

# Melbourne Genomics Health Alliance & Australian Genomics Health Alliance

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Australian Genomics Health Alliance

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Executive Director: Melbourne Genomics Health Alliance



# Melbourne Genomics Health Alliance

Exec. Director: Assoc. Prof. Clara Gaff

## Founding members



## New members



**FUNDING:** Members \$3.4 million 2014-15, State Govt & Members \$35 million 2016-19

# Collaboration focused on **health care** is needed

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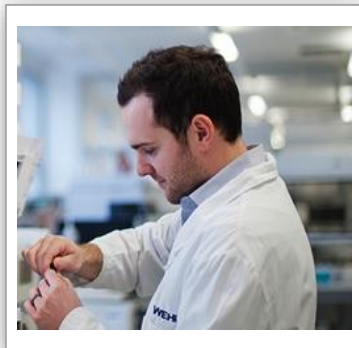
Patients



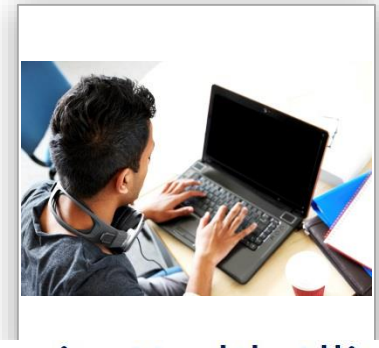
Clinicians



Diagnostic lab



Researchers



# 2014 -2015 Demonstration Phase

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## Build a 'prototype'

Testing policies

Counselling & consent

Single bioinformatics platform

Shared variant curation db

Variants linked to clinical data

Patient data entry

Researcher access to data

*Multiple organisations*

*Different conditions*

**Evaluate** *compared to standard care*

## Process

what worked

what didn't

potential solutions

## Impact

detection rate

change in management

Cost effectiveness

*Clinicians*

*Patients*

*Diagnostic scientists*

*Data scientists*

# Demonstration Project

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**Prospective:** Singleton Whole Exome Sequencing with targeted analysis prospective *i.e.* in parallel with usual investigations

## Five flagship diseases:

- Hereditary peripheral neuropathies (CMT)
- Childhood syndromes (CS)
- Focal epilepsy (Epil)
- Hereditary colorectal cancer syndromes (hCRC) - germline
- Acute myeloid leukaemia (AML) - somatic

**n= 305 patients**

# Shared approaches



**Common clinical consent form  
(germline)**



**Data  
standards**



**Curation guidelines**

Lab name/logo

**Diagnostic Exome Sequencing report – targeted analysis.**

<b>Patient Details:</b> Name: DOB: Sex: URN: Referring doctor: [insert referring dr details]	<b>Sample details:</b> Lab ID: Source: Date collected: Date received: Report date:
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Clinical indication: Clinical diagnosis (and family history) of XXXXX  
Test performed: Whole exome sequencing (WES) with targeted analysis of [insert #] genes known to be associated with [name of condition].

<b>Primary result:</b>	A (likely) pathogenic variant consistent with a diagnosis of [condition] was detected.
<b>Secondary result:</b>	No secondary findings detected.

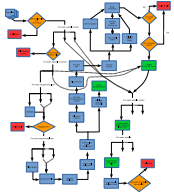
**Common report format**



**Multidisciplinary review  
meetings**

# Proof of concept for State-wide approach

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**Analysis:** Common Bioinformatics Pipeline (Cpipe)

*VLSCI*

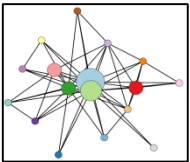


**Interpretation & Variant Curation Database (MG-LOVD) Reporting**

*NeCTAR*

**Storage & compute**

*VLSCI*



**Access to clinical data:** Data linkage

*BioGrid*



**Access for researchers:** Research Data Storage

*RDSI*



**Patient data entry**

*BioGrid*

# Patients: pathogenic variants – interim results

Participants	Total	AML	CRC	CS	CMT	EPIL
Analysed	<b>171</b>	24	25	80	35	41
Pathogenic variant detected	<b>31%</b>	38%	20%	57%	29%	10%
Not detected by Std care	TBD	TBD	none	45%	29%	10%

# Melbourne Genomics – cost analysis

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## 40 children with suspected syndromes

### Standard investigations

A total of  
**\$190,007**  
was spent on diagnostic investigations, an average of  
**\$4,750 per patient.**

**7 diagnoses** were made

Cost per diagnosis of  
**\$27,143**

### Singleton exome

A total of  
**\$80,000**  
was spent on singleton exomes at  
**\$2,000 per patient.**

