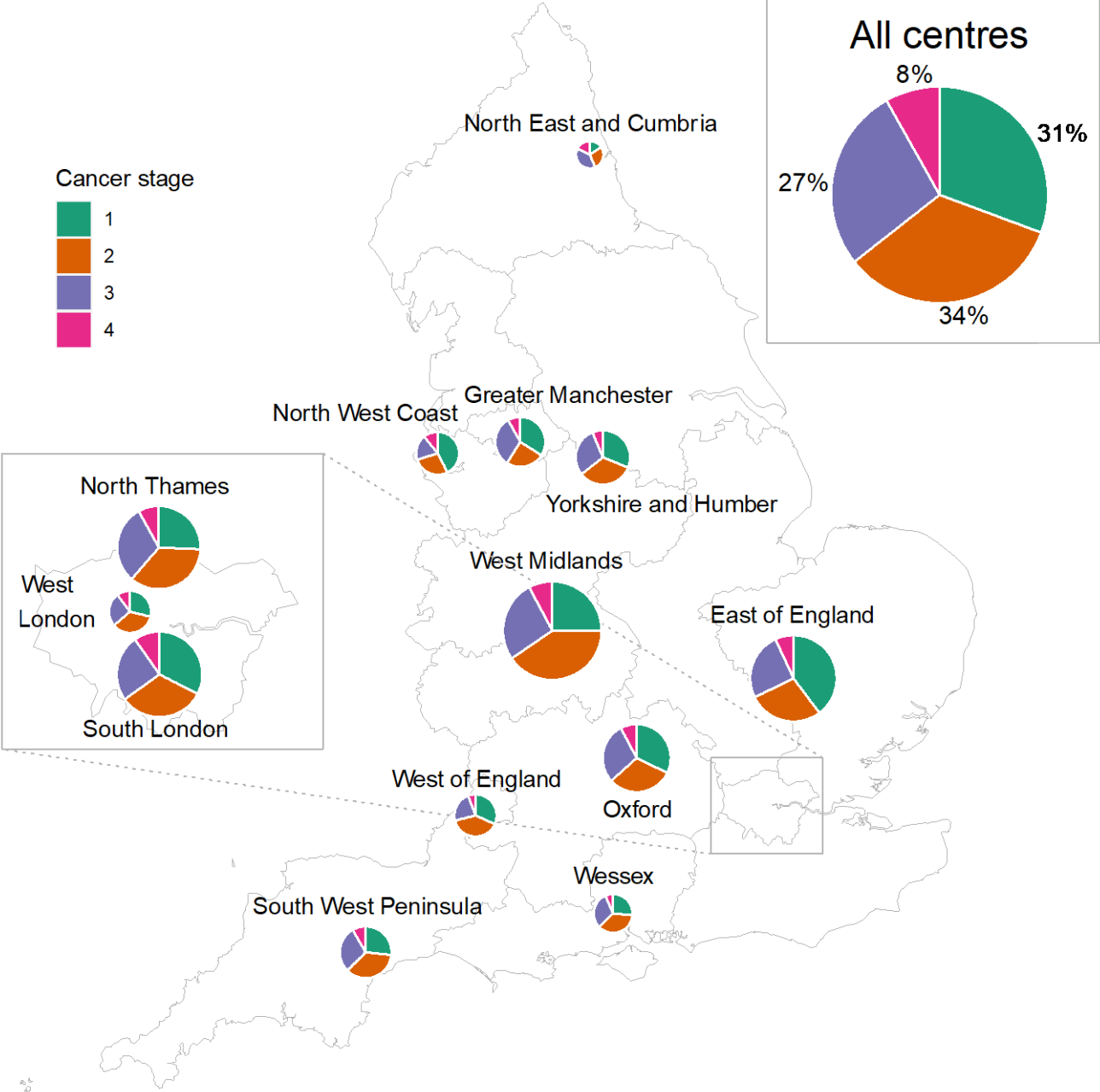
	AT dropout	CG dropout	Evenness of coverage	Chimeric reads, %	SNVs	Indels
GL	2.61	1.91	6.77	0.32	NA	NA
FF	5.22	2.48	11.56	0.65	10083	1573
FFPE	17.30	-17.30	41.26	1.27	698797	41645

