

PURPOSE OF GUIDE

This guide aims to support Australian-based health professionals to:

- obtain patient consent for tissue-targeted (somatic) genomic testing for clinical purposes,
- provide clear explanations of the purpose, potential benefits, risks and outcomes of this testing to patients, and
- standardise the consent process for tissue-targeted (somatic) genomic testing for all patients.

This guide, developed by Australian Genomics (2025), should be used in conjunction with the:

- **Clinical Consent Form for Tissue-targeted (Somatic) Genomic Testing**
- **Tissue-targeted (Somatic) Genomic Testing Patient Fact Sheet**

CONSENT FORM

Written consent forms for tissue-targeted (somatic) genomic testing support health professionals to provide appropriate information to patients and provide evidence that a consent process took place.

A copy of the consent form should be offered to the patient and retained in the patient's clinical record.

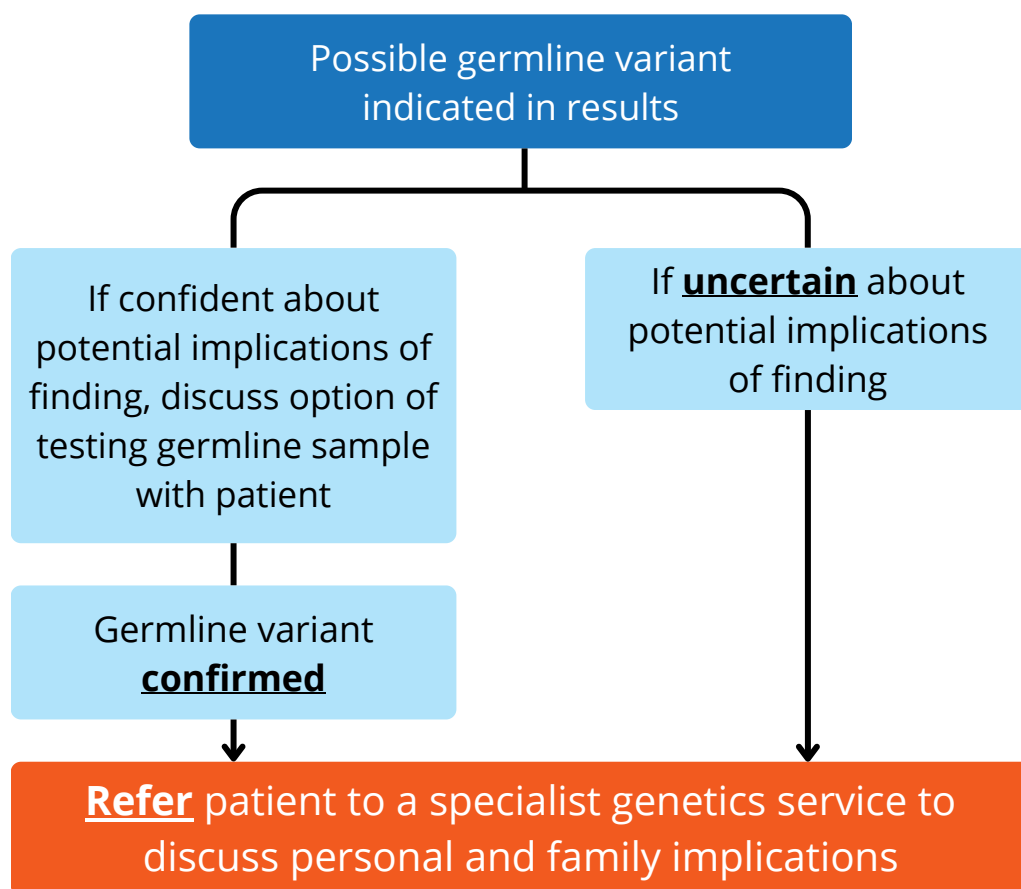
The following table explains the clauses of the Clinical Consent Form for Tissue-targeted (Somatic) Genomic Testing:

CLAUSE	EXPLANATION
1. This test aims to look for genetic changes in the tissue sample that may be related to the condition.	Clinically significant somatic variants may predict response to a specific therapy, provide diagnostic or prognostic information, and/or help identify management/treatment options.
2. The test does not detect all genetic changes or all genetic conditions.	The discussion with patients should include: • the purpose of testing, • genes/conditions covered by the test, • what the test might or might not reveal about their condition, • any limitations of the test (e.g. current limitation of genomic knowledge, such that not all types of genetic variants can be detected, and that the results cannot predict all future health conditions or outcomes) • types of results and what they might mean, and • the possibility of uncertain results, the meaning of variant of uncertain significance, the potential for reclassification as knowledge evolves and who is responsible for follow-up if new knowledge emerges. Please refer to the methodology section of test results for specific information about the limitations of the test performed. Specific consideration must be given to the limited availability of genomic reference data for a number of ethnic backgrounds, including Aboriginal and Torres Strait Islander Peoples, which may impact the ability to interpret results. The Patient Fact Sheet provides a short definition for the different purposes of testing.

CLAUSE	EXPLANATION
3. Although not intended, this test may find a result that is unrelated to the current condition and/or could have implications for blood relatives.	Patients should be informed that variants detected by this test are generally not inherited. However, there is a small possibility (usually less than 10%) of identifying a possible/likely germline variant, and that this may have health implications for them and their biological family/children. If a possible/likely heritable germline variant is identified, germline confirmation testing can be requested by the clinician, or the patient might be referred to a clinical genetics service (see figure below). A list of clinical genetic services can be found here. Patients should also be informed that germline (or somatic) variants may be unrelated to the current condition. This can include: • Germline conditions with additional health implications ◦ e.g. a child with a soft tissue hamartoma has tissue-targeted (somatic) genomic testing, which identifies a likely germline PTEN variant. PTEN hamartoma syndrome would explain the soft tissue hamartoma but also increases the risk of certain other cancers. • Incidental findings, i.e. a gene or chromosome change unrelated to the testing indication ◦ e.g. the identification of a germline sex chromosome aneuploidy on cytogenetic testing of tumour tissue. Please refer to the methodology section of test results for policy information about germline and incidental findings.
4. To better understand the test results, more testing, a new tissue sample or further review of the current sample may be needed.	Consideration should be given to the potential for further testing and/or future re-analysis of a sample and/or genomic data. Reasons for this may include: • The somatic or germline origin of a variant may not be clear. • The test may fail and may require another sample. • If a suspected germline variant is detected, a 'germline' sample may be required to confirm this. This will be carried out as a separate second test and will require additional consent. Patients should be made aware that the rapid expansion of genomic knowledge may allow for future re-examination of data/samples when test results are inconclusive. Currently there is no standard process for the re-analysis of genomic data or samples. This process can be driven by the clinician, through re-referral to a genetics service, or by the patient.
5. As part of patient care, results and related health information may be shared with clinical databases. All identifying information will be removed.	To enhance the understanding of human genetics, patient genomic information may be shared with clinical databases. By consenting to this test, patients agree for their de-identified data to be included on clinical databases. For example, ClinVar is an international clinical database that collates information about genomic variation and its relationship to human health, and Shariant Australasia shares evidence between laboratories to improve the accuracy of genomic variant classification.

CLAUSE	EXPLANATION
6. Results are confidential and will only be shared with my consent, or as required or permitted by law.	You should be aware of relevant law, regulation, policy, or guidelines regarding the disclosure of genomic health information as applicable to you or your organisation. This will enable you to inform your patients of circumstances in which lawful disclosure of genomic health information may occur without their consent, such as to prevent a serious threat to the health of a blood relative.
7. I can change my mind about testing and choose not to be told the results, but if testing has started a report will remain in patient medical records and/or My Health Record.	The testing process can be stopped at any time, and patients can choose not to be told the results of the test. However, the report may remain in medical records depending on what stage they make this decision. Results cannot be removed if they have already been entered into the medical record. You should refer to local policies and guidelines in the case that the patient withdraws consent.

WHEN TO REFER A PATIENT TO A SPECIALIST GENETICS SERVICE



A comprehensive list of specialist genetics services can be found on the Human Genetics Society of Australasia webpage.

