The clinical utility of whole genome, transcriptome and methylation sequencing and proteomics in classifying “unclassifiable” tumours

Project summary: Tumour classification is becoming increasingly defined by the underlying molecular changes in any given cancer. However, using current morphological and molecular methodologies many tumours defy characterization and classification. The use of whole genome DNA sequencing, whole transcriptome sequencing and proteomics will help identify the underlying molecular basis of unclassifiable cancers, enable biological insight as to aetiology and potentially enable new diagnostic categories to be determined.

Justification

The combination of expert pathologists together with access to high throughput genomics, bioinformatic pipelines and curation of variants is very limited. It is hypothesized that a pan-genomic approach will provide a deeper understanding of unclassifiable cancers and enable improved classification of such diagnostic dilemmas and identification of new entities

Vision

Rendering a pathologic diagnosis in all patients.

Goal

To improve the diagnostic, prognostic and therapeutic options for patients with unclassifiable cancers

Target audience

Clinicians and pathologists, cancer researchers

This project is being developed under Peter MacCallum Cancer Center ’s leadership, led by Dr Stephen Fox and in collaboration with:

- University of Melbourne
- University of Queensland,
- NSW Health Pathology
- Children's Medical Research Institute.

IC3R collaboration for cancer classification