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# Event Agenda

Australasian Genomic Technologies Association (AGTA) Annual Conference 2025

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## Monday, October 13, 2025

9:00 AM - 10:30 AM

**Registration and Coffee**

10:00 AM - 10:30 AM

**Welcome to Country and Opening Remarks**

Convenor: Martin Smith, Sandra Fitzgerald, Mark Cowley

10:30 AM - 12:00 PM

**Clinical Genomics and Precision Oncology**

Location: Main Stage

Moderator: Mark Pinese

**Roche Introduction**

10:30 AM - 10:35 AM

Speaker: Jaedon Scott

**Molecular Second Opinions**

10:35 AM - 10:55 AM

Speaker: Sean Grimmond

**Breaking the Bottleneck in Genomic Testing: Accelerating Variant Analysis using Large Language Models**

10:55 AM - 11:15 AM

Speaker: Simon Sadedin

**Connecting the Transcriptome and Epigenome to Uncover Hidden Insights in AML**

11:15 AM - 11:25 AM

Speaker: Reza Ghamsari

**Nanopore direct RNA sequencing reveals transcriptome and epitranscriptome regulation by long non-coding RNAs in childhood acute lymphoblastic leukemia**

11:25 AM - 11:35 AM

Speaker: Qing Wang

**AI-Driven Integrative Frameworks to Advance Precision Therapeutics in Retinopathies**

11:35 AM - 11:40 AM

Speaker: Diya Prabhuram

**Panel Discussion**

11:40 AM - 12:00 PM

Speakers: Sean Grimmond, Simon Sadedin, Reza Ghamsari, Qing Wang, Diya Prabhuram, Mark Pinese

12:00 PM - 1:00 PM

**Lunch**

**Roche SBX unveiling**

12:30 PM - 1:00 PM

Location: Roche Lounge

1:00 PM - 2:30 PM

## Population Genomics, Indigenous Genomics, and Rare Disease Genomics

Location: Main Stage

Moderator: Hugh French

### Olink Introduction

1:00 PM - 1:05 PM

Speaker: Renu Balyan

### Precision Psychiatry for Mental Health – It's Not all in the Mind

1:05 PM - 1:25 PM

Speaker: Clarissa Yates

### African Genomes – untapped potential

1:25 PM - 1:45 PM

Speaker: Vanessa Hayes

### Combinatorial multivariate epigenomic patterns reveal the genomic basis of cell phenotypes underpinning complex traits and disease

1:45 PM - 1:55 PM

Speaker: Woo Jun Shim

### Pangenome interrogation exposes the limitations of Hg38 in capturing population-specific diversity

1:55 PM - 2:05 PM

Speaker: Aria Pestonji

### SpliceTraceR identifies atypical splicing events driven by splice-site variants using targeted next-generation sequencing data.

2:05 PM - 2:10 PM

Speaker: Muneeza Maqsood

### Q&A Panel

2:10 PM - 2:30 PM

Speakers: Renu Balyan, Clarissa Yates, Vanessa Hayes, Aria Pestonji, Woo Jun Shim, Muneeza Maqsood

2:30 PM - 3:00 PM

## Afternoon Tea

3:00 PM - 4:00 PM

## Keynote: Aziz Al'Khafaji, Advances in Transcriptomics, Methods and Applications

Location: Main Stage

Moderator: Martin Smith ; Speaker: Aziz Al'Khafaji

### Advances in Transcriptomics, Methods and Applications

3:05 PM - 4:00 PM

Location: Main Stage

Speaker: Aziz Al'Khafaji

**Uncovering Germline Structural Variants in Paediatric Acute Myeloid Leukaemia**

4:03 PM - 4:06 PM

Location: Main Stage

Speaker: Luis Arriola-Martinez

**Hypoxia-related germline variants associated with ancestral disparities in prostate cancer clinical presentation**

4:06 PM - 4:09 PM

Speaker: Kangping Zhou

**AGTA Ads: Mettler Toledo**

4:09 PM - 4:11 PM

Location: Main Stage

**Using spatial transcriptomics to understand the molecular mechanisms underlying cardiac rhabdomyomas**

4:11 PM - 4:14 PM

Speaker: Natalie Charitakis

**Development of an ancestry-aware EPIC array filtering resource reveals heavy metal-associated DNA methylation in prostate cancer**

