Australian Genomics Policy on Data Access and Sharing for Secondary Use

Introduction

The purpose of this policy is to create a framework for reasonable access to data collected through clinical flagship projects of Australian Genomics for the purpose of secondary research use. This policy is designed to reflect the opinions of flagship leads and investigators, and respect the wishes of flagship participants. Data collected will strictly be used in accordance with a participant's consent for collection, use and data sharing.

Australian Genomics' data access policy and agreements comply with all relevant Australian laws and guidelines including the Privacy Act (1988)[1] and its Australian Privacy Principles (APPs); the Health Record Act (2001)[2] ; the National statement on Ethical Conduct in Human Research (2018)[3]; the Australian Code of Responsible Conduct of Research[4] and its supporting guide: Management of Data and Information in Research[5] . The policy also aligns with the guidelines and policies set out by the Global Alliance for Genomic Health (GA4GH)'s Framework for Responsible Sharing of Genomic and Health-Related Data[6]. See Appendix 1 for a summary of the Foundational Principles and Core Elements.

Scope

This data access policy establishes the principles and processes for reasonable access for researchers and clinicians both *internal* and *external* to the Australian Genomics collaboration (as defined below). The focus of this policy is data resulting from participants' genomic sequencing as well as data captured through their clinical care (such as pathology results, reports, or clinical examinations) or research participation (such as survey responses).

References and bibliography:

[1] Privacy Act (1988): https://www.legislation.gov.au/Details/C2014C00076

[2] Health Record Act (2001): http://www.legislation.vic.gov.au/Domino/Web_Notes/LDMS/LTObject_Store/LTObjSt6.nsf/DDE300B846EED9C7CA257616000A3571/77FAA53ECDC0DA44CA2579030015D701/%24FILE/01-2aa023%20authorised.pdf

[3] National Statement on Ethical Conduct in Human Research: https://www.nhmrc.gov.au/_files_nhmrc/file/publications/national-statement-2018.pdf

[4] The Australian code for responsible conduct of research (2018) from NHMRC: https://www.nhmrc.gov.au/sites/default/files/documents/attachments/grant%20documents/The-australian-code-for-the-responsible-conduct-of-research-2018.pdf

[5] Management of Data and Information in Research from NHRMC: https://www.nhmrc.gov.au/sites/default/files/documents/attachments/Management-of-Data-and-Information-in-Research.pdf

[6] Framework for responsible sharing of genomic and health-related data (GA4GH): https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4685158/pdf/11568_2014_Article_3.p

Definitions and Role Descriptions

Aggregated, Anonymised Data: Genomic data can never be fully anonymised due to its identifying nature. The term Anonymised Data refers here to data that has personal identifiers removed, and is grouped in cohorts or subsets to eliminate individualised data access, and reduce risks of indirect identifiability due to specific or rare characteristics.

Data Access Committee: The Data Access Committee objectively and systematically reviews data access requests from Data Requestors, in accordance with Australian Genomics policies and protocol. The Australian Genomics Data Access Committee may include, but not be limited to: senior operational personnel, data stewards, data domain leads, bioinformatician(s), patient representative(s), and/or invited members of the relevant Flagship(s) and additional expert advisors.

Data Author: Lead investigators of clinical flagship projects enrolling participants into the study and providing the clinical data.

Data Custodian: The Data Custodian is responsible for the safe custody, aggregation and storage of data.
For Australian Genomics: University of Melbourne and Murdoch Children's Research Institute.

Data Donor: a research participant, whose data have been collected, held, used for the primary research purpose and potentially shared for secondary research use.

Data Steward: The role of the Data Steward is to manage, oversee and utilise the organisation's data governance processes to ensure fitness of data elements - both the content and metadata.
For Australian Genomics: Australian Genomics Managing Director and Data Manager.

Data User or Requestor: the researcher or clinician seeking access to data.

Data Sharing: defined as per the GA4GH Framework: data transfer or data exchange between data users, or where data are made available to secondary researchers, either openly or under specified access conditions[vi].

