

# Use of phenotype data to obtain novel insights into disease causes and mechanisms

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# Overview



- Introduction to the 100,000 Genomes Project
- Role of clinical and model organism phenotypes
  - Clinical data collection and panel assignment
  - Automated variant prioritisation
  - Precision mouse models for validation and functional characterisation of the variants

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# The 100,000 Genomes Project



**100,000** genomes



**70,000** 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  
**85** NHS Trusts within them are involved in recruiting participants



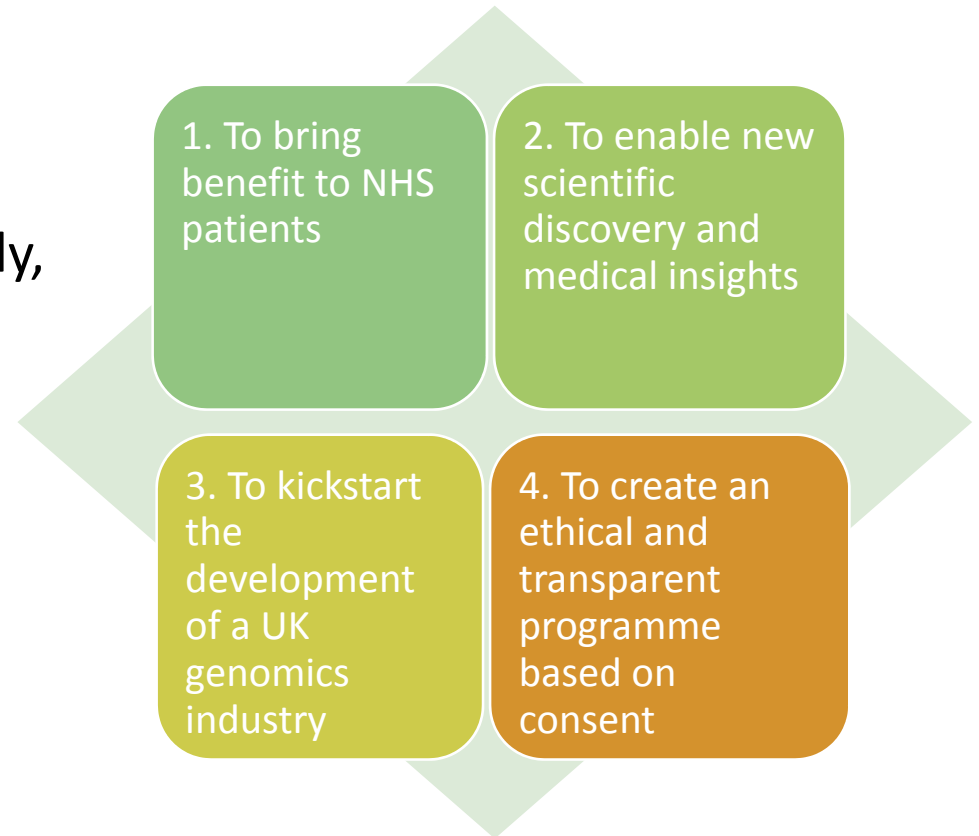
**1,500** NHS staff  
(doctors, nurses, pathologists, laboratory staff, genetic counsellors)



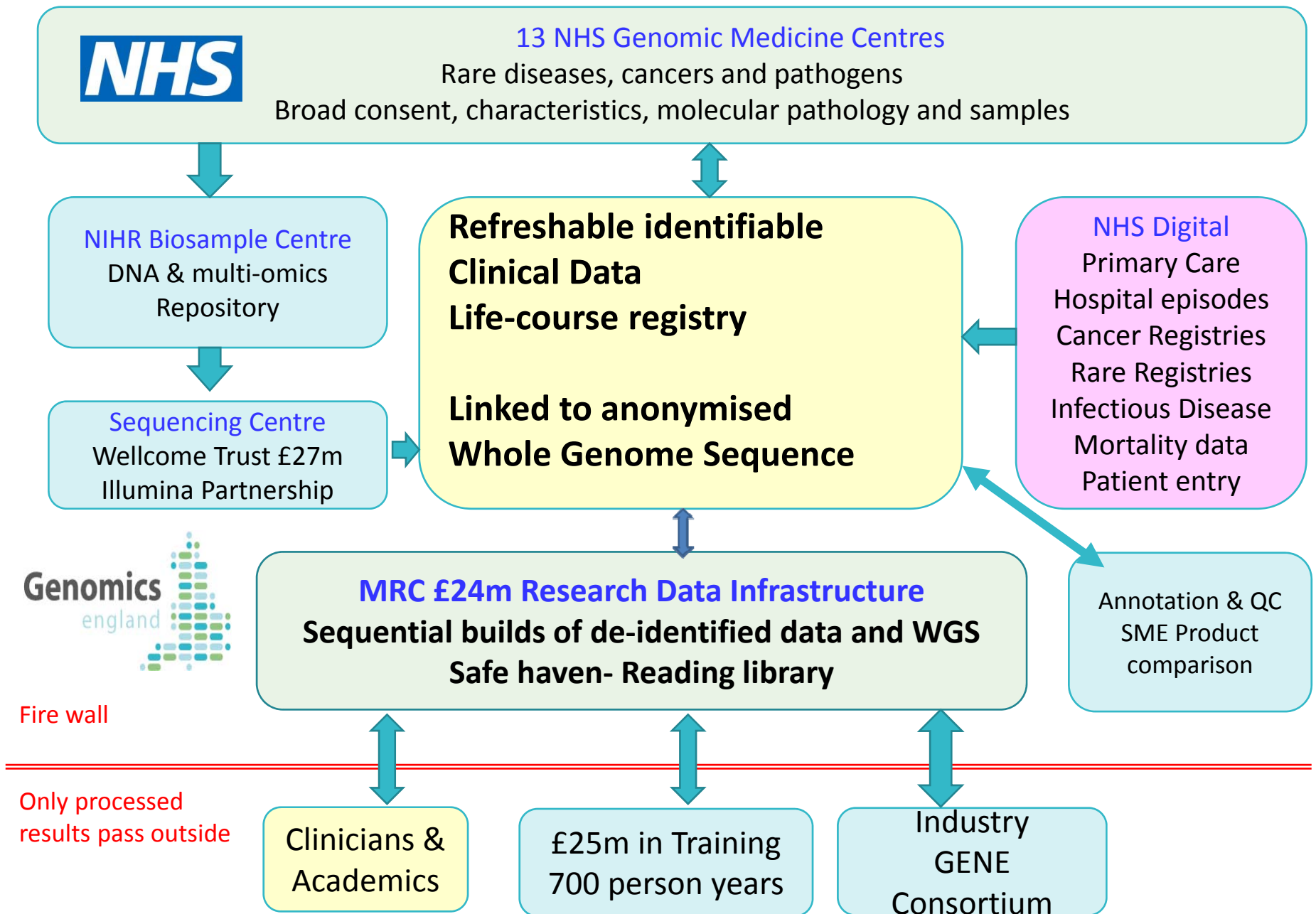
**2,500** researchers and trainees from around the world