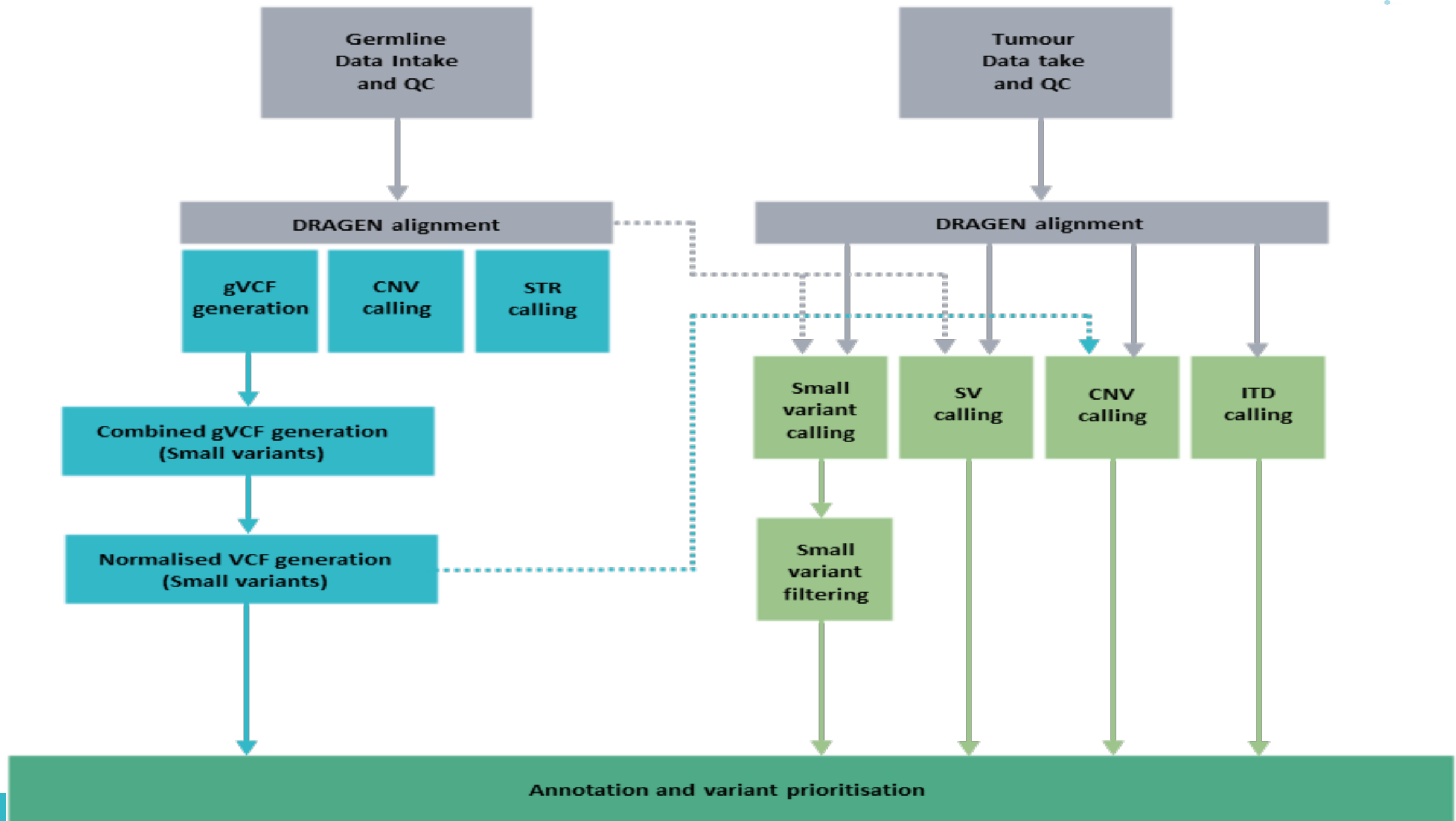
Cancer Patients by Tumour Type



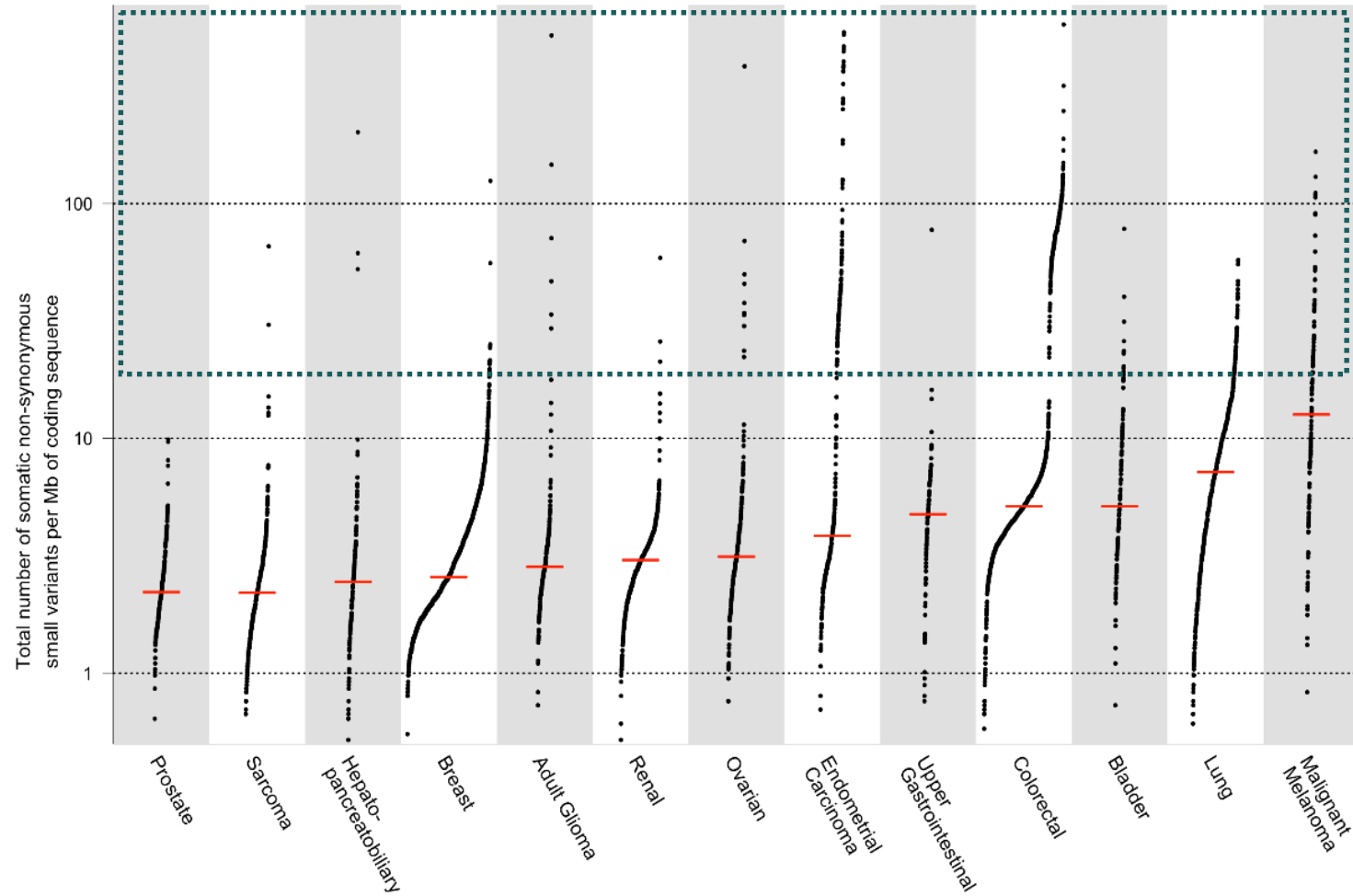
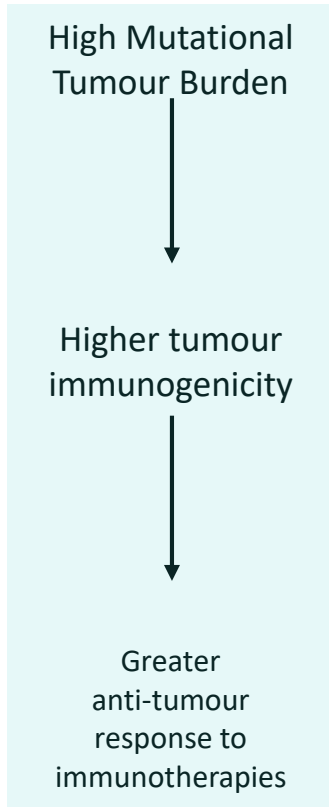
Cancer Type	No. of Tumours
Adult Glioma	572
Bladder	401
Breast	3244
Childhood	153
Colorectal	2980
Endocrine	60
Endometrial Carcinoma	868
Haematology Oncology	1267
Hepatopancreatobiliary	364
Lung	2043
Malignant Melanoma	350
Nasopharyngeal	9
Oral or Oropharyngeal	274
Other	7
Ovarian	697
Prostate	694
Renal	1519
Sarcoma	1652
Sinonasal	19
Testicular Germ Cell Tumours	61
Upper Gastrointestinal	254
Grand Total	17488

