



**20TH ANNIVERSARY  
CONFERENCE**  
30 October – 2 November 2022  
Novotel Twin Waters  
Sunshine Coast, Queensland

## POSTER PROGRAM

as at 13 October

Poster Number	AUTHOR	AFFILIATION	POSTER TITLE
1	Brad Balderson	The University of Queensland	Selective requirement for polycomb repressor complex 2 in the generation of specific hypothalamic neuronal subtypes
2	Gulrez Chahal	Murdoch Children's Research Institute	CaraVaN: Prioritising Cardiac Variants in the Non-coding genome
3	Jessie Chang	The Peter Doherty Institute for Infection and Immunity	Short and long-read scRNA-seq uncovers age and strain-dependent responses in human nasal epithelia infected with SARS-CoV-2
4	Natalie Charitakis	Murdoch Children's Research Institute	Benchmarking Methods for the Identification of Spatially Variable Genes in Spatial Transcriptomics Datasets
5	Kazzem Gheybi	The University Of Sydney	Evaluating germline testing panels in Southern African men with advanced prostate cancer
6	Andreas Halman	Peter MacCallum Cancer Centre	Using human sequencing data to detect microbes and host integration sites
7	Mehedi Hasan	The University Of Sydney	Optical genome mapping – new insights from rare inherited structural variants to tumour complexity
8	Jue Jiang	The University Of Sydney	ANO7 Ethnic Diversity and Advanced Prostate Cancer
9	Mathew Jones	University of Queensland Diamantina Institute	Decoding DNA Replication Dynamics Using Nanopore Sequencing
10	Joey Lai	The Westmead Institute for Medical Research	High-dimensional spatial transcriptomic capability at the Westmead Research Hub core facilities
11	Vanessa Lakis	QIMR Berghofer Medical Research Institute	Is Cytology Slides an Alternative Source of DNA for Genomic Testing for Metastatic Lung Cancer



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12	Peter Lau	Australian Genome Research Facility	Low Input Long-read Methylome Sequencing
13	Andrew Lonsdale	Peter MacCallum Cancer Centre	Toblerone: detecting exon deletion events in cancer using RNA-seq
14	Isabelle McGrath	The University of Queensland	Genomic Insights into the Relationship between Endometriosis and its Comorbidities
15	James Miller	PacBio	A New Standard: High MAG Recovery and Precision Species Profiling of a Pooled Human Gut Microbiome Reference using PacBio HiFi Sequencing
16	James Miller	PacBio	Extracting CpG Methylation from PacBio HiFi Whole Genome Sequencing
17	Sally Mortlock	The University of Queensland	Unravelling disease risk using multi-omic data: The role of genetic regulation in endometriosis risk and pathogenesis
18	Ebtihal Mustafa	Peter MacCallum Cancer Centre	Establishing functional drivers and novel therapeutic targets in oesophageal adenocarcinoma
19	Felicity Newell	QIMR Berghofer Medical Research Institute	Genomics of melanoma subtypes: whole-genome sequencing of 570 tumours
20	Hieu Nim	Murdoch Children's Research Institute	Mining cis-regulatory elements data to identify cardiac disease-causing genes
21	Katia Nones	QIMR Berghofer Medical Institute	Comparing Comprehensive Genomic Profile Platforms in EBUS-TBNA Samples from NSCLC.
22	Katherine Pillman	Centre For Cancer Biology, University Of South Australia	Network analysis of microRNA/transcription factor-driven cascade reveals the regulatory structure
23	Miranda Pitt	University of Melbourne	Evaluating the "-omes" of Extensively Drug-Resistant <i>Klebsiella pneumoniae</i> using Native DNA and RNA Nanopore Sequencing
24	Zuwei Qian	Pacific Biosciences	Enablement of Long-Read Targeted Sequencing Panels Using Twist Hybrid Capture and PacBio HiFi Sequencing
25	Daniel Rawlinson	University of Melbourne	Imputation of single-cell surface protein abundances using linear models of single-cell transcript expression



