The 100,000 Genomes Project
Transforming Healthcare

Berlin Institute of Health

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Chief Scientist

William Harvey Research Institute
Queen Mary University of London
Disclosures

• 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

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

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

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

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

29 January 2021
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
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

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
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/

**Genomics England PanelApp**
A crowdsourcing tool to allow gene panels to be shared, downloaded, viewed and evaluated by the Scientific Community.

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

### Step 1
**Creation of initial gene panel for each disorder**

### Step 2
**Crowdsourcing of Expert Knowledge**

### Step 3
**Consolidation of reviews & further curation**

Use other resources to verify reviews:
- OMIM
- Gene2Phenotype
- Orphanet
- ClinGen
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
NHS Reporting portal

View family pedigree

Download the report

Review variants and close case
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

<table>
<thead>
<tr>
<th>Dataset</th>
<th>Number of episodes</th>
<th>Total cost</th>
</tr>
</thead>
<tbody>
<tr>
<td>Critical care</td>
<td>347</td>
<td>£387,085</td>
</tr>
<tr>
<td>Accident and Emergency care</td>
<td>16,696</td>
<td>£2,530,399</td>
</tr>
<tr>
<td>Inpatient care</td>
<td>43,714</td>
<td>£77,276,982</td>
</tr>
<tr>
<td>Outpatient care</td>
<td>177,125</td>
<td>£26,243,354</td>
</tr>
<tr>
<td><strong>TOTAL</strong></td>
<td><strong>237,882</strong></td>
<td><strong>£106,437,820</strong></td>
</tr>
</tbody>
</table>

$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
Cancer Patients by Tumour Type

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

Cancer stage
1
2
3
4

North East and Cumbria
North West Coast
North Thames
West London
South London
Yorkshire and Humber
West Midlands
East of England
West of England
Oxford
Wessex
South West Peninsula

All centres
31%
27%
34%
8%
Pan genomic markers 5700 patients 136 actionable genes (Genome Oncology)

High Mutational Tumour Burden

Higher tumour immunogenicity

Greater anti-tumour response to immunotherapies
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**

- Predictive test: BRCA2 carrier
  - Daughter will receive breast screening with scans yearly from age 30
  - consider risk reducing surgery
  - consider chemoprevention

- Males awaiting testing
  - If carriers, self examination for breast lumps
  - Eligible for prostate cancer screening from age 40
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

 Samples 3244

 Still with GEL 169 5.20%

 Result Back 3075 94.80%

 Awaiting Review 268 8.71%

 RIP 277 9.00%

 Listed for GTAB 781 25.40%

 Clinically Excluded 1416 46.05%

 No Actionable Domain 1 Variant 333 10.84%

 GTAB – Action 477 61.08%

 GTAB - No Action 304 38.92%

 DPYD 53 11.11%

 Clinical Action – Licensed 21 4.40%

 Clinical Action – Unlicensed 11 2.30%

 Clinical Trial 204 42.78%

 High TMB Report 43 9.01%

 Refer to Clinical Genetics 69 14.47%

 Validated - No specific recommendation 76 15.93%
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.
Infections
Infections & Pathogens

- 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

<table>
<thead>
<tr>
<th>Genomes</th>
<th>Primary clinical data</th>
<th>89,139 participants</th>
</tr>
</thead>
<tbody>
<tr>
<td>111,232 genomes</td>
<td>• 37,224 Cancer</td>
<td>• 17,339 Cancer</td>
</tr>
<tr>
<td>• 74,008 Rare Disease</td>
<td></td>
<td>• 71,800 Rare Disease</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Secondary data</th>
<th>Quick view tables</th>
</tr>
</thead>
<tbody>
<tr>
<td>• Hospital Episode Statistics (HES)</td>
<td>• Final genomes from the 100,000 Genomes Project</td>
</tr>
<tr>
<td>• Patient Reported Outcome Measures (PROMs)</td>
<td>• A new aggregate VCF file with v8 data</td>
</tr>
<tr>
<td>• Mental Health Services Data Set (MHSDS)</td>
<td>• COVID ICNARC data</td>
</tr>
<tr>
<td></td>
<td>• PHE cancer and SACT data</td>
</tr>
<tr>
<td></td>
<td>• PHE Mental health data</td>
</tr>
</tbody>
</table>