# Goals of the Genomics England project

- Sequence 100,000 genomes
- Cancer and rare genetic disease
- Capture data delivered electronically, store it securely and analyse it within an English data centre (reading library)
- Combine genomes with extracted clinical information for analysis, interpretation, and aggregation
- Create capacity, capability and legacy in personalised medicine for the UK



# Organisation of the 100,000 Genomes Project



# GeCIP Domains



## Rare

- Cardiovascular
- Endocrine and Metabolism
- Gastroenterology and Hepatology
- Hearing and Sight
- Immunology and Haematology
- Inherited Cancer Predisposition
- Musculoskeletal
- Neurological
- Paediatric Sepsis
- Paediatrics
- Renal
- Respiratory
- Skin

## Cancer

- Adult Glioma
- Bladder
- Breast
- Colorectal & upper
- Lung
- Melanoma
- Renal Cell
- Sarcoma
- Testis
- Ovarian
- Prostate
- Childhood Solid Cancers
- Haematological Malignancy
- Pan Cancer
- (Ca of) Unknown primary

## Functional

- Electronic Health Records
- Validation and Feedback
- Ethics and Social Science
- Functional Effects
- Health Economics
- Machine Learning, Quantitative Methods and Functional Genomics
- Population Genomics
- Enabling Rare Disease Translational Genomics via Advanced Analytics and International Interoperability
- Functional Cross Cutting
- Education and Training
- Stratified Medicine & Pharmacogenomics

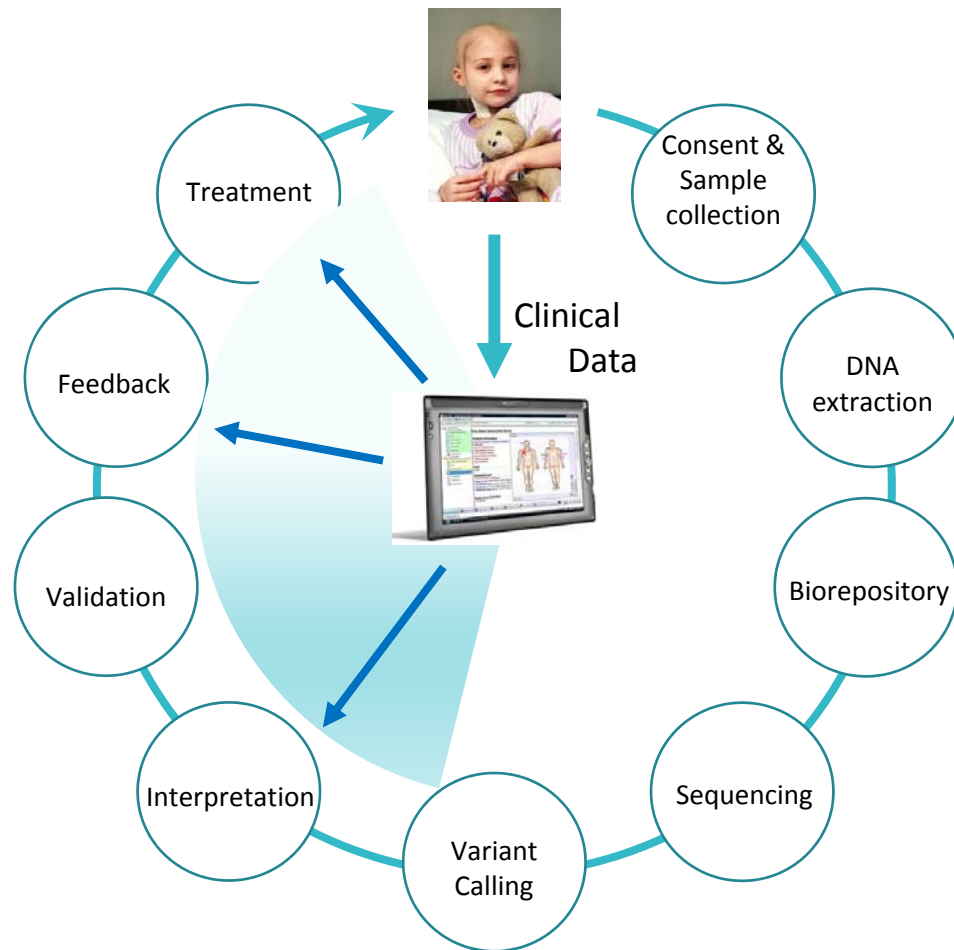
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# Genomics England is about helping complete the cycle



- Treatment cycle for just one patient requires a complex chain of operations
- Most of these operations have not been designed or optimised for the purposes of Genomic Medicine.
- So the task is one of catalysing a **Transformation** in Medical Practice, particularly relating to routine use of coordinated data.
- To achieve this one needs to develop/adopt **standards** across the system