Tumour stage





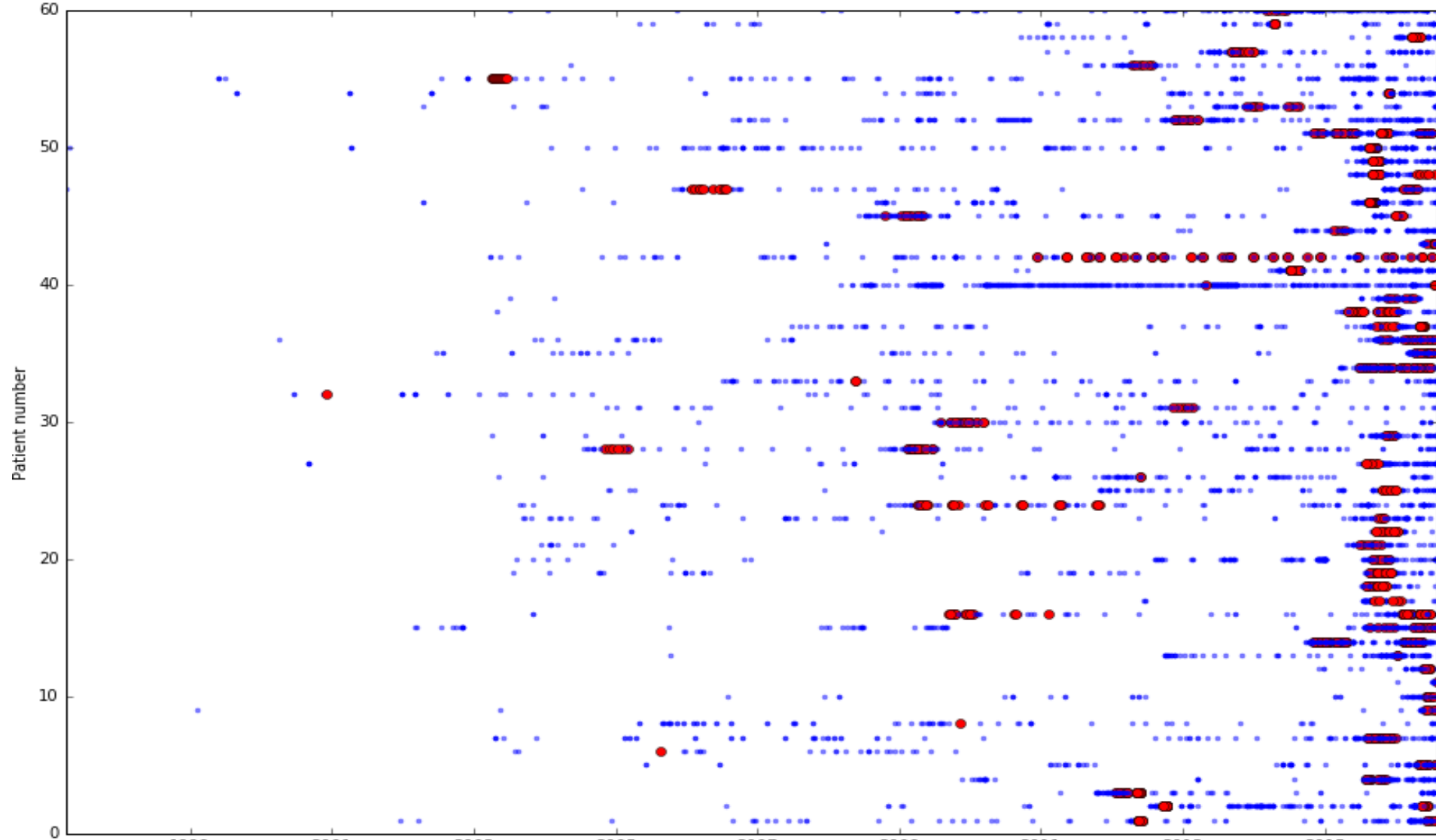
Pan genomic markers 5700 patients 136 actionable genes (Genome Oncology)



Hospital Episodes delving deeper 1997-2005

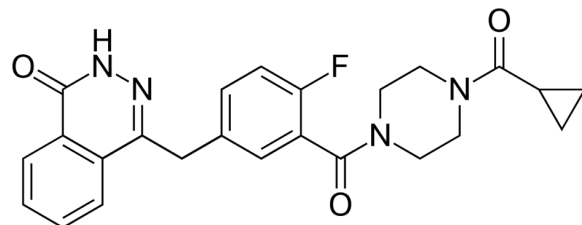
Previous treatment, 61 patients care pathways

- = Cancer treatment
- = Non-Cancer treatment



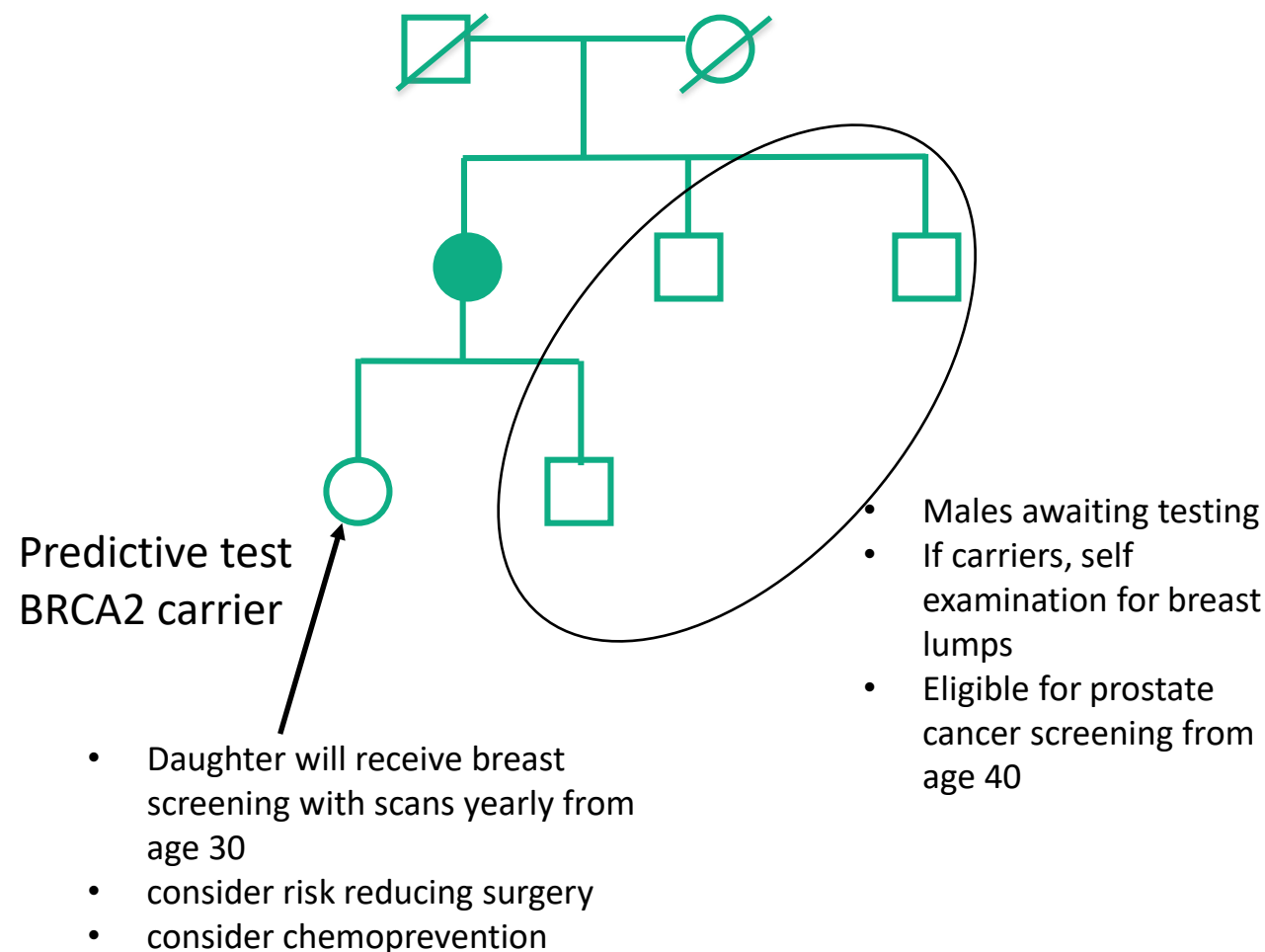
Cancer Case: Implications of result

For the patient



- Targeted therapy with Olaparib through clinical trial (OLYMPIA)
- 1-3/10 women develop ovarian cancer
- Offer risk reducing surgery
- 1 in 2 lifetime chance of left sided breast cancer – requires ongoing screening or consideration of risk reducing surgery