De-identified Data: Data with all associated personal Identifiers and other indices removed and replaced with a unique study identifier, such that there is a low or no risk of re-identification from data that are made accessible to Data Users/ Requestors.

External Access: Data access request(s) from individual(s) affiliated with an institute that is not a partner of Australian Genomics (see '*Internal Access*').

Genomic Sequencing Data: Binary Alignment Map (BAM), Variant Calling Format (VCF) and FASTQ text file format storing biological sequence and corresponding quality scores.

Human Research Ethics Committees (HREC): Review all research proposals involving human participants to ensure that they meet ethical standards and guidelines.[7]

Identifier or Identifying Information: Information where the identity of an individual is apparent or can reasonably be ascertained by the holder of the information. Information that may directly, or ndirectly, lead to identifying an individual from whom the samples and associated information are collected as a link (or multiple links) exists between the participant's personal Identifiers and the data.[8]

[7] HRECs definition from NHMRC:
https://nhmrc.gov.au/research-policy/ethics/human-research-ethics-committees

[8] Government of Western Australia, Department of Health: "Guidelines for human biobanks, genetic research databases and associated data:
https://ww2.health.wa.gov.au/-/media/Files/Corporate/Policy-Frameworks/Unallocated/Policy/Guidelines-**australiangenomics.org.au**

Internal Access: Data access request(s) from individual(s) affiliated with an Australian Genomics partner institute, i.e. a participating institution as a signatory of the Australian Genomics Multi-Institute Agreement or Secondary Research Collaboration Agreement.

Metadata: Information about the primary data, including but not limited to: quality metrics; methodological information; laboratory information; and possible coded Identifiers and clinical information.

Moratorium: The temporary restriction on access to documents or data for a specified period of time.

Governance Framework

National and International Frameworks.
The international standards setting organisation in genomics, the Global Alliance for Genomics and Health (GA4GH), has developed a Framework for Responsible Sharing of Genomic and Health-Related Data. This framework's scope includes personal health data and other types of data that may have predictive power in relation to health. In particular, it highlights, and is guided by, Article 27 of the 1948 *Universal Declaration of Human Rights*, which guarantees the rights of every individual in the world "*to share in scientific advancement and its benefits*"[9]. For this to best occur the rights of the individual must be weighed against the rights of the community to benefit from information sharing.

The framework clearly outlines the requirement to provide clear information on the purpose, collection, use and exchange of genomic and health-related data, including, but not limited to: data transfer to third parties; international transfer of data; terms of access; duration of data storage; identifiability of individuals and data; limits to anonymity or confidentiality of data; communication of results to individuals and/or groups; oversight of downstream uses of data; commercial involvement; proprietary claims; and processes of withdrawal from data sharing.

The NHMRC also encourages researchers to disseminate and share their research data through publicly accessible databases or repositories. Researchers are therefore encouraged to share data with as much breadth and depth as possible, while considering their jurisdictional and ethical-legal obligations, and providing sufficient metadata to allow others to reuse their data.

In order to balance disclosure risk with data utility, this policy also follows, where adequate and sustainable, the Five Safe Framework[10]. The five related but separate dimensions of this framework are listed in Appendix 3. The use and sharing of data are to be limited to what is relevant and necessary to accomplish the pre-defined research purpose; minimise privacy risks for participants; and be in line with participant consent.

The GA4GH framework, the NHMRC guidelines for data sharing and the Five Safe Framework are informing the data governance framework for the Australian Genomics Health Alliance described here.

The Australian Genomics Framework
The Australian Genomics access identification process will follow the registered access policy model

for-human-biobanks-genetic-research-databases/OD299-Guidelines-for-human-biobanks-and-genetic-research-databases.pdf

[9] Universal Declaration of Human Rights 1948: https://www.un.org/en/universal-declaration-human-rights/

[10] The Five Safes Framework: http://www.fivesafes.org/

as set out by the GA4GH (Dyke et al, EJHG 2016; Dyke et al EJHG 2018) and will be limited to bona fide researchers with approved HREC relevant for the research purpose. This registered access model ensures the access process implements Authentication (proof of researcher's identity), Attestation (data use request meets consent, ethical approval and agreement to comply with terms of use) and Authorisation (permission to access the data and perform the specific action).