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26	Jack Royle	Australian Genome Research Facility	Metagenomic insights of a complex soil sample using the PacBio Sequel II
27	Adrian Salavaty	Children's Cancer Institute	InCRIMP: a versatile computational model for the integrative analysis of multi-omics data
28	Pamela Soh	The University Of Sydney	Profiling prostate cancer genetic risk associated with African ancestry
29	Dhanya Sooraj	Australian Genome Research Facility	Allegro: a low-cost high throughput targeted genotyping approach for sustainable genetic breeding
30	Qiao Wen Tan	Nanyang Technological University	Cross-stress gene expression atlas of Marchantia polymorpha reveals the hierarchy and regulatory principles of abiotic stress responses
31	Jiang Tao	Garvan Institute of Medical Research	Development of a Customised Targeted Panel for Circulating Tumour DNA (ctDNA) Analysis in Prostate Cancer
32	Michael Vacher	CSIRO	Integrating multiple omics platforms to identify biological signatures of Alzheimer's disease
33	Carter Wright	Hudsonalpha Institute For Biotechnology	Contribution of rare genetic variation in patients with early-onset or atypical dementia
34	Lijun Xu	QIMR Berghofer	Characterisation of Homologous Recombination Status with BRCA1 or RAD51C Methylation in a Pan-cancer Context
35	Fei Yang	The University of Queensland	A comprehensive analysis for transcriptome-wide isoform level dysregulation in endometriosis
36	David Yoannidis	Peter MacCallum Cancer Centre	MAC-seq: high-throughput, low-cost RNA-seq from cell lysates



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## LIGHTNING POSTER PROGRAM

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Poster Number	AUTHOR	AFFILIATION	POSTER TITLE
37	Denis Bienroth	Murdoch Children's Research Institute	Spatially Resolved Transcriptomics Exploration in Virtual Reality
38	Ashton Curry-hyde	University of New South Wales	Investigating the epitranscriptome in human tissues
39	Macabe Daley	Children's Cancer Institute	Hey Siri, how can I use Deep Learning for Variant Calling in my Familial Whole Genome Sequencing Studies?
40	Gunjan Dixit	Australian National University	Predicting cell-type specific combinatorial binding of neuronal transcription factor network by Deep Learning
41	Jillian Hammond	Garvan Institute of Medical Research	Assembling high-quality sea snake genomes to investigate the genetic basis of aquatic adaptation
42	Kaitao Lai	University Of Sydney	Shotgun microbial profiling reveals geo-ethnic disparities in aggressive prostate cancer
43	Lingchen Liu	Qimr Berghofer Medical Research Institute	Application of Long read sequencing (LRS) in cancer genomics
44	Chelsea Mayoh	Children's Cancer Institute	Value of RNA-sequencing in precision medicine expands beyond fusion detection
45	James Miller	PacBio	Sequencing By Binding (SBB) Shows Superior Sensitivity and Specificity of Detection of Low Frequency Variants from ctDNA
46	Mark Pinese	Children's Cancer Institute	Having our Cake and Eating it Too: Building Speculative Research into Clinical Genomics Studies
47	Michael Rhodes	NanoString Technologies	The Spatial Biology Revolution: multi-omic whole-transcriptome GeoMx profiling combined with sub-cellular resolved Spatial Molecular Imaging



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48	Hiruna Samarakoon	Garvan Institute of Medical Research	Flexible and efficient handling of nanopore sequencing signal data with slow5tools
49	Kira Xiaohuan Sun	BGI International Pty Ltd	Stereopy as an advanced tool in interpreting spatial transcriptomics data
50	Berivan Temiz	University of Otago	Characterization of Botrylloides diegensis whole body regeneration through single-cell RNA-sequencing
51	Erik Thompson	Queensland University of Technology	Identifying Metabolic Shift Gene Signature Pattern In The Wnt-Associated Epithelial-Mesenchymal Plasticity Of The PMC42 Breast Cancer Model System
52	Janette Tong	TrendBio	Automated processing of solid tissues into single cells or nuclei for genomics and cell biology applications with the Singulator™ 100 system
53	Kent Zaitlik	Lifebit Biotech Limited	A novel reference architecture for multi-party federation: enabling joint analysis of large-scale clinical-genomic data across distributed Trusted Research Environments