ADDITIONAL CONSENT FORM CLAUSES

CLAUSE	EXPLANATION
8. If a genetic change is found that may be relevant to blood relative/s, I consent that test results and related information can be shared with health professionals to help with the genetic testing of relative/s. I understand that identifying information will not be shared with relative/s wherever possible.	Consent processes should include patient consideration of the release of test results for the care of blood relatives. This option allows your patient to consent for their result to be released to health professionals caring for their relatives, so they can access testing for any germline variant identified through tissue-targeted (somatic) genomic testing. When discussing the sharing of results for the health care of blood relatives, the following point should be communicated to your patient: if your patient's results show that a germline variant may be present, and testing is available to other family members, you should recommend that patients advise their relatives of this. If a germline variant is confirmed, a referral to a genetics service is advised to aid with this family communication and family testing (as per figure). It should be emphasised that health professionals will generally not contact relatives without patient permission.
Test results may be uploaded to My Health Record (MyHR).	Patients can be given the option of whether their results are uploaded to MyHR. However, states and organisations will have their own policies regarding opt out procedures and what results are uploaded to MyHR. You should be aware of relevant policies in your state/organisation.
Interpreter/Liaison Officer Signature <i>Optional (added based on jurisdictional policy or procedural requirements)</i>	In some jurisdictions where an interpreter has been involved in the consent consultation, they are required to sign the consent form as well as the patient.

OTHER POINTS FOR DISCUSSION

DISCUSSION POINT	EXPLANATION
The sample will be stored and may be shared with other laboratories to assist with genomic testing	The patient should be informed that their sample may be used for the purpose of quality control, internal validation, test improvement, and training purposes by the accredited laboratory that is organising testing. The sample may also be used as a positive control for the testing of blood relatives. This is part of usual testing processes and does not require additional consent. Refer to local guidelines and policies if a patient asks to have their sample destroyed earlier or returned to them.

DISCUSSION POINT	EXPLANATION
Patient Fact Sheet	The Patient Fact Sheet has been developed to assist patients in understanding the benefits, consequences, and limitations of tissue-targeted genomic testing, as well as provide a resource to guide discussions with their health care providers and family members to decide whether to have testing or not. Patients should be given sufficient time to read, understand and ask questions about this fact sheet before giving consent. Some patients may wish to delay giving consent until they have had time to give it further consideration. The Patient Fact Sheet is not an exhaustive list of answers to the questions that patients might have and should not replace the pre-test discussion between you and your patient.

OTHER POINTS FOR CONSIDERATION

CONSIDERATION	EXPLANATION
Aboriginal and Torres Strait Islander Peoples	The storage, use, and disclosure of genomic clinical data and information may uniquely impact Aboriginal and Torres Strait Islander Peoples and have possible impacts on the broader Aboriginal and Torres Strait Islander community. Specific consideration must be given to the limited availability of genomic reference data for Aboriginal and Torres Strait Islander Peoples and the significant implications this has on the degree of certainty of results and the management of incidental findings. Initiatives such as that of the Australian Alliance for Indigenous Genomics (ALIGN) and the Centre for Population Genomics in Australia are working to increase representation of First Nations peoples in reference databases. The approach to obtaining consent should consider cultural practice, belief, and support systems of Aboriginal and Torres Strait Islander Peoples. This will facilitate the appropriate people to be part of the decision-making process, while supporting people to make a choice about testing that is consistent with their values, whether individual or cultural. This applies to all patients, regardless of ethnicity or ancestry. Resources to support Aboriginal and Torres Strait Islander people: • Culturally safe communication resources can be found here. Further resources • Online course by the Australian Alliance for Indigenous Genomics (ALIGN): Genomics Our Way. • Publications pertaining to structure and variation Indigenous genomics: ◦ The landscape of genomic structural variation in Indigenous Australians ◦ Indigenous Australian genomics show deep structure and rich novel variation

CONSIDERATION	EXPLANATION
Cultural, ethnic, and linguistic diversity	Consideration must be given to cultural, ethnic and linguistic diversity, and the relevant implications for consent. Health professionals should follow local policies and guidelines relevant to the delivery of health services to culturally and linguistically diverse populations, including the use of interpreters for non-English speaking patients.
Patients with disabilities	Where a patient has particular communication needs due to visual and/or hearing impairments, appropriate actions should be taken to assist them to understand the implications and benefits of testing. You should follow the protocols of your particular organisation, specific to the delivery of health care for patients with disabilities and/or communication. People should be offered Easy Read resources to ensure they have the opportunity to provide fully informed consent. Gene Equal has developed a toolkit for health professionals that can be found here .