Underpinning the whole framework and the data sharing of participant's data is the informed consent of adult participants or the parent/guardians of paediatric participants. Some participants will dynamically and granularly update their consent preferences through an online platform (CTRL). The up-to-date participants' preference is, in either case, stored in the REDCap record of each participant and referred to prior to any data sharing as per the processes described below. Each participant consent is mapped to GA4GH Data Use Ontology (DUO) codes[11] [12] to facilitate standards in data access restrictions and permissions.

In the case of a participant withdrawing from the study, the status and management of data sharing will be dependent upon the timing of withdrawal. Retrospective withdrawal (i.e., applying restrictive/cancelling data sharing once participant data has been released to Data Users) will not be possible. However, upon participant withdrawal, prospective data sharing will cease. The REDCap database will be updated to record the withdrawal to prevent any further on-sharing.

Data under Australian Genomics Custodianship

Data Infrastructures and Tools

Within the scope of Australian Genomics, data is stored in, or accessible from, different locations depending on its type. Appendix 2 details the data tools created and developed by Australian Genomics, including contacts for each tool. A brief summary is listed here:

- *REDCap study Database* - The REDCap study database stores identifiable data, including but not limited to: personal information; demographics; clinical (phenotype) and genotype information; pathology reports and results; study survey responses; study logistics and tracking information.
- *Genomic Data Repository (GDR)* - The raw genomics sequencing data (BAM/VCF/FASTQ files) as well as a minimal subset of Metadata is stored in the GDR, managed by University of Melbourne Centre for Cancer Research (UMCCR).
- *Variant Atlas* - Aggregated variant data (VCF) of clinical flagship cohorts can be visualised and filtered by key clinical features via the tool hosted at Garvan Institute.
- *CTRL ("control")* – Based on dynamic consent, this platform is a new online research consent and engagement platform for Australian Genomics' participants. It enables participants to give or revoke consent in real time and in a granular fashion.
- *Shariant* - Clinically curated variant classifications, the evidence underpinning the classification, and information of the providence of the classification (submitting laboratory and/or curator) is shared via the online platform *Shariant*, hosted by SA Pathology. The Shariant platform is hosting curated variant classifications for laboratories all around Australia.

[11] GA4GH Data Use Ontology Codes: https://www.ga4gh.org/news/data-use-ontology-approved-as-a-ga4gh-technical-standard/

[12] Dyke SOM, Philippakis AA, Rambla De Argila J, Paltoo DN, Luetkemeier ES, Knoppers BM, et al. (2016) Consent Codes: Upholding Standard Data Use Conditions. PLoS Genet 12(1): e1005772. https://doi.org/10.1371/journal.pgen.1005772

- *Standardised, computer-readable clinical descriptions (FHIR)* - The clinical information in REDCap is translated into standardized phenotype ontology codes to allow computerised search, discovery and coding.

Categories of Data

Three categories of data are available. These are classified based on the sensitivity of the data (re-identifiability), and the permissions associated with the data - rather than the tool they are stored in. Although the identifiability of data is accepted to be a spectrum rather than discrete tiers, we are using the "tier" terminology to categorise the different data types stored and accessed by Australian Genomics. A visualisation of the data tiers described below along the data identifiability spectrum is shown in Figure 1. A summary of the different data types, tiers and tools is presented in Table 1:

- ***Tier 1: Individual (unit) level, personally identifiable data.***
  Identifiable clinical and genomic information will only be available to the participant's treating team, the Australian Genomics Managing Director, Australian Genomics Data Stewards and Australian Genomics operational team members on a need-to-know basis. Data in this tier will not be available for secondary research use.
- ***Tier 2: Unit-level, coded, de-identified data.***
  Genomic and clinical information identified only with the Australian Genomics Study Identifier, with participants' personal information removed, will be made available to the flagship research teams for the purpose of resolving undiagnosed participants and/or furthering understanding of their condition. De-identified data might also be made available to bona fide researchers who demonstrate HREC permission or equivalent for use of data of this tier; for a purpose in line with data permissions; and following participant's consent. De-identified flagship data will be available for secondary research use from the Genomic Data Repository, Variant Atlas (Gen-Phen interface), FHIR server (standardised clinical data) and REDCap (clinical data), pending Data Access Committee review. As there is a slim chance of re-identification of participants, these data are still considered sensitive and researchers and institutes granted access to the data will sign a Data Access and Sharing Agreement stipulating that any attempt to re-identify individuals is expressly forbidden.
- ***Tier 3: Aggregate, anonymous data***
  Datasets that are not identified with either personal information or code will be made available upon registration with an institutional email and attestation to statement as described in Appendix 4, as summarised information across the patient cohort, or across subsets of the cohort. Given the chance of re-identification is low-to-nil, these datasets will be classed as low sensitivity.

In support of data re-analysis and sharing, the data and any associated metadata will be kept accurate, verifiable, unbiased and annotated with providence and date.

Figure 1: Spectrum of Identifiability

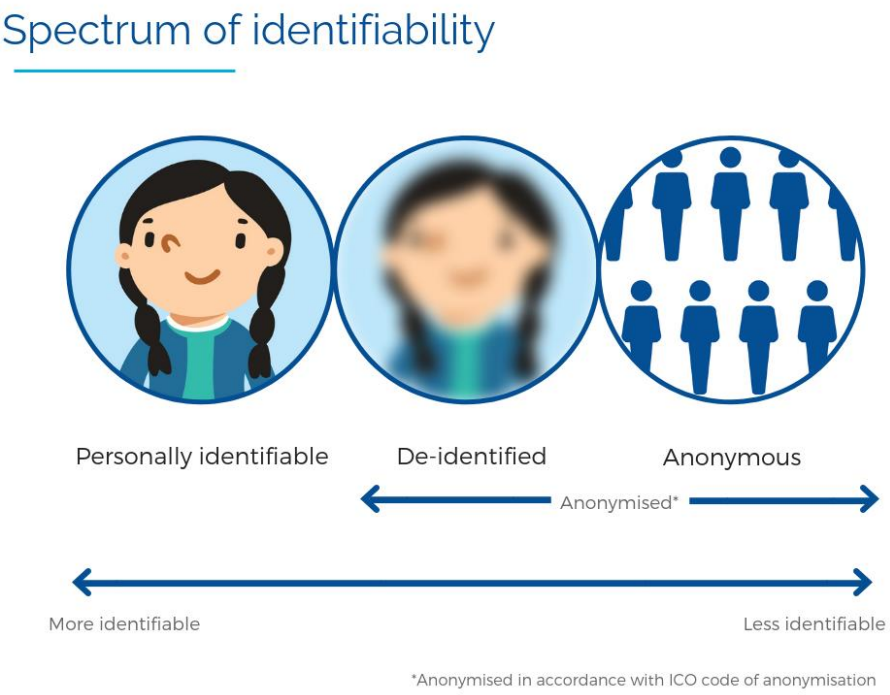

Table 1: Summary of data types, tools and tiers

	Data Access type		
Data storage tool	Personally Identifiable Data (Tier 1)	Re-identifiable Data (Tier 2)	Anonymous data (Tier 3)
REDCap	Participant's treating clinical team as well as coordination and required operational staff	Researchers with HREC and DAC approval	Researchers with HREC and DAC approval
Genomic Data Repository	N/A	Clinicians or HREC and DAC approved researchers	N/A
Variant Atlas	N/A	Restricted to Flagship team only	Registered Access with institutional email
CTRL ("Control")	N/A	Australian Genomics flagship investigators and collaborators	Researchers with HREC and DAC approval
Shariant	N/A	N/A	Participating Laboratories
FHIR server	N/A	Australian Genomics flagship investigators and collaborators	Australian Genomics flagship investigators and collaborators

Data Access Procedures

Timelines and Moratoria

In recognition of the role of flagship clinicians and researchers as data Authors and lead investigators, a Moratorium on sharing the data is in place. This Moratorium will be 6 months for Internal and 12 months for External Access to the data, from when the final report is issued for each flagship, unless alternative arrangements are made with Flagship leads. After this Moratorium period, data access requests will be accepted for consideration as per the processes described below. The Data Access Committee, in consultation with the flagship leads, may choose to waive the Moratorium period.