# Developing a clinical data capture system for RD genome diagnostics

Genomics  
england

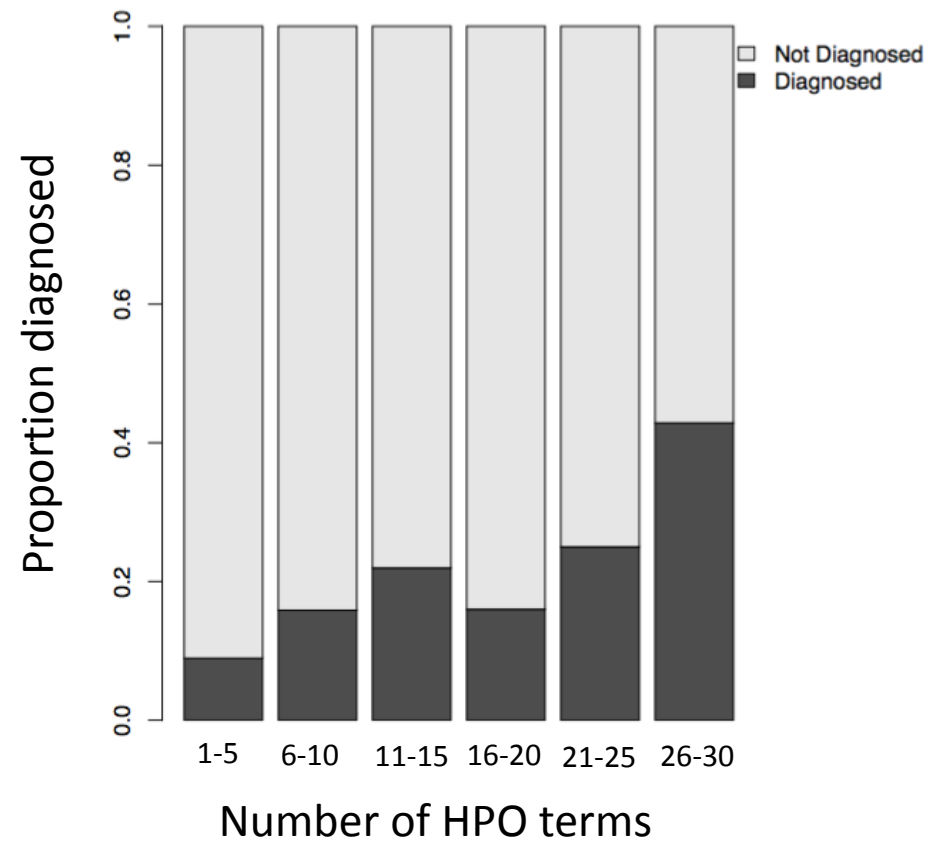
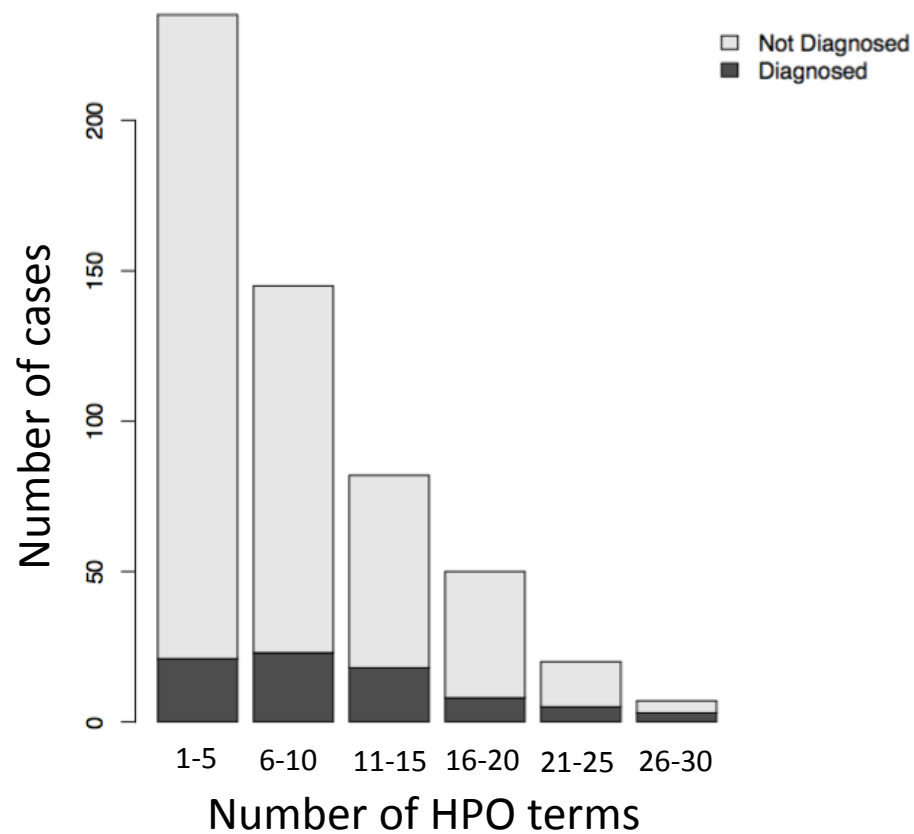


Standardised clinical data questionnaire forms

- OpenClinica or their own systems exporting in XML schemas
- Defined HPO terms for each disease category; collect positive and negative and additional terms