Clinically interpreted data & QC

- 33,827 families with Tier 1, 2 and 3 variants from interpretation pipeline
- 20,032 families with GMC exit questionnaires
- 61,138 tiered and quality checked rare disease genomes;
- 31,590 quality checked cancer genomes

Quick view tables

- 89,139 participants
  - 17,339 Cancer
  - 71,800 Rare Disease

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

**Genomic Medicine Services Alliances** (announcement pending)

**National Laboratory Network**
- 7 Genomic Laboratory Hubs

**National Genomics Research Library**

**Whole Genome Sequencing Provider**

**Clinical Interpretation Pipeline**

**Workforce development**
- upskilling of existing staff

**Industry/ academic/ international partnerships**

**Whole Genome Sequencing Provider**

**Clinical Interpretation Pipeline**

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

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

<table>
<thead>
<tr>
<th>Cancer</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Majority of testing</strong></td>
</tr>
<tr>
<td>Pan-solid cancer large panel</td>
</tr>
<tr>
<td>Pane-haematological large panel</td>
</tr>
<tr>
<td>Paediatrics, Sarcoma - WGS</td>
</tr>
<tr>
<td><strong>Smaller volume tests</strong></td>
</tr>
<tr>
<td>Single gene tests</td>
</tr>
<tr>
<td>Karyotype, FISH</td>
</tr>
<tr>
<td>Methylation tests</td>
</tr>
</tbody>
</table>
National Genomics Informatics Service

A platform for digital genomic health
Genetic mechanisms in severe COVID-19 Illness
Kenneth Baillie

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

<table>
<thead>
<tr>
<th>Patient Characteristics</th>
<th>GenOMICC (n=2109)</th>
<th>ISARIC 4C (n=134)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Female sex</td>
<td>624 (30%)</td>
<td>46 (34%)</td>
</tr>
<tr>
<td>Age (yrs, mean ± SD)</td>
<td>57.3 ± 12.1</td>
<td>57.3 ± 2.9</td>
</tr>
<tr>
<td>European ancestry</td>
<td>1573 (75%)</td>
<td>103 (76%)</td>
</tr>
<tr>
<td>South Asian ancestry</td>
<td>219 (10%)</td>
<td>18 (13%)</td>
</tr>
<tr>
<td>African ancestry</td>
<td>174 (8%)</td>
<td>8 (6%)</td>
</tr>
<tr>
<td>East Asian ancestry</td>
<td>143 (7%)</td>
<td>6 (4%)</td>
</tr>
<tr>
<td>Significant comorbidity</td>
<td>396 (19%)</td>
<td>49 (2%)</td>
</tr>
<tr>
<td>Invasive ventilation</td>
<td>1557 (74%)</td>
<td>35 (2%)</td>
</tr>
<tr>
<td>Died (60 days)</td>
<td>459 (22%)</td>
<td>338 (16%)</td>
</tr>
</tbody>
</table>
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

**Reciprocity**
- Turn up to appointments, don’t waste resources, appreciate value of care
- Collect taxes; manage and deliver service efficiently
- Provide best, evidence-based care; patient data used for clinical care only

**Altruism**
- Choose to benefit others e.g. blood donation, participate in health research (if explained)
- Provide services that are free at point of delivery and not based on citizenship e.g. emergency care

**Solidarity**
- Accept progressive taxation and comply with healthy lifestyle advice to reduce public health burden
- Triage across whole system to allocate resource based on need and to balance books
- Treat all equally and with respect

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Commercial uses for healthcare

Genetic manipulation

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 |
|---------------------------------|------------------|
| Pharmacogenomics                | 72%              |
| Current medical conditions      | 71%              |
| Health risks in later life      | 68%              |
| Ancestry                        | 67%              |
| Carrier status                  | 63%              |

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)
Diversity Genomics and PGX

GEL Core Funding inc. NHSInformatics
Rare Disease Diagnoses from WGS

Cancer 2.0

PRS Common Diseases

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

NHSE/I Genomics services
Funded via core NHS budget

Not in scope of this SR bid
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

Email Mark Caulfield
m.j.caulfield@qmul.ac.uk

@genomicsengland  #genomes100k

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www.genomicsengland.co.uk
# UK Precision Medicine – Life Sciences Strategy

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