For her family

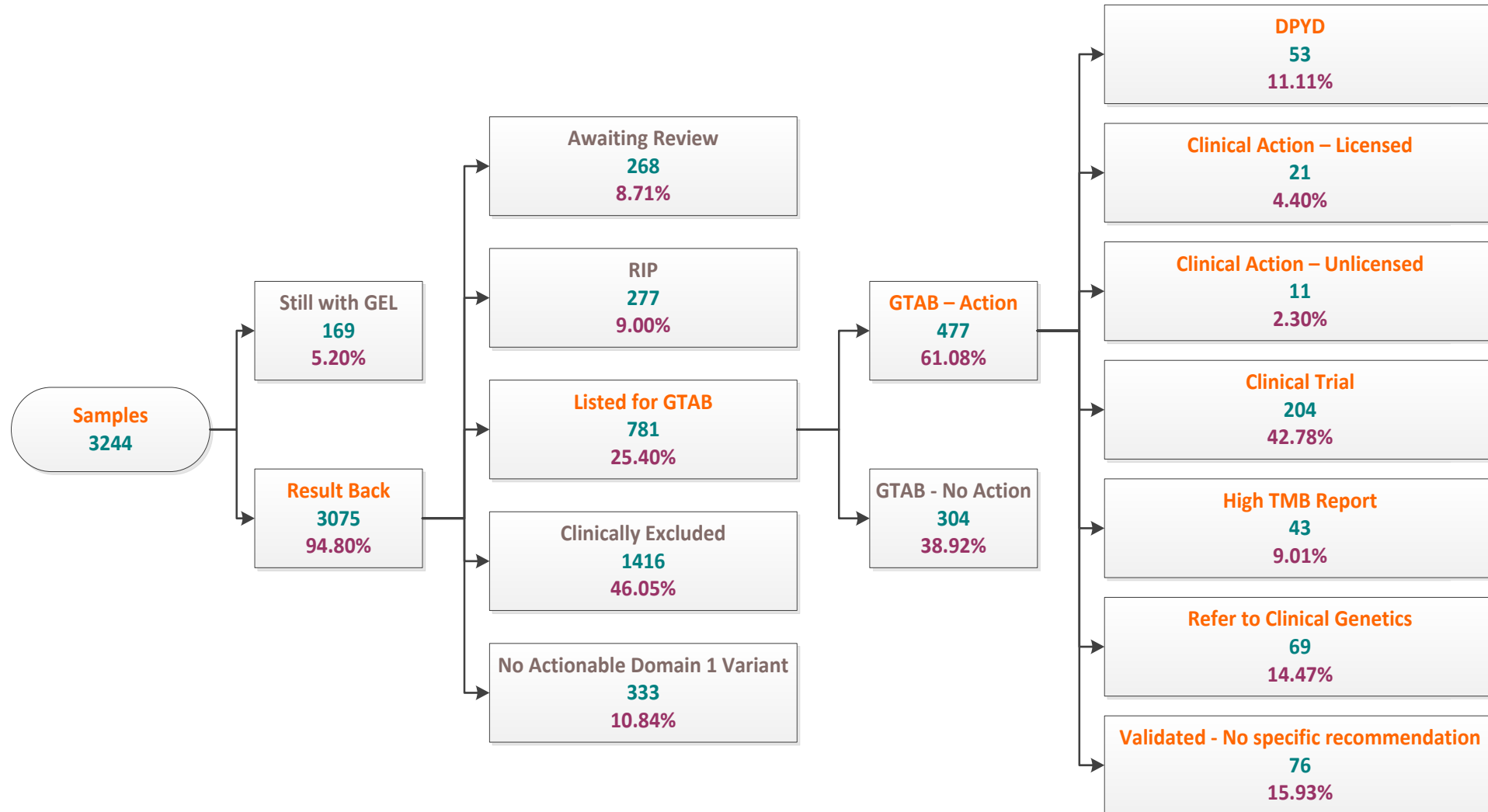


Metastatic Colorectal Case – 42 year old male

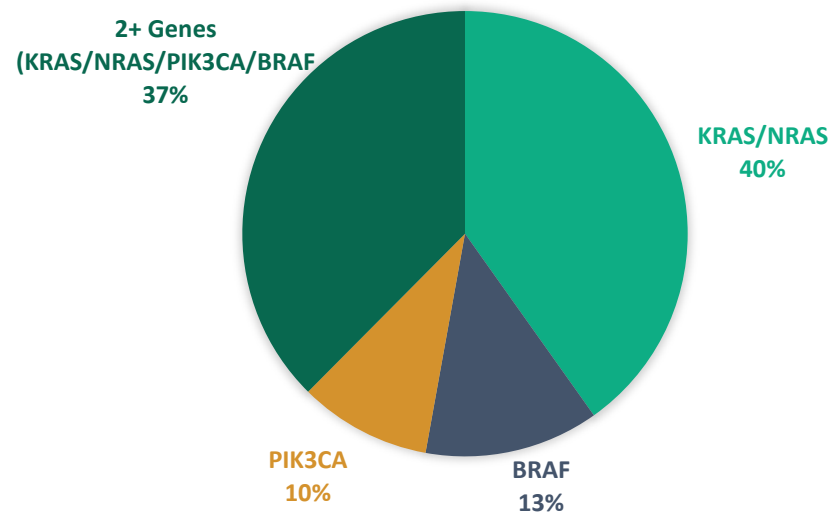
- Past history of well-controlled HIV (off-therapy) and previous Hepatitis B infection
- Weight loss and jaundice
- CT
 - Circumferential sigmoid thickening
 - Liver lesion & possible satellite
 - Nodule
- Sigmoid biopsy
 - Moderately differentiated adenocarcinoma
 - NewGene mutation testing (Usual Care)
 - MSI/MMR not done via NHS (as biopsy)
 - 100K fresh frozen sample sent
- Received 6 cycles of usual chemo but the liver lesion was enlarging liver
- WGS report
 - 83 domain 1 variants including
 - *NRAS* c.175G>A VAF 0.13
 - *KRAS* c.38G>A VAF 0.11
- **Germline *MSH6* mutation**
- Next steps
 - Immunotherapy trials