Disease							
1	Disease Group	Renal and urinary tract disorders					
2	Disease Subgroup	Syndromes with prominent renal abnormalities					
3	Specific disease	Alport syndrome					
Basic Phenotyping							
4	Phenotype Description	5	Phenotype Identifier	7	Phenotype Present	Modifiers	Actions
	Proteinuria		HP:0000093		<input checked="" type="radio"/> Unknown <input type="radio"/> Yes <input type="radio"/> No		Edit
	Hematuria		HP:0000790		<input checked="" type="radio"/> Unknown <input type="radio"/> Yes <input type="radio"/> No		Edit
	Nephrotic range proteinuria		HP:0012593		<input checked="" type="radio"/> Unknown <input type="radio"/> Yes <input type="radio"/> No		Edit
	Renal insufficiency		HP:0000083		<input checked="" type="radio"/> Unknown <input type="radio"/> Yes <input type="radio"/> No		Edit

# Diagnostic rate for trios

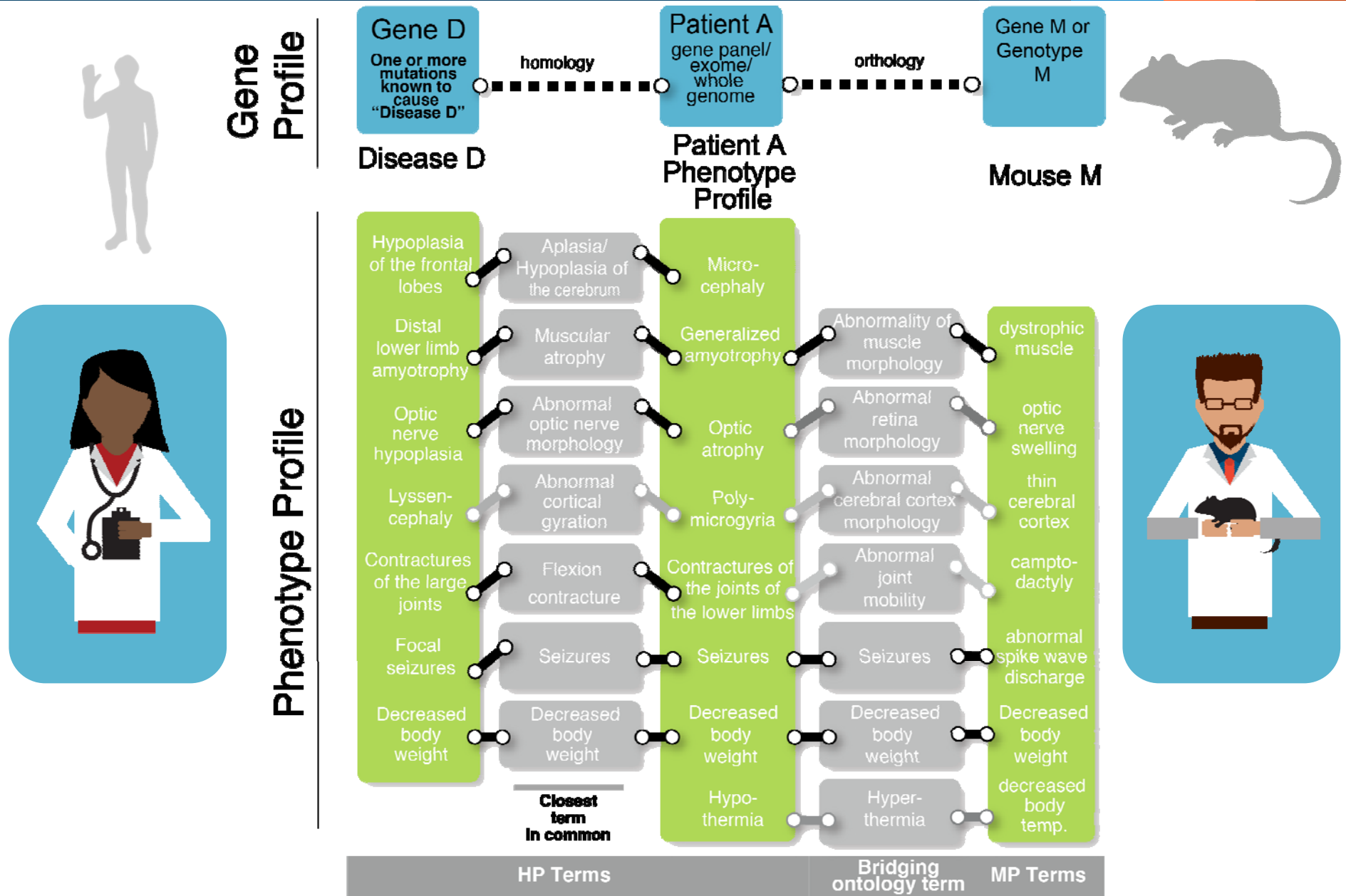


# Overview

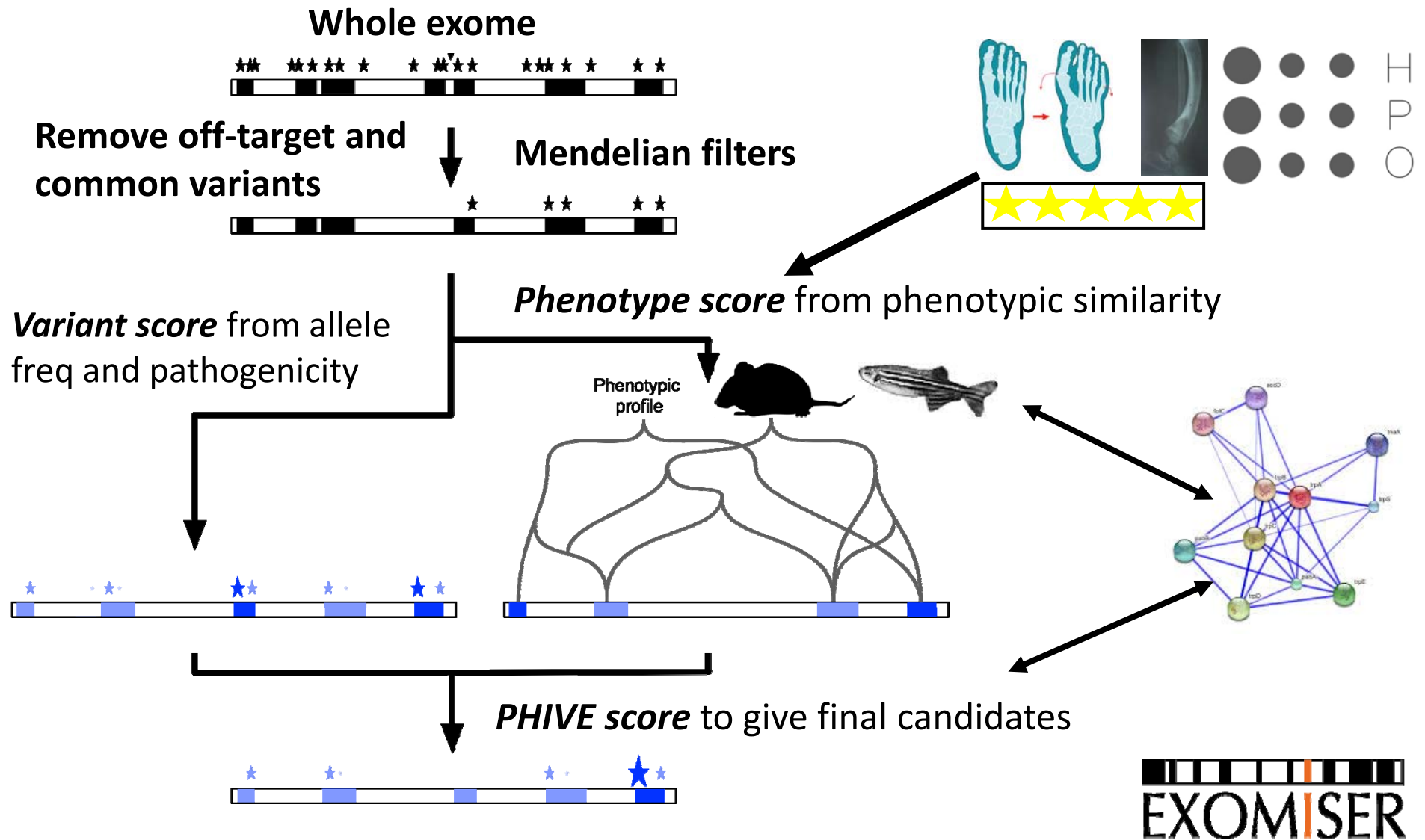


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# Precision fuzzy phenotype matching

