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. It is hypothesized that a pan-omic approach will provide a deeper understanding of unclassifiable cancers and enable improved classification of such diagnostic dilemmas and identification of new entities..

Justification

The combination of expert pathologists together with access to high throughput genomics, bioinformatic pipelines and curation of variants is very limited. The use of complex 'omics to underpin a diagnosis is performed in the context of case reports or small series and has/is not to the best of our knowledge performed in a systematic manner for the purpose of tumour classification.

Goal

The use of whole genome DNA and 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..

Target audience

Pathologists

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,
- Pathology Queensland,
- University of Sydney, Royal North Shore Hospital
- Children's Medical Research Institute.

IC3R collaboration for cancer classification