FURTHER RESOURCES

'Requirements for Human Medical Genome Testing Utilising Massively Parallel Sequencing Technologies' (First Edition 2017): Information on laboratory requirements for reporting of variant of uncertain origin and the management of incidental findings

NPAAC Laboratory Retention of Records and Samples (Ninth edition 2022): National Pathology Accreditation Advisory Council guidelines

EviQ- Mainstreaming genetic testing for oncology teams: A focus on genetic testing in cancer patients: This learning activity for healthcare professionals takes a step-by-step approach to the mainstreaming process and its role in the management of cancer patients. It also outlines how oncology teams can implement mainstream genetic testing in their oncology units.

RCPA test directory: This website contains a comprehensive listing of all genes from the Human Gene Nomenclature Committee (HGNC) database alongside laboratories and tests available in the country. You can browse genes and tests or, if you are a laboratory member, add and edit tests available.

Somatic variant classification principles:

Standards and Guidelines for the Interpretation and Reporting of Sequence Variants in Cancer: Somatic variant classification principles.

Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology: Non-cancer pathogenicity (often use adaptations of germline guidelines)

Standards for the classification of pathogenicity of somatic variants in cancer (oncogenicity): Joint recommendations of Clinical Genome Resource (ClinGen), Cancer Genomics Consortium (CGC), and Variant Interpretation for Cancer Consortium (VICC): Cancer oncogenicity

GLOSSARY

Germline variant: a genetic variant that can be found in all cells of the body and has been present since conception. These variants can be inherited or *de novo* (new in the individual from the point of conception). Germline variants may be passed on to offspring.

Somatic variant: a genetic variant that has been acquired *after* conception in a confined set of cells or tissues. A somatic variant may arise during embryogenesis (somatic mosaicism), or may occur after birth as part of disease/cancer or as a normal part of ageing. Somatic variants cannot usually be passed on to offspring

Variant Allele Frequency (VAF): the number of times a variant is detected within reads of a gene compared to the total number of times that gene is sequenced. VAF gives an indication of the proportion of cells in the sample harbouring the variant. When testing a tumour sample, tumour purity can also influence the VAF. Not all laboratories will report VAF.

Variant classification: the process undertaken by diagnostic laboratory specialists to annotate and classify genetic variants detected during testing with available evidence, to determine the likelihood that the variant is responsible for the patient's phenotype, and/or has clinical significance. This is done according to specific guidelines and can differ between germline and somatic variants. It usually includes assessments of:

- **Somatic:**

- a. **Pathogenicity/Oncogenicity (non-malignant/malignant conditions, respectively)**

- Patho/Oncogenic (Class 5): variant is causative
 - Likely Patho/Oncogenic (Class 4): variant is likely causative
 - Variant of uncertain significance (Class 3): it is uncertain at this time whether it is or is not causative, commonly referred to as VUS or VOUS
 - Likely benign (Class 2): variant is not likely to be causative
 - Benign (Class 1): variant not causative

- b. **Clinical significance (if relevant to condition)**

- Clinically significant (Tier I - Strong, & Tier II - Potential)
 - Uncertain clinical significance (Tier III)
 - Likely benign/ \benign (Tier IV)

- See 'Further resources' section for references on somatic variant classification.

- **Germline:**

- a. **Pathogenicity**

- Pathogenic (Class 5): variant is causative
 - Likely pathogenic (Class 4): variant is likely causative
 - Variant of uncertain significance (Class 3): it is uncertain at this time whether it is or is not causative, commonly referred to as VUS or VOUS
 - Likely benign (Class 2): variant is not likely to be causative
 - Benign (Class 1): variant not causative