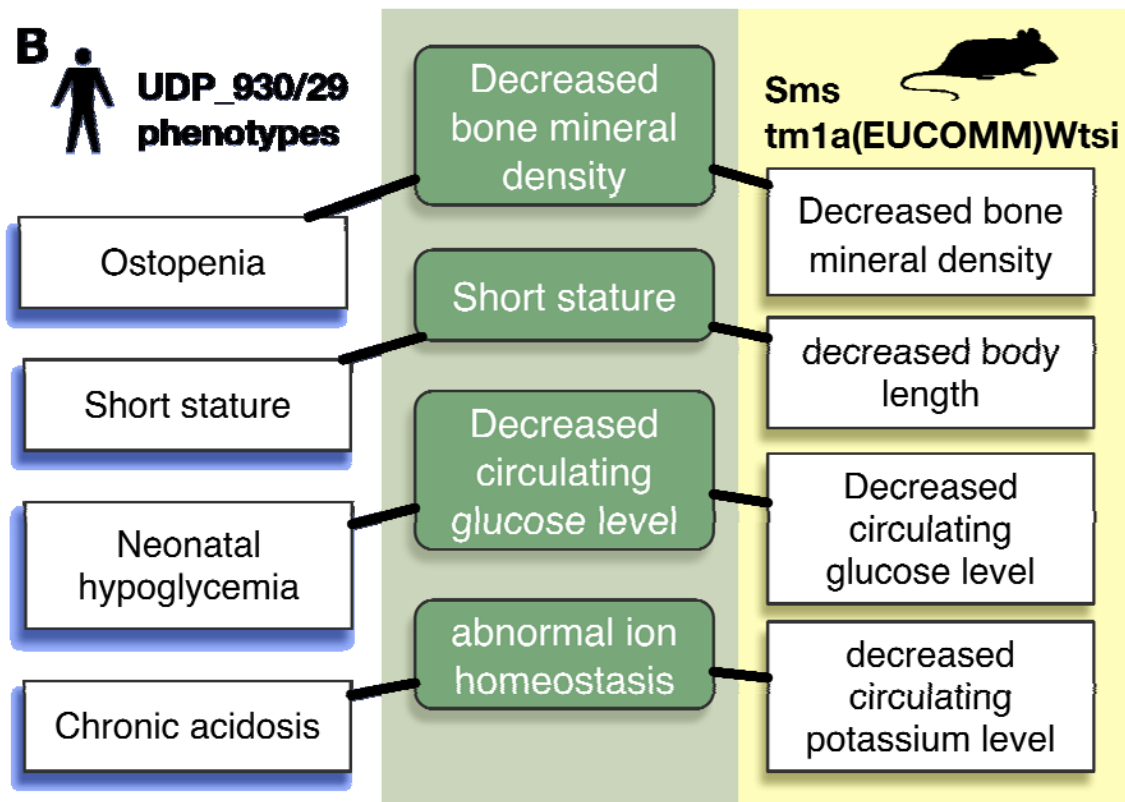


# Combining G2P data for variant prioritization

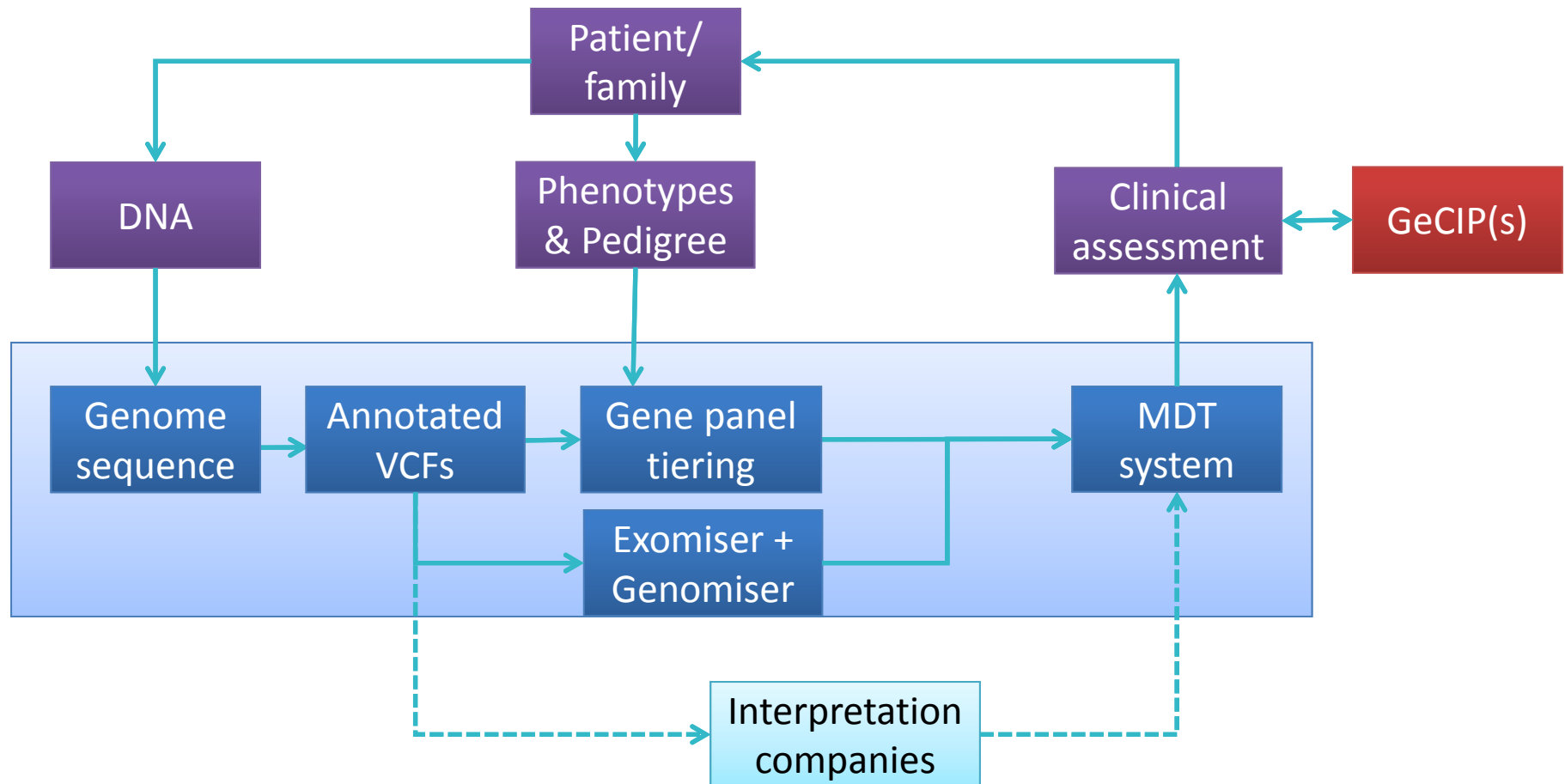


# Exomiser software suite

- **How-To guide:** Smedley D et al *Nature Protocols* 2015 **10**(12):2004-15.
- **Exomiser:** Robinson PN et al. *Genome Research* 2014. **24**(2):340-8.
- **Genomiser:** Smedley D et al. *Am J Hum Genet.* 2016. **99**(3):595-606.
- **Undiagnosed Disease Program:** Bone W et al. *Genetics in Medicine* 2015.