Genomic Tumour Board – Clinical Utility

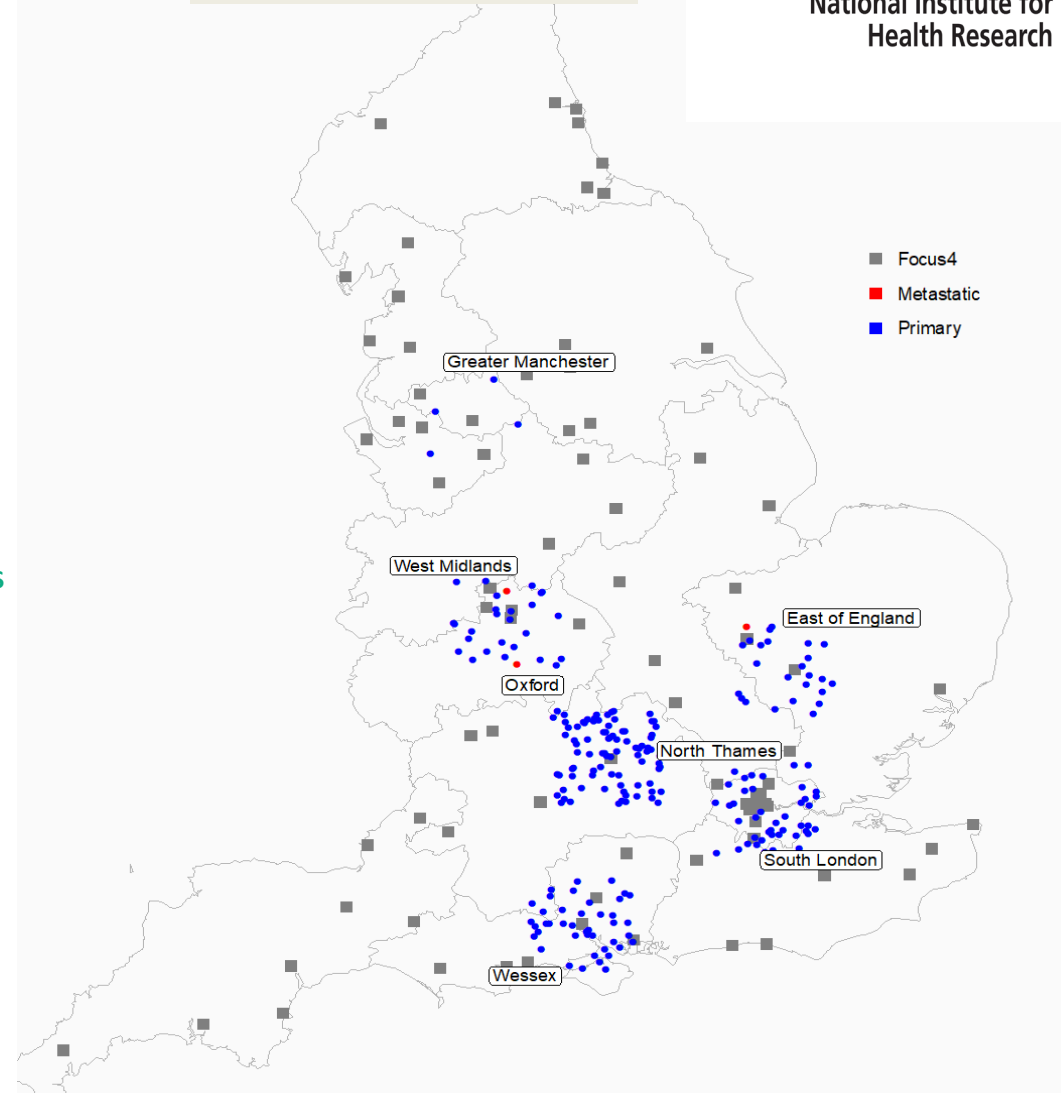


Facilitating recruitment of patients to clinical trials



229 colorectal cancer patients were identified with mutations which could be eligible for FOCUS4 trial, if they were to develop a recurrence

FOCUS-4 Trial



Infections



Infections & Pathogens



The NEW ENGLAND JOURNAL of MEDICINE

ORIGINAL ARTICLE

Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing

The CRyPTIC Consortium and the 100,000 Genomes Project

- 10,000 TB strains sequenced
- WGS correctively predicted drug sensitivity enabling precision care for TB
- NHS implemented TB sequencing for diagnosis (1000 organisms/month)
- Global registry of TB resistance



Clinical Pharmacogenetics International Consortium - actionable allele summary

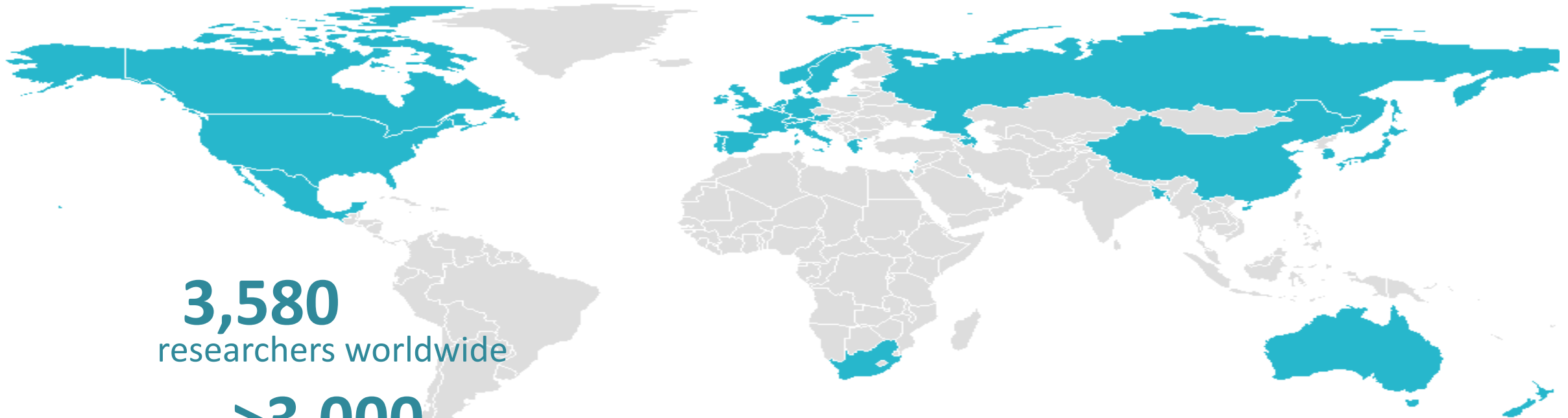


- **CYP2C9 & phenytoin** – 13% (861) have a genotype that could increase toxicity, reduced starting dosage is recommended.
- **CYP2C19 & clopidogrel** – 30% (1988) have a risk genotype for adverse CV events due to lack of efficacy.
- **Warfarin dosing algorithm** – 27% (1789) had a CYP4F2 genotype including *3 (rs2108622 T), 12.5% (828) have a CYP2C9 genotype affecting dosage.
- **CYP3A5 & tacrolimus** – tacrolimus has a narrow therapeutic window; 2% (132) have a genotype that may require higher dose to achieve target INR.
- **DPYD & fluoropyrimidines** – could be at increased risk for severe or even fatal drug toxicity.
- **Testing algorithms for HLA region and CYP2D6**
- 60,000 whole genomes – 100% possess a CPIC actionable gene-drug pair
- Median of 4 gene drug pairs