**25 diagnoses** were made

Cost per diagnosis of  
**\$3,200**

# Clinicians have a better understanding

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- Designed to **promote change in clinician behaviour**
- Capability Opportunity Motivation Behaviour (COM-B) Model  
(Michey *et al.* 2011)
- All clinicians interviewed as part of the process evaluation (n=28)

**“So it's given us hands-on experience with the data and being able to understand how the test works and how the curation process works. I definitely have a much better understanding about the limitations of the test and also how it's supposed to look.”**

# And they report they want...

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**Decision support**: algorithm with capacity to indicate whether exome is appropriate based on phenotype data (or recommend a different test)

**Knowledge resource** encompassing evidence and clinical actions

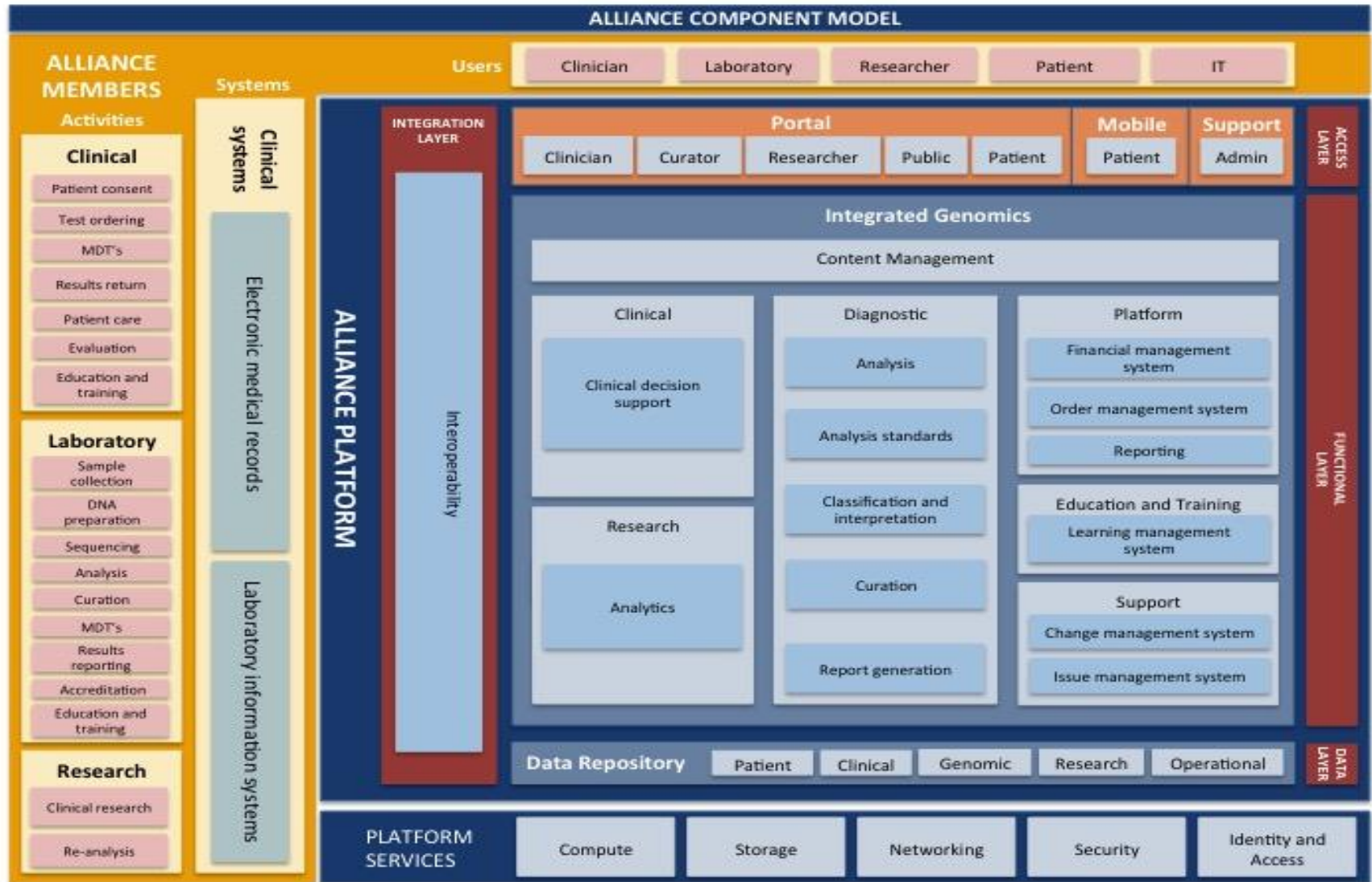
**Reports integrated** into hospital systems and electronic patient records that **link genotype and phenotype data**