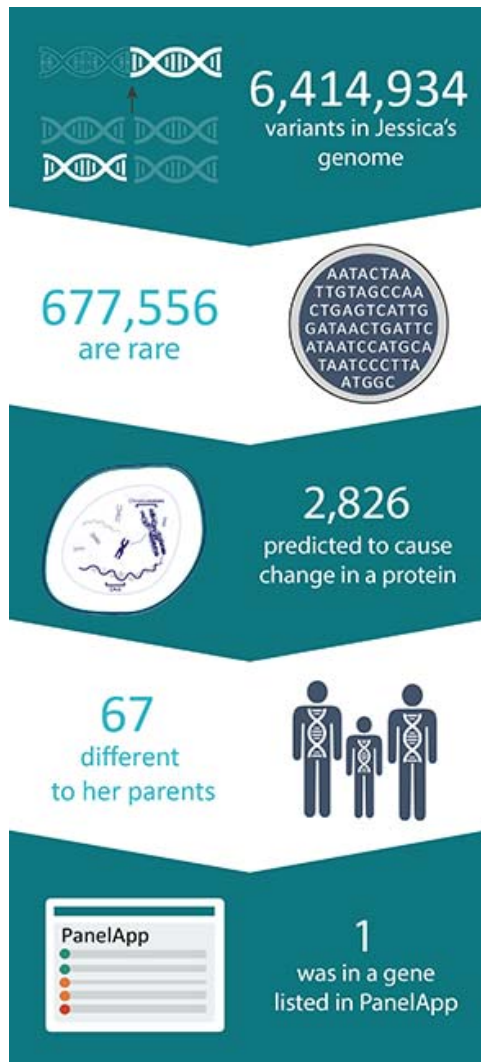


# Scalable rare disease diagnostics





# First families diagnosed

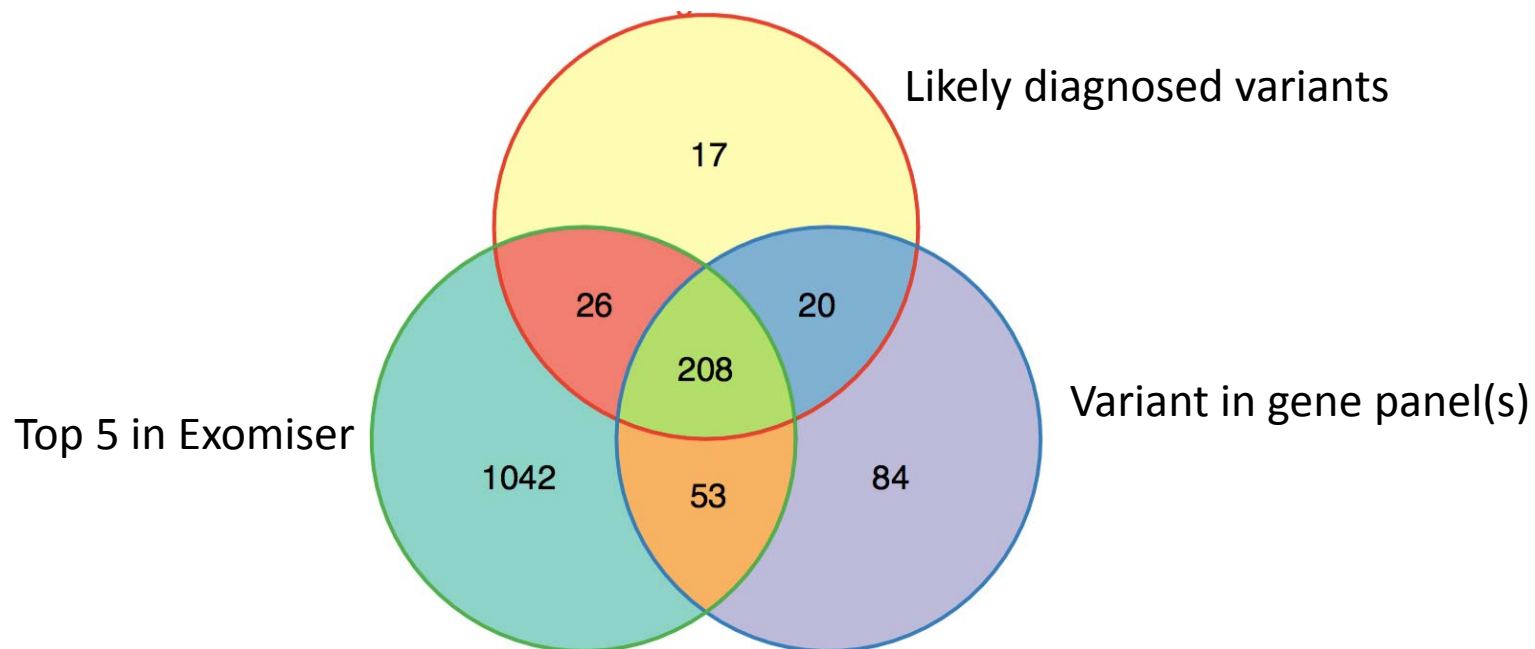


- Jessica (aged 4) has a rare condition which causes epilepsy, affects her movement and developmental delay. Standard genetics tests negative.
- De novo deletion in *SLC2A1* identified as the cause of her Glut 1 deficiency syndrome
- Now being successfully treated with a a ketogenic, low-carb diet
- Low risk for future pregnancies



# Likely diagnoses in first 1000 reports

- Top Exomiser hit in 59% of cases
- In top 5 Exomiser hits in 88% of cases
- Confirms variants found in gene panel(s)
- Identifies missing genes from applied panels



# Addition diagnoses from phenotypes

- Rare, frameshift deletion in *SORD* for a patient with congenital cataracts
- Not in our panel as limited evidence in OMIM and literature
- Highlighted by Omicia's clinical team and top 5 Exomiser match based on existing mouse (spontaneous mutation removing all functional protein) used as a model of cataract development in diabetes

Omicia Opal

Menu

Clinical Reporter

Genomics England

damian.smedley@genomicsengland.co.uk

Help

Sign Out

Clinical Reports

Variant Selection

Variant Interpretation

Test: Solo

Scoring Rubric: ACMG Mendelian

VAAST Release: 3.0.4.2

Pipeline Version: 6.0.4

Interpreted By: Melanie Babcock

HPO Terms:

Congenital cataract

Show/Hide Columns

Reset Filters

Bulk Update

Variant Selection

Review Report

	Review	Gene	Position	Change	Effect	Zygosity	Quality	1KG AF	Omicia		Class	VAAST	Phavor	VAAST	Complete	Scoring	Confirmation	Report	Latest Classificati	
	Priority		dbSNP				GQ	GeL AF	Score	Evidence	(Condition)	gene	gene	Inheritance	Tier	Penetrance	Status	Status	Section	(Date Classified, Confirmation Stat
1	<input type="checkbox"/>						Coverage	ExAC AF				rank	rank	Model						
2	<input type="checkbox"/>		SORD	chr15:45361216	CG → C	frameshift	149	-	0.800		Uncertain	11	13	Dominant			Classified	To Be Confirmed	Not Reported	-
3			rs55901542	c.757delG			99	0.00502			Significance									
				p.Ala253GlnfsTer27			16 : 10 : 6	-			(Cataract)									

1 Items

Items per page: 25

# Research candidates



- Likely to have 10-15k rare disease cases without a clear diagnosis from standard pipeline
- Exomiser and Genomiser candidates, especially those based on **model organism phenotypes critical for new disease gene discovery**
- Interactions with GeCIP communities to validate
  - Transcriptomics
  - **Crispr/Cas9 precision animal models for functional validation and ultimately improved treatment**

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# Aims and Objectives

Use sophisticated tools  
developed within IMPC  
to further support  
genome engineering