Authorisation and Approvals

For requestors seeking External Access, an Authorisation process must first be conducted to establish bona fide researcher status. Data requests will subsequently be reviewed for proposed research use, appropriate Attestations, confirmation of ethical approval for the study, and approval by the Data Access Committee.

For a requestor involved with the Australian Genomics program or affiliated with a participating institution, the Authentication process is pre-approved as the bona fide status of that researcher is known. Further, the terms of research collaboration have been defined and agreed under a Multi Institute Agreement, or other Research Collaboration Agreement. Should the proposed research application of the requestor be defined under Australian Genomics Ethics protocol (MH2016/224), and attestation has been established – Approval shall be granted. Should the internal data access request be for research use that falls outside the remit of Australian Genomics Ethics protocol, the proposal shall be reviewed for HREC approval and alignment with the permissions associated with the data to establish Attestation, and approval granted.

Please note the flagship lead(s) has the right to deny an application for access to their respective cohort data, only if there is a robust justification to deny that data access.

Data Access Options

Data under the custodianship of Australian Genomics can be accessed via two separate methods: data querying or data sharing.

Data querying: Data can be queried without being downloaded or otherwise accessed via the Variant Atlas and FHIR server platforms.

Variant Atlas

In this platform, two types of queries can be performed:

- Anonymised, Aggregated Data Queries

Access to the aggregated data queries is managed by the Australian Genomics Data Governance Officer. Researchers request access via an online REDCap registration form that collects Data Requestor details that includes, but is not limited to, institutional email address and purpose of access. Additional details may be requested over time or if required. Requestors are provided with this Policy, the Data Breach Policy and Statement on Secondary Data Use Research Findings, and must attest to conditions of use. Approved requestors are then required to set up a password-protected user account on Variant Atlas using their institutional email address.

- Restricted Access Individual and Clinical Data Queries

Appropriately credentialed flagship investigators and collaborators, via direct request to the Australian Genomics Data Governance Officer, data custodian, or data officers, may be granted access to query the individual-level, coded flagship genomic and clinical data via the Variant Atlas portal. Cross-flagship gene panels and queries may be used to support the resolution of undiagnosed

cases and flagship research activities. Some data may have additional limitations of use, which will be controlled by Variant Atlas administrators.

FHIR server

The FHIR server hosts data from the Redmatch ontology and standardisation tool that provides the transformation rules that converts clinical information in REDCap into standardised clinical terminology and machine-readable FHIR format. The FHIR server can connect to other tools providing queries of the phenotype data, such the CSIRO Pathling analytic tool. Only approved and credentialed investigators will be able to query aggregated and de-identified coded phenotypic data.

Data Access Submission Procedure

Data access requests are submitted to the Australian Genomics Data Governance team via an online application form. All requests will be managed and tracked via a dedicated REDCap database, to ensure appropriate access to approved data requestors; and that the purpose of access is ethically-compliant and meets patient consent. A Data Access Committee (DAC) will review all data access applications. Terms of use will be outlined in a Data Access and Sharing Agreement that will be signed and executed by the project's Principal Investigator, an authorised representative of the named institution, and MCRI legal. Users will be provided with this Data Access and Sharing for Secondary Use Policy, the Data Breach Policy, and the Statement on Secondary Data Use Research Findings. Once all agreements have been executed, the requestor will receive access to the data..