Systems that **prompt for review** when gene lists are significantly updated

Professional **upskilling**, particularly opportunities for experiential learning (“learning by doing”)

Support and reallocation of resources within the **workforce**

# Single shared Statewide platform



# Benefits of a single platform

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Economies of scale



Scalable according to need



Rapid adoption of new knowledge and discoveries



Meets the needs of and provides consistency for all users



Facilitates sharing and use of data internally and externally



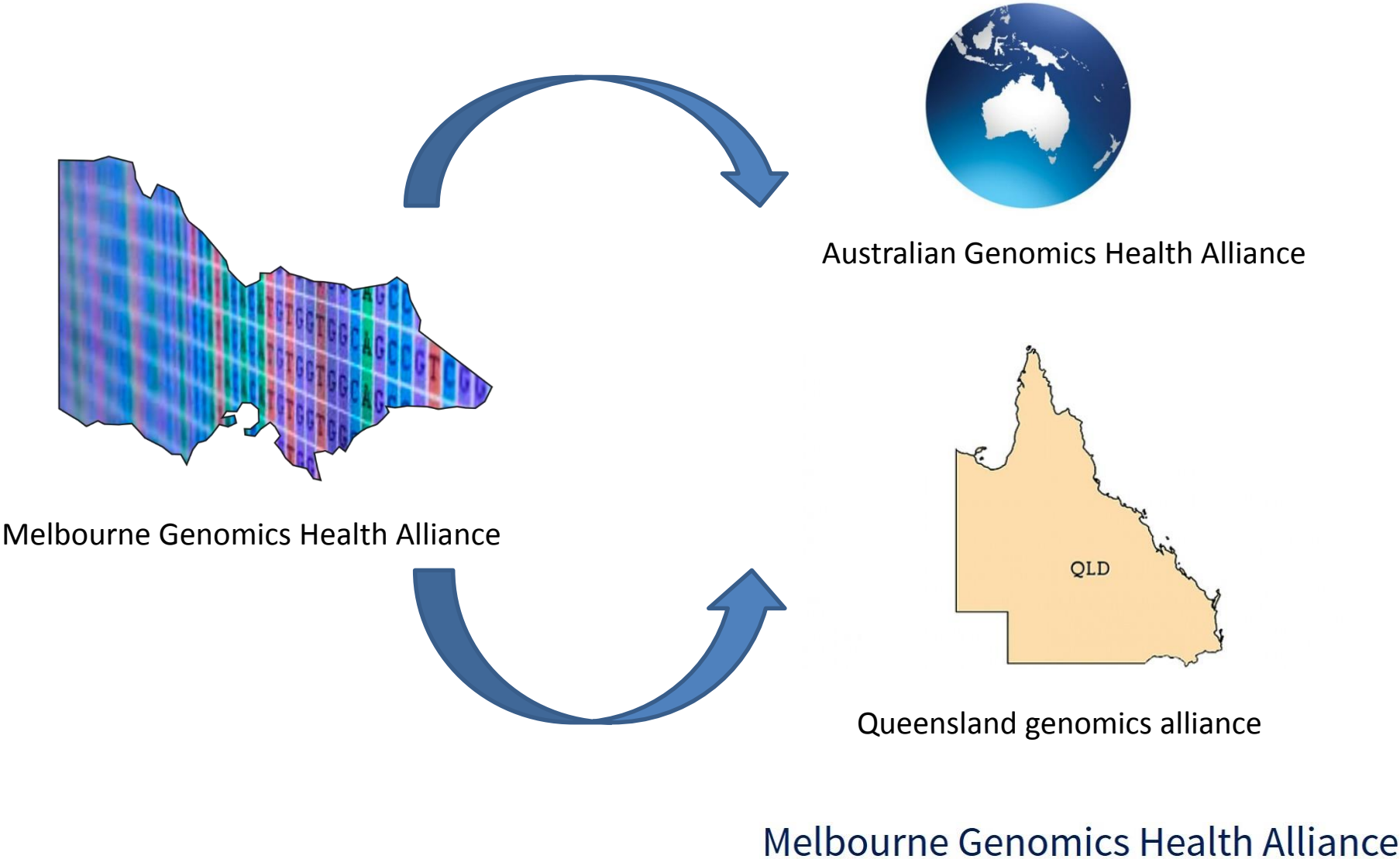
Adaptable for other –omics



Collaborative approach optimises funding opportunities

# Others are adopting our model

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# Australian Genomics Health Alliance