Make the technical skills  
of Harwell available  
widely



# GEMM

GENOME EDITING MICE FOR MEDICINE

Shorter timescales  
responsive to scientific  
and clinical needs

Offer a wider range of  
genetically quality  
controlled lines to UK  
scientists

Nominations from UK  
Clinicians and academics

Call 1= 87

Call 2= 93

Peer reviewed by a  
panel of experts



# GEMM

GENOME EDITING MICE FOR MEDICINE

Nominations scored by MRC

Harwell for

1) Resource

2) Feasibility

Mouse strains  
delivered but also  
available in public  
archives

# Research candidates for functional validation



1200 negative reports (currently based on GeL clinical review of gene panel and company candidates)

390 gene panel or  
company candidates

221 de novo variants  
(outside gene panel)

934 high scoring  
Exomiser variants  
(outside gene panel)

1545 candidate variants

Final submissions came from targeted discussions with GMCs and GeCIP members and also include diagnosed variants where therapeutic and mechanistic studies would be useful





### **Call 1- Summer 2016**

- 87 application
- 23 selected
- 12 point mutations

### **Call 2- Spring 2017**

- 93 application
- 19 selected
- 12 point mutations

X-linked intellectual disability

Non-ketotic hyperglycinemia

Thyroid Cancer

Pain

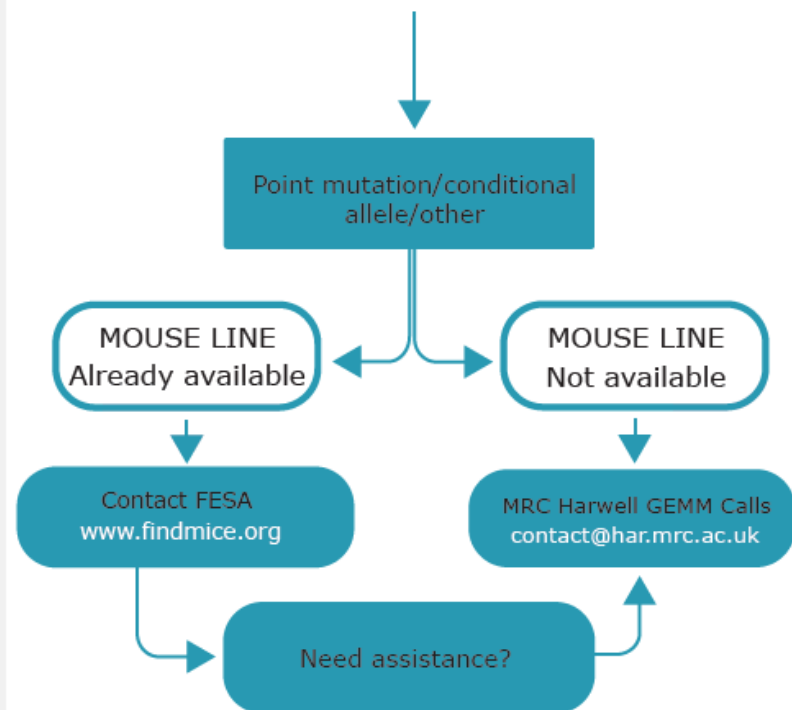
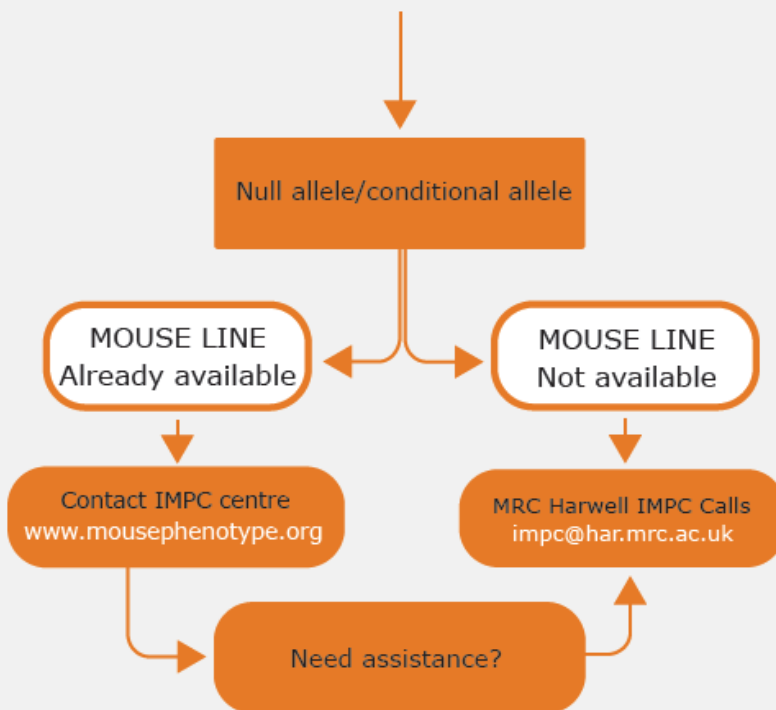
Charcot-Marie-Tooth

Cardiac Myopathy

Epilepsy

infantile-onset dyskinesia and chorea

# Opportunities for Mouse Strains



# Building the future of genomic medicine



***Clinical and model organism phenotypes as well as precision animal models are key to achieving this vision***

- 100,000 WGS on NHS patients and pathogens
- The NHS, academics and industry partnerships at the outset to drive Genomic Medicine into the NHS and create wealth
- Building the human capacity and capability
- Key international partnerships to add value
- NHS is preparing to commission WGS from April 2018 as part of a re-procured Genomic Health service
- Concentrating the UK Genomics Knowledgebase in one location
- New diagnostics and therapies and opportunities for patients

# Acknowledgements

- 100,000 Genomes Project
  - The patients and their families
  - NHSE staff
  - Genomics England colleagues
  - UK biobank and Illumina
  - Interpretation companies
  - GeCIP members