The Genomics England Clinical Interpretation Partnership



Genomics England Clinical Interpretation Partnership



3,580
researchers worldwide

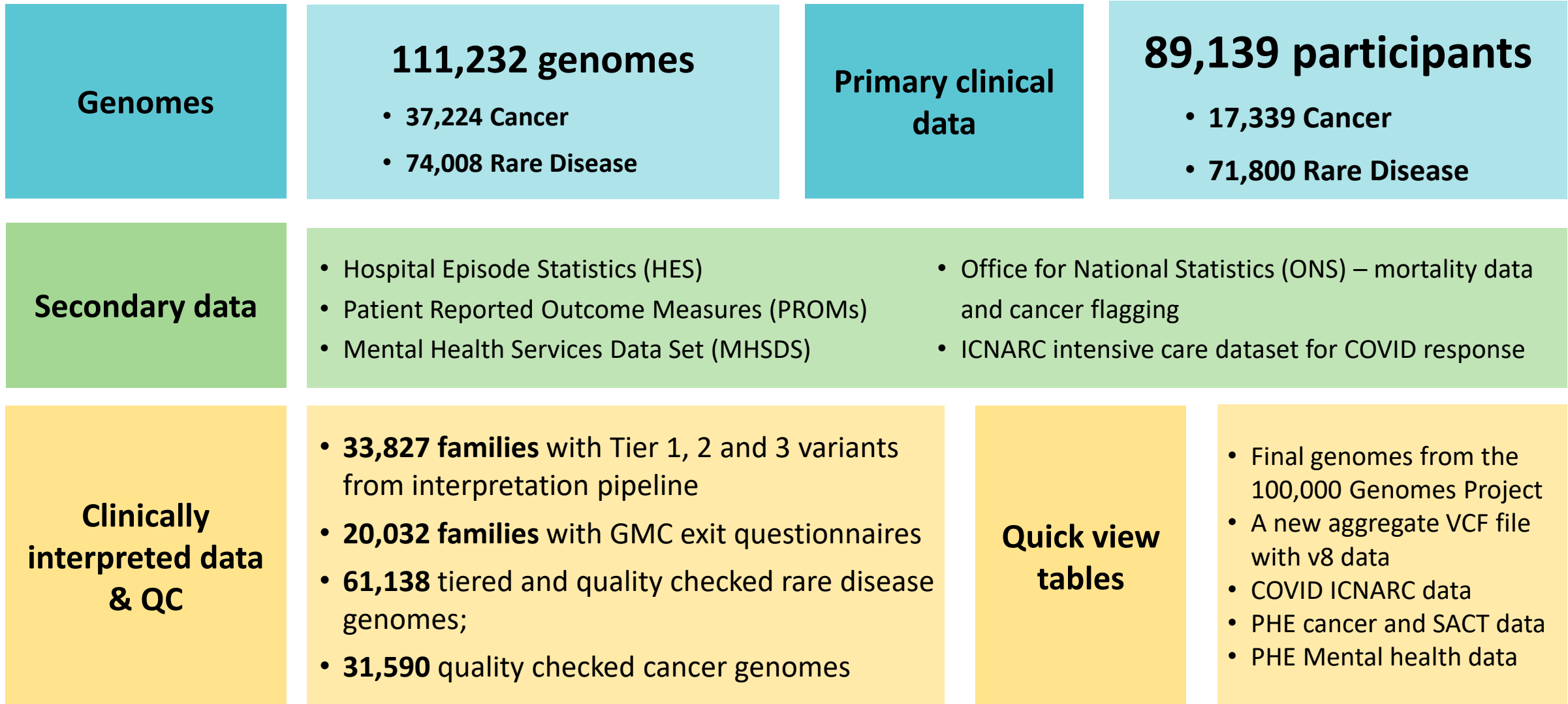
>3,000
researchers with data
access

413 academic institutions

£50 million in grants won

Discovery Forum of 130
companies partnering us to add
value for patients

Genomics England - Sept 2020 release – 3.8 billion clinical data points alongside 111,000 genomes



Primary care datasets – SNOMED Codes and quantitative data under COPI Notice imminent

Transforming healthcare



National Genomic Medicine Service

National Genomic Medicine Service

National Test Directory

300,000 Tests reviewed
25% upgraded to new technologies

21 categories of rare disease

4 Cancers for WGS

More edge cases in cancer

Annual Directory Review

Pharmacogenomics from April 2021

29 January 2021

Genomic Medicine Services Alliances
(announcement pending)

National Laboratory Network
7 Genomic Laboratory Hubs

NHS Lead

National Genomics Research Library

Whole Genome Sequencing Provider

Clinical Interpretation Pipeline

Genomics England Lead

Workforce development
upskilling of existing staff

Industry/ academic/ international partnerships

500,000 whole genomes sequenced from the NHS in the next 5 years

- Offered consent for research
- Longitudinal Life Course
- Recall for research
- International researchers and industry