For researchers seeking access to Australian Genomics data, prior to ethics approval for their proposed project, an in principle agreement may be granted, however access to data will only be made available following ethical approval of the project and once a Data Access and Sharing Agreement is fully executed.

Inclusion in Databases

Where possible, Australian Genomics will inlcude de-identified genomic data associated with non-identifying clinical summary data in national or international databases, in line with participants' consent to future ethically approved research projects, in order to make the gathered data available to advance knowledge. Furthermore, in compliance with the requirement of many academic journals that data used in publications are required to be archived in long-term community-endorsed repositories and, where possible, made accessible to other researchers, Australian Genomics data may be stored and available from restricted and controlled access databases such as the European Genome-phenome Archive (EGA) or similar. The EGA, or similar databases, will purely serve as an approved and registered storage facility, with the Australian Genomics Data Access Committee retaining full access-granting authority. Any data access request will follow the same processes in place as described above. The Data Access Agreement will require full execution by any investigator and their host institution prior to data release.

Findings from secondary research

At this time, Australian Genomics will not accept from researchers, or return to participants, research findings unrelated to the condition they were tested for. If you identify a variant through your research that may be the cause of the condition the participant was originally tested for, and you have supporting evidence for this assertion, you are invited to contact Australian Genomics via email (australian.genomics@mcri.edu.au). Please review the Statement on Secondary Use Research Findings for a more detailed notice on the use of Australian Genomics cohort data.

Requests from participants to access their genomic data

We understand that study participants may have a strong interest in their own information into their raw genomic data. However, these data will not be returned to individual participants due to resource, ethical and legal considerations associated with returning sequencing data. Therefore, if a participant would like for their data to be re-analysed, they must be referred to a genetics service that will be able to request the sequencing data for re-analysis.

Outputs and publication

Any publication or output resulting from analyses of the data, or part thereof, collected and stored by Australian Genomics shall acknowledge Australian Genomics (NHMRC GNT1113531, GNT2000001 and the Medical Research Future fund) and the relevant Data Author(s). It should also cite the REDCap database[13, 14] if using any data that has been stored during its lifetime in REDCap.

Audit to be performed on data usage

Audits shall be performed on a regular basis on the usage of data released to Data Users in order to ensure access is granted to relevant parties and used appropriately. Audits would also allow for feedback and potential improvements on the usefulness of the repository and systems in place. Audit can be performed by means of approved requestors or their institution providing an annual update and a list of resulting publications and outcomes. Timely reports will ensure maintenance of access to required data. In the case of overdue reporting, access will be suspended by the Data Steward until the audit report is completed.

Data Breach process

Researchers who suspect or are made aware that a data breach has occurred, must immediately notify: security@australiangenomics.org.au.

Researchers must provide all available information they have regarding the data breach such as, but not limited to: what type of data is affected; which individual or cohort of individual is affected; the time when the breach first occurred; the type of breach (see Australian Genomics Data Breach Policy); etc. The data breach response team, comprised of the manager, Data Steward, as well as relevant members of the data Custodian institutions, will then follow the relevant steps to contain, stop and, where possible, revert the data breach as mapped in the Australian Genomics Data Breach Policy. The data breach response team will subsequently contact the researchers for any further details, as required.

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[13] PA Harris, R Taylor, R Thielke, J Payne, N Gonzalez, JG. Conde, Research electronic data capture (REDCap**)** – A metadata-driven methodology and workflow process for providing translational research informatics support, *J Biomed Inform. 2009 Apr;42(2):377-81*
http://www.sciencedirect.com/science/article/pii/S1532046408001226

[14] PA Harris, R Taylor, BL Minor, V Elliott, M Fernandez, L O'Neal, L McLeod, G Delacqua, F Delacqua, J Kirby, SN Duda, REDCap Consortium**,** The REDCap consortium: Building an international community of software partners**,** *J Biomed Inform. 2019 May 9 [doi: 10.1016/j.jbi.2019.103208]*
https://www.sciencedirect.com/science/article/pii/S1532046419301261

Appendix 1: GA4GH Framework principles and core elements [vi]