Vision: to provide evidence based genomic medicine that will improve healthcare outcomes in the most cost-effective way

## Partners

Harry Perkins Institute of Medical Research  
Path West  
Genetic Services of Western Australia  
Telethon Kids Institute  
University of Western Australia

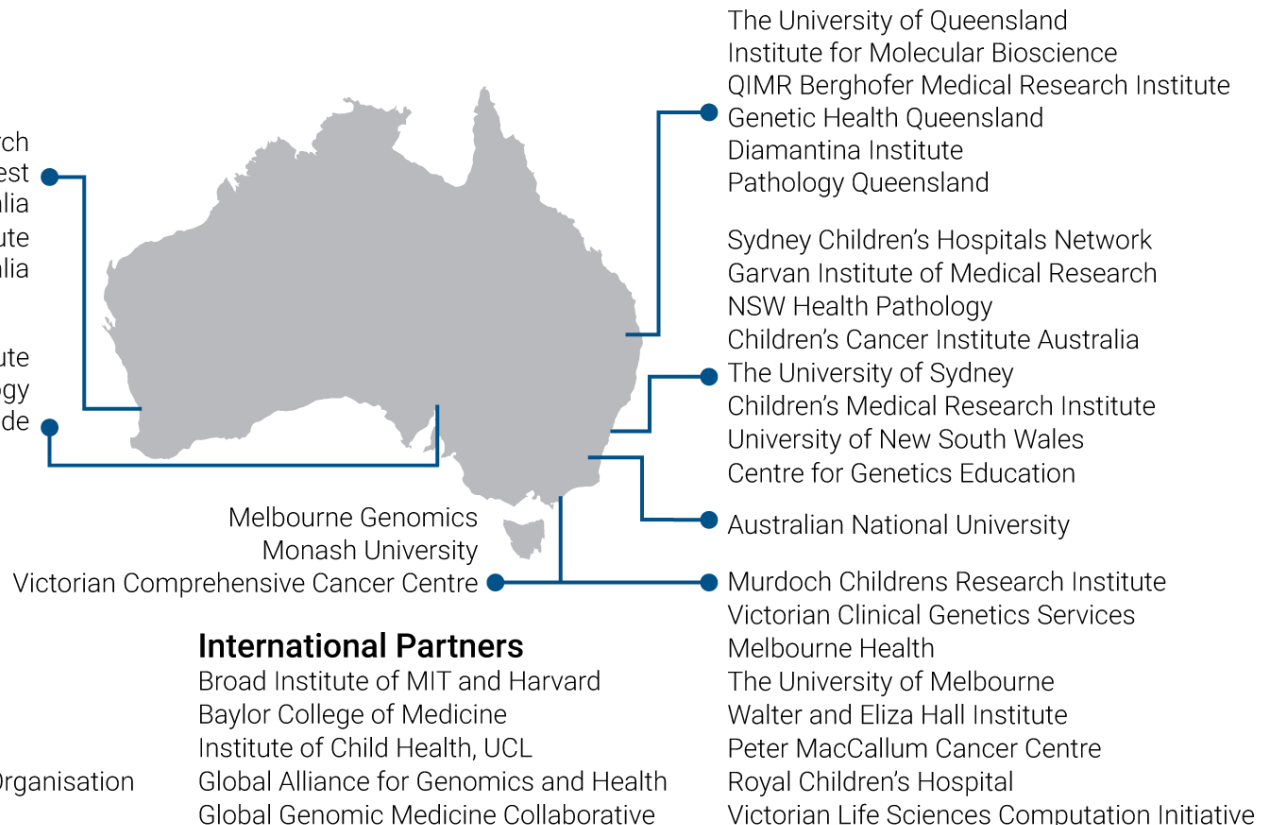
South Australian Health & Medical Research Institute  
SA Pathology / Centre for Cancer Biology  
University of Adelaide

## Peak Professional Bodies

Royal College of Pathologists of Australasia  
Human Genetics Society of Australasia

## National Partners

Bioplatforms Australia  
Australian Genome Research Facility  
BioGrid Australia  
National Computational Infrastructure  
Commonwealth Science and Industrial Research Organisation  
Rare Voices Australia



## Program 1

A national diagnostic and research network

*Developing the most appropriate diagnostic approach for each specific disease area.*

## Program 2

A national data repository

*Registries and linkage to genomic data.*

## Program 3

Evidence and policy for genomics in healthcare

*Health economics, policy development, communication and engagement.*

## Program 4

Genomic education and workforce

*Training for healthcare professionals, development of online information tools for clinicians and public.*