The range of genomic testing available

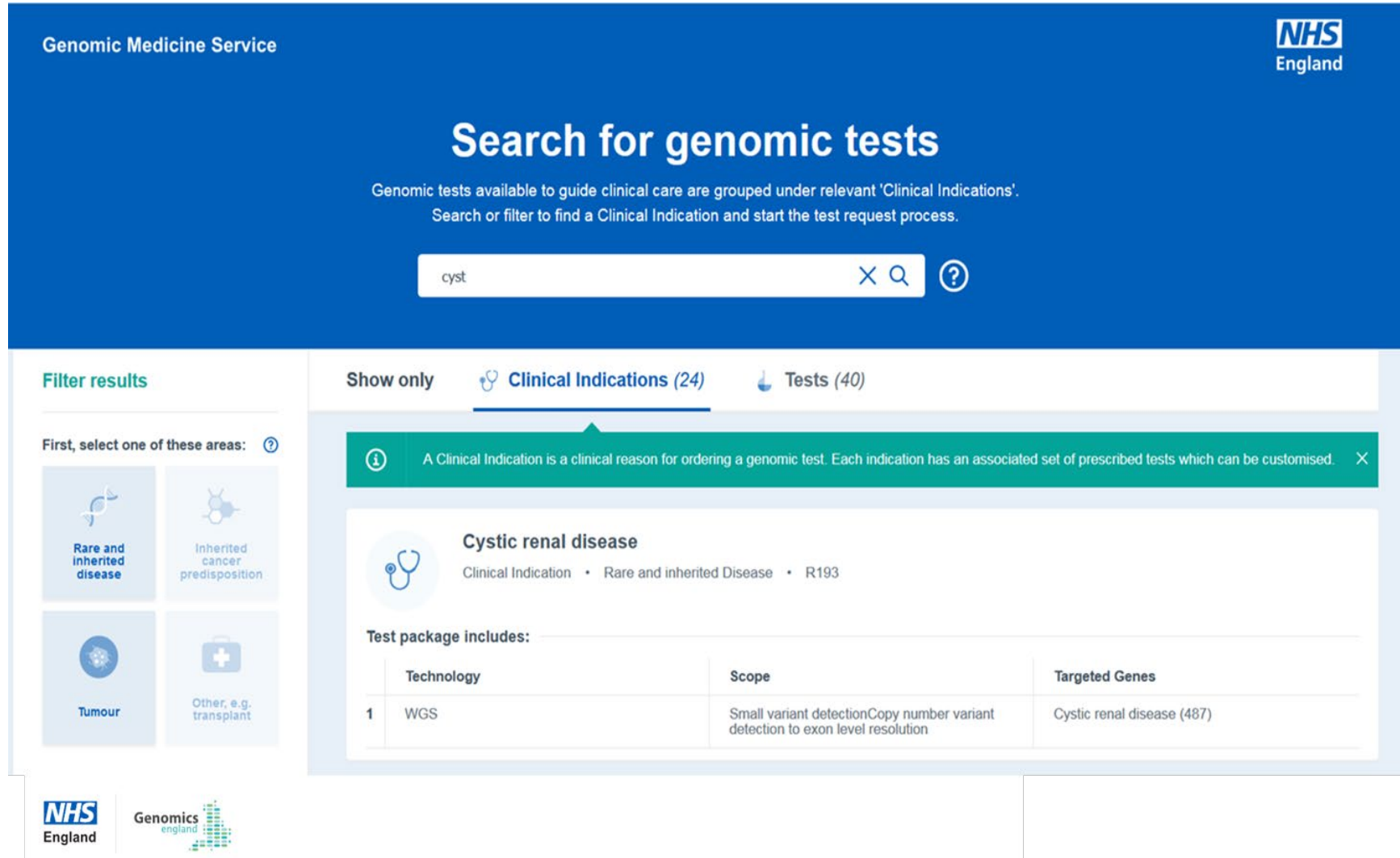


- Test for ~300 rare disease clinical indications and 120 cancer clinical indications identified across 22 test technologies with ~75 panels/subpanels
- Builds upon the substantial evidence base and evaluation by UKGTN since 2003
- The Test Directory identifies core tests provided by all centres together with specialist tests to be provided by a limited number of centres

Cancer
Majority of testing
Pan-solid cancer large panel
Pan-haematological large panel
Paediatrics, Sarcoma - WGS
Smaller volume tests
Single gene tests
Karyotype, FISH
Methylation tests

Rare Disease	Est prop'n of reports
Targeted mutation testing	20-25%
Microarray	10-20%
WGS	10-25%
Small panel	10-15%
STR testing	10-15%
WES or large panel	2-14%
MLPA or equivalent	5-7%
Common aneuploidy testing	5-7%
Karyotype	3-5%
Single gene sequencing	3-5%
FISH; DNA repair defect testing; Methylation testing; UPD testing; X-inactivation testing; Identity testing; Microsatellite instability; NIPT; NIPD; PGD	each <2%
Other	2-5%

A platform for digital genomic health



The screenshot shows the 'Genomic Medicine Service' search interface. At the top, it says 'Search for genomic tests' and provides instructions: 'Genomic tests available to guide clinical care are grouped under relevant 'Clinical Indications'. Search or filter to find a Clinical Indication and start the test request process.' A search bar contains the text 'cyst'. Below the search bar, there are filters for 'Clinical Indications (24)' and 'Tests (40)'. A sidebar on the left offers filters for 'Rare and inherited disease', 'Inherited cancer predisposition', 'Tumour', and 'Other, e.g. transplant'. A notification banner states: 'A Clinical Indication is a clinical reason for ordering a genomic test. Each indication has an associated set of prescribed tests which can be customised.' The main content area displays 'Cystic renal disease' as a Clinical Indication, categorized under 'Rare and inherited Disease' with ID 'R193'. Below this, a table lists the test package details.

	Technology	Scope	Targeted Genes
1	WGS	Small variant detection Copy number variant detection to exon level resolution	Cystic renal disease (487)

Genetic mechanisms in severe COVID 19 illness

4
3

Kenneth Baillie

- 2224 severe COVID-19 cases from 209 ITUs genotyped matched controls and cases from Biobank UK, GEL, International collaboration

Patient Characteristics	GenOMICC (n=2109)	ISARIC 4C (n=134)		
	<i>missing data</i>	<i>missing data</i>		
Female sex	624 (30%)	46 (34%)		
Age (yrs, mean \pm SD)	57.3 \pm 12.1	57.3 \pm 2.9		
European ancestry	1573 (75%)	103 (76%)		
South Asian ancestry	219 (10%)	18 (13%)		
African ancestry	174 (8%)	8 (6%)		
East Asian ancestry	143 (7%)	6 (4%)		
Significant comorbidity	396 (19%)	42 (28%)	31 (21%)	
Invasive ventilation	1557 (74%)	35 (2%)	25 (19%)	31 (23%)
Died (60 days)	459 (22%)	338 (16%)	22 (16%)	30 (22%)



CHIEF
SCIENTIST
OFFICE

Genomics
england



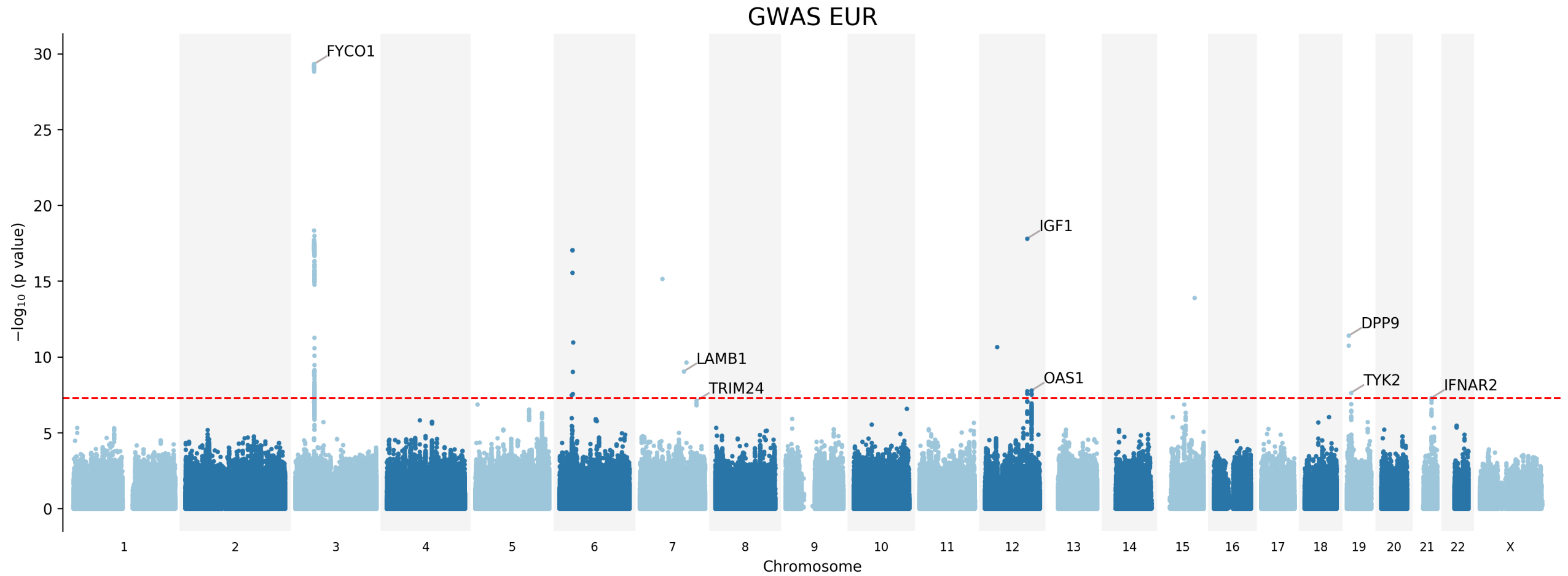
GenOMiCC



UK Research
and Innovation



wellcome




GenOMICC first paper published in Nature 2020

- **7 genome wide significant loci detected**
- **3 potential therapies**
 - Interferon 2 Receptor – potential target interferon
 - Tyrosine kinase 2 – Jak1/Jak 2 inhibitors used in cancer
 - e.g. Baracitinib
 - CCR2 – biologic tested in rheumatoid arthritis and psoriasis