The foundational principles and core elements for responsible sharing of genomic and health-related data as highlighted in the GA4GH guidelines are as follows and founded on Article 27 of the 1948 Universal Declaration of Human Rights:

Principles:

- Respect Individuals, Families and Communities
- Advance Research and Scientific Knowledge
- Promote Health, Wellbeing and the fair Distribution of Benefits
- Foster trust, Integrity and Reciprocity

Core elements:

- Transparency
- Accountability
- Engagement
- Data quality and security
- Privacy, data protection and confidentiality
- Risk-benefit analysis
- Recognition and attribution
- Sustainability
- Education and training
- Accessibility and dissemination

Appendix 2: Australian Genomics Data Management

REDCap

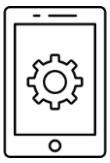
REDCap is the Australian Genomics study database. The clinical, demographic and survey data of all our participants is stored and managed in REDCap, which is hosted at MCRI.
Contact: Australian Genomics data team: AGHAdatabase@mcri.edu.au

Genomic Data Repository (GDR)

The cloud-based GDR stores Australian Genomics' Genomic Sequencing Data (BAM/VCF/FASTQ) and is hosted at University of Melbourne. A subset of a participant's clinical data is linked to their genomic data, to facilitate meaningful analysis and sharing.
Contact: Oliver Hofmann: oliver.hofmann@unimelb.edu.au

Variant Atlas

Variant Atlas is an interactive Genotype-Phenotype data platform, hosted at Garvan Institute. With this tool, researchers can visualise aggregated Flagship variant data, and filter by key clinical features to describe the cohort.
Contact: Sarah Kummerfeld: s.kummerfeld@garvan.org.au



CTRL ("Control")

CTRL is an online platform where research participants can dynamically and granularly manage their consent and data sharing preferences, as well as kept up to date with news and information about the study.
Contact: Matilda Haas: matilda.haas@mcri.edu.au

Shariant

Shariant is an online platform for laboratories to share curated variant classifications. Hosted at SA Pathology, Shariant builds upon international variant databases like ClinVar to display not only the variant information – but also the submitting lab, and the evidence underpinning the classification.
Contact: Emma Tudini: emma.tudini@qimrberghofer.edu.au
Amanda Spurdle: amanda.spurdle@qimrberghofer.edu.au

Standardised, computer-readable clinical descriptions (FHIR)

The clinical information in REDCap is translated into standardized codes (phenotype ontologies: HPO/SNOMED) to allow computerized search, discovery and coding.
Contact: Madonna Kemp: madonna.kemp@csiro.au
David Hansen: david.hansen@csiro.au

Data Access Agreements and Policies

Our participants provide consent to both national and international Data Sharing, for the benefit of healthcare. Clinicians and researchers can request access to Australian Genomics datasets, and this will be granted according to the level of data sensitivity; the specific consent of the participant; and the researcher's HREC, where applicable. Australian Genomics ascribe to GA4GH policies and standards.
Contact: Data Governance Officer: ag-datarequest@mcri.edu.au

For general Australian Genomics Data Management enquiries, contact Marie-Jo Brion, Data Program Manager: mariejo.brion@mcri.edu.au

Appendix 3: The Five Safes Framework

The Five Safes breaks down the decisions surrounding data access and use into five related but separate dimensions:

- Safe Projects: Is the use of the data appropriate, lawful, ethical and sensible?
- Safe people: Can the user be trusted to use it in an appropriate manner?
- Safe data: Does the data itself contain sufficient information to allow confidentiality to be breached?
- Safe settings: Does the access facility limit unauthorised use or mistakes
- Safe outputs: Is the confidentiality maintained for the outputs of the management regime?

Policy Revision History

Policy Version	Date effective	Summary of Revision
V 1.0	Ratified by NSC November 2018	Original Document
V2.0	7thMay 2020	Updated contact details in appendix 2 and removed library card model.
V3.0	18th March 2021	Update to match current Data Program activities and processes
V3.1	7th June 2022	Update contacts