Existing Activities

Disease Area I

Rare Disease

Clinically driven

Disease Area II

Cancer

Patient focused

Enabling research

Clinical Outcomes



Early Diagnosis



Prevention



Early Intervention



Surveillance



Targeted intervention or therapy

## Analysis

To provide a strong evidence base for applying genomics to clinical medicine

## Policy

Practical strategies to inform Australian Health system planners and policy makers

# Melbourne Genomics Acknowledgements

CEOs/Leadership	Project Team	Flagships	Laboratories	Working Groups	Information Systems
<p>Gareth Goodier (RMH) Christine Kilpatrick (RCH) Stephen Smith (University of Melbourne) Doug Hilton (WEHI) Kathryn North (MCRI) Lynne Cobiac (CSIRO) Sue Forrest (AGRF)</p>	<p>Clara Gaff (Exec Director) Ivan Macciocca (Clinical) Brenda Greyling (Clinical) Natalie Thorne (Bioinf) Tim Bakker (Info Mgmt) Karen Meehan (Comms) Michele Cook (Admin)</p>	<p>AML Andrew Roberts Ian Majewski Seong Lin Khaw Francoise Merchinaud Eddie Chew</p>	<p>CTP Paul Waring Graham Taylor Tiffany Cowie Sebastian Lunke Renata Marquis-Nicholson Greg Corboy Michael Christie Arthur Hsu</p>	<p>Pipeline platform</p>	<p>DIAGNOSTIC SYSTEMS <i>Cpipe / MG-LOVD</i> Simon Sadedin John-Paul Plazzer Anthony Marty Guido Grazioli Richard Sinnott Glenn Tesla Advanced Users Group <i>VLSCI</i> Andrew Lonie Peter Georgeson Charlotte Anderson Gayle Phillips Harriet Dashnow Clare Sloggett</p>
<p>Steering Group</p>	<p><i>Evaluation Team</i> Melissa Martyn Bill Wilson Emily Forbes Nessie Mupfeki</p>	<p>CMT Monique Ryan Paul James Tim Day Lynette Kiers Adrienne Sexton</p>	<p>VCGS Andrew Sinclair Graham Taylor Damien Bruno Steven Nasioulas Belinda Chong Shannon Cowie Melanie Smith Clare Love Chris Guest</p>	<p>Computing</p>	
<p>James Angus (Chair) Julian Clark Sue Forrest Clara Gaff (Exec Director) Trevor Lockett / David Hansen Andrew Sinclair Mike South Paul Waring / Jon Emery Ingrid Winship</p>	<p><i>Genetic Counsellors</i> Gemma Brett Emma Creed Ella Wilkins</p>	<p>CRC Alex Boussioutas Finlay Macrae Alison Trainer Ingrid Winship Michael Bogwitz</p>	<p>AGRF Sue Forrest Kirby Siemerling Melanie O'Keefe Matthew Tining Lavinia Gordon Rust Turakulov</p>	<p>Variant database</p>	
<p>Community Advisory Group</p>	<p><i>Advisory Groups</i></p>	<p>CS Sue White Zornitza Stark Paul Ekert Christiane Theda David Amor Tiong Tan Maie Walsh Patrick Yap</p>		<p>Database users</p>	
<p>Ingrid Winship (Chair) Louisa Di Pietro Heather Renton Margaret Sahhar Janney Wale Christine Walker Liat Watson</p>	<p>Genomics and Bioinformatics Chair: Graham Taylor / Alicia Oshlack</p>	<p>EPILEPSY Patrick Kwan Terry O'Brien Ingrid Scheffer Piero Perucca Paul James</p>		<p>Clinical bioinformatic workforce</p>	
	<p>Clinical Interpretation and Reporting Chair: Paul James</p>			<p>Sequencing</p>	
	<p>Information Management Chair: David Hansen</p>			<p>Patient survey</p>	
				<p>Cost-effectiveness</p>	
				<p>Research access</p>	
				<p>Patient-entered data tool</p>	
				<p>Workshop Groups</p>	
				<p>Information requirements</p>	
				<p>Lifestyle data</p>	
				<p>Business case</p>	
				<p>Education symposium</p>	
				<p>Evaluation</p>	
				<p>Reporting</p>	
					<p>CLINICAL SYSTEMS <i>Biogrid</i> Maureen Turner Leon Heffer Alice Johnstone <i>MCRI &amp; REDCAP</i> Jane Halliday Susan Donath Leanne Mills Ross Dunn Luke Stephens</p>
					<p>DATA ACCESS Yousef Kowsar Kurt Lackovic Steven Manos Candice McGregor Owen O'Neill Gayle Phillips Bernie Pope Melissa Southey</p>