The Public and Patients at the heart of the Programme



Public views of key behaviours
in the social contract now

 Public don't understand how research ecosystem works / feeds clinical care

Genetic manipulation



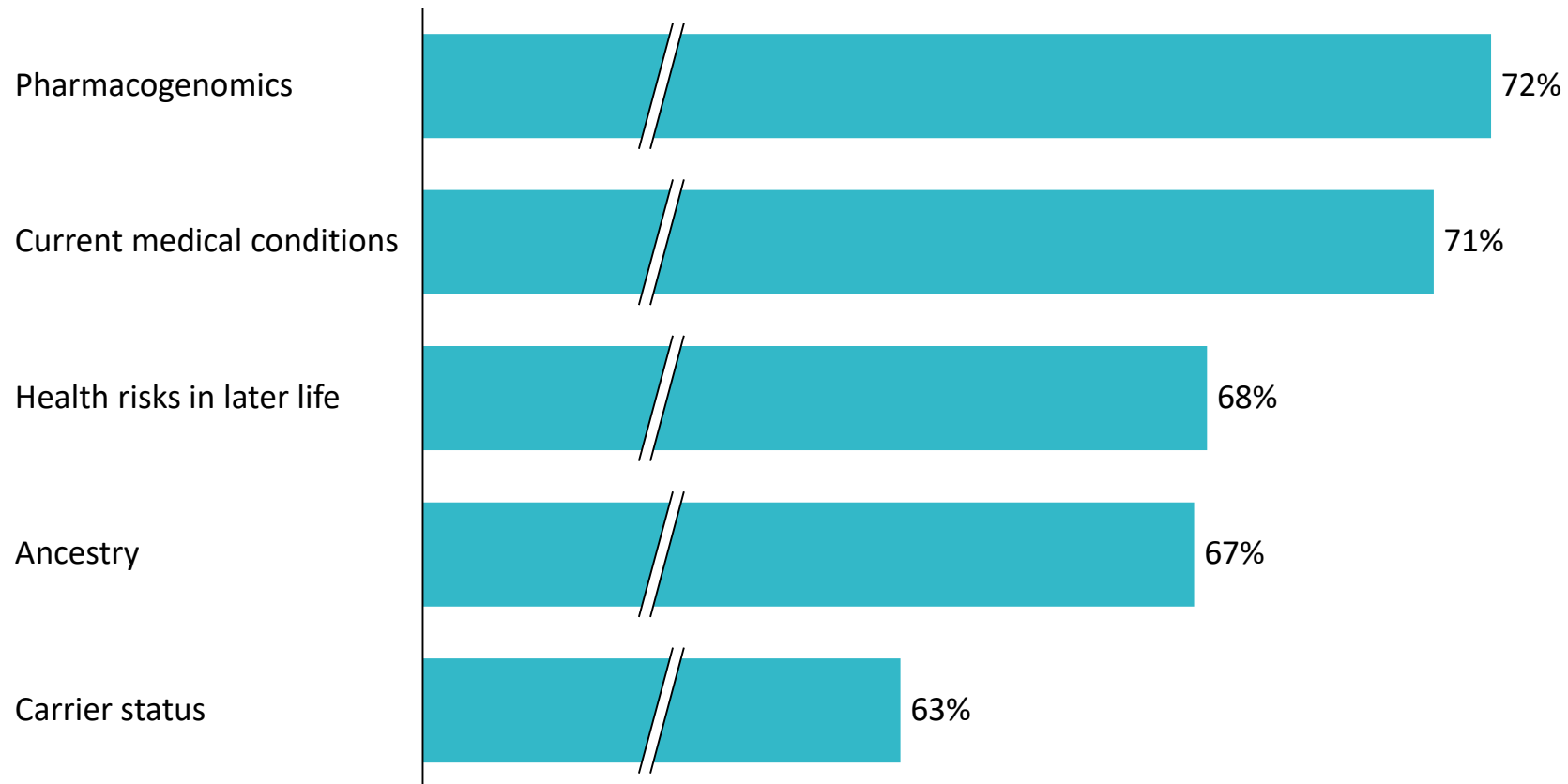
Commercial uses for healthcare

 Commercial interests aren't spontaneously seen as part of the system

No surveillance society

Public survey showed significant interest in receiving personalised genomic results as Genomic Volunteers

Proportion of respondents interested in personally receiving specific genomic results



Source: Ipsos-Mori survey of the public perspectives of genomic volunteers. Electronic survey of 1,866 people (selected to be a representative sample of adults aged 16 – 75 across England)



HM Government

GENOME UK
The future of healthcare



Diversity
Genomics
and PGX

Cancer 2.0

Not in scope
of this SR bid

PRS
Common
Diseases

GEL Core
Funding inc. NHS
Informatics

Rare Disease
Diagnoses from
WGS

NHSE/I
Genomics
services
*Funded via core
NHS budget*

Newborns
“Generation
Genome”
Early diagnosis
1 in 190 births
9 children
every day

Future – UK Life Sciences Strategy

- International Partnerships with
- France, Australia, Hong Kong, Qatar, British Columbia, Japan

Multi-omics and new technologies

- Long read technologies
- cftDNA
- Transcriptomics
- Multi-omics
- Standardisation
- Other disease areas
- Population cohorts





The National Health Service will have:

- A national Genomic Medicine Service providing consistent & equitable care for 55 million population
- Operating to common national standards, specifications & protocols
- Standardised genomic consent for NHS care and Research
- Delivering an approved national testing directory covering use of single gene to WGS
- Building a single UK Genomic Knowledgebase
- national NHS database with all tests that will enable care, effectiveness, and outcomes
- De-identified data for academic & industry research
- An ambition for 5 Million Genomic Tests & Early Detection Cohorts
- The future is a global coalition of intellects driving genomics into healthcare and our goal is for the UK to be at the heart of that



Thank you to everyone who has taken part in the 100,000 Genomes Project



Stay in touch



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@genomicsengland #genomes100k



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UK Precision Medicine – Life Sciences Strategy

	Diagnosis and Precision Care		Prevention	Research
Key UK Infrastructure:	The 100,000 Genomes Project and Genomic Testing in the NHS		Accelerating Detection of Disease	UK Biobank
Population	100,000 participants with rare diseases and cancer	Genomic testing across the UK includes 500,000 WGS by 2024.	5 million healthy people at the time of recruitment	500,000 participants healthy at the time of recruitment
Genomic data	Whole Genome Sequencing	Whole Genome Sequencing and non-whole genome sequencing	Genotyping – Polygenic Risk Scores	Genotyping Whole Exomes and Whole Genome Sequencing
Complementary data	Phenotypic and long-term clinical data	Phenotypic and long-term clinical data collection	Health-related data	Deep phenotyping and health-related data
Bio-sampling	✓	✓	✓	✓
Clinical feedback	✓	✓	✓	✗
Recontact	✓	✓	✓	✓
UK Wide	✓	✓	✓	✓