4:14 PM - 4:17 PM

Speaker: Jenna Craddock

**AGTA Ads: TECAN**

4:17 PM - 4:19 PM

Location: Main Stage

**Integrative Analysis of microRNA, circRNA, and Alternative Splicing in Neuroblastoma**

4:19 PM - 4:22 PM

Speaker: Roopan Giri

**Neo-Antigen Identification in Tumors Harboring Splice Factor Mutations as a Step Towards Cancer Immunotherapy**

4:22 PM - 4:25 PM

Speaker: Esther Güse

**AGTA Ads: Dovetail Genomics**

4:25 PM - 4:27 PM

**Uncovering Aberrant Mesenchymal Programs in Neuroblastoma Using a Sympathoadrenal iPSC Model**

4:27 PM - 4:30 PM

Speaker: Tayla Albertini

**A Specialised Knowledge Graph to Semi-automate the Curation of Germline Variants in Paediatric Cancer Patients**

4:30 PM - 4:33 PM

Speaker: Weilin Wu

**Ensemble approach for somatic L1 discovery in paediatric neuroblastoma using whole-genome sequencing**

4:35 PM - 4:38 PM

Speaker: Nandan Deshpande

**From Variants to Cell Types: CLEAR Mapping of Breast Cancer Genetic Risk**

4:38 PM - 4:41 PM

Speaker: Lefei Wang

**AGTA Ads: Ramaciotti Centre for Genomics**

4:41 PM - 4:43 PM

**Characterising TAL1\_AB-like and TAL1\_DP-like Subtypes in Paediatric T-ALL with a DP-AB Axis Score**

4:43 PM - 4:46 PM

Speaker: Susan Corley

**Scaling for African Inclusion in High-Throughput Whole Cancer Genome Bioinformatic Workflows**

4:46 PM - 4:49 PM

Speaker: Jue Jiang

**AGTA Ads: TrendBio**

4:49 PM - 4:51 PM

**AEon: Improving Ancestry Estimation For Diverse Populations**

4:51 PM - 4:54 PM

Speaker: Naomi Warren

**Dynamic and ongoing de novo L1 retrotransposition in tumors of high-grade serous ovarian cancer patients**

4:54 PM - 4:57 PM

Speaker: Barun Pradhan

**Affinity proteomics in elucidating clinical disease pathways and development of diagnostic biomarker panels**

4:59 PM - 5:02 PM

Speaker: Sam Olechnowicz

**Revealing the landscape and characteristics of trans-splicing in health and cancer**

5:02 PM - 5:05 PM

Speaker: Minghan Wu

5:05 PM - 7:00 PM

**Poster Session + Drinks & Canapés**

Location: Upstairs Atrium

**Poster Session I**

5:05 PM - 7:00 PM

Location: Upstairs Atrium

7:00 PM - 9:00 PM

**Student Function**

Location: Level 1 Bar (Roundhouse)

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**Tuesday, October 14, 2025**

8:00 AM - 9:30 AM

**AGTA Junior - Student & ECR Breakfast Mentoring Session**

Location: Level 1 Bar (Roundhouse)

Facilitator: Safaa Al Haj Hussein, Isabela Almeida, Kangping Zhou ; Mentor (Academia): Mark Pinese, Mark Cowley, Vanessa Hayes, Ruby Lin, Fatemeh Vafaei ; Mentor (Industry): Mark Crowe, David Barda, Kay Anantanawat, Ebru Boslem, Kerith-Rae Dias

9:30 AM - 11:00 AM

**Innovative & Emerging Genomic Technologies I**

Location: Main Stage

Moderator: Brian Gloss

**DKSH & PacBio: Launching a Partnership**

9:30 AM - 9:35 AM

**Advancing long-read sequencing methods for human genomics**

9:35 AM - 9:55 AM

Speaker: Andre Reis

**The basis for L1 retrotransposon enrichment on the human X chromosome**

9:55 AM - 10:15 AM

Location: Main Stage

Speaker: Geoffrey Faulkner

**Cornetto: Adaptively integrated sequencing and assembly of near-complete genomes**

10:15 AM - 10:35 AM

Location: Main Stage

Speaker: Ira Deveson

**SemanticST: Spatially Informed Semantic Graph Learning for Clustering, Integration, and Scalable Analysis of Spatial Transcriptomics**

10:35 AM - 10:45 AM

Speaker: Roxana Zahedi Nasab

**A comprehensive benchmarking study of spatial transcriptomics methods to help make informed experimental and analytical decisions**

10:45 AM - 10:50 AM

Speaker: Daniela Zalcenstein

**Q&A Panel**

10:50 AM - 11:00 AM

Location: Main Stage

Speakers: Andre Reis, Ira Deveson, Geoffrey Faulkner, Daniela Zalcenstein, Nadia Davidson

11:00 AM - 11:30 AM

**Morning Tea**

**KiloBrains: A Conversational AI Platform for Accessible Genomics and Bioinformatics Analysis**

11:33 AM - 11:36 AM

Speaker: Zheng (John) Su

**Multi-omics signatures indicative of status and effectiveness of vaccination against SARS-CoV-2 in ferrets**

11:36 AM - 11:39 AM

Speaker: Laurence Wilson

**AGTA Ads: SeekGene**

11:39 AM - 11:41 AM

**A new pathway for methylation sequencing at Garvan: 5-base and 6-base workflows for simultaneous 5hmC, 5mC detection on top of genomes**

11:41 AM - 11:44 AM

Speaker: Orion Tong

**Utilizing Ampli-Fi assemblies to advance pangenomic applications in conservation.**

11:44 AM - 11:47 AM

Location: Main Stage

Speaker: Samuel Bagot

**AGTA Ads: Sequins**

11:47 AM - 11:49 AM

**Identifying the evolution of synergistic mutations in Influenza using association rule mining**

11:52 AM - 11:55 AM

Speaker: Carol Lee

**AGTA Ads: AGRF**

11:55 AM - 11:57 AM

**Interpretable Machine Learning for Mutation Rule Discovery in Pathogen Genomes: A Case Study on SARS-CoV-2**

11:57 AM - 12:00 PM

Speaker: Nehleh Kargarfard

**Accelerating Analysis on UK Biobank 500,000 WGS: RAPpoet Boosts Speed and Cut Costs**

12:00 PM - 12:03 PM

Speaker: Letitia Sng

**AGTA Ads: Garvan Genomics Platform**

12:03 PM - 12:05 PM

**LINDTIE: Identify Novel Structural and Splice Variants in Long-read Transcriptome Sequencing**

12:05 PM - 12:08 PM

Speaker: Jia Wei Tan

**Using Kolmogorov-Arnold Networks, an ExplainableAI Method, to Integrate Multiomics and Interpret the Relationships Underpinning Complex Traits**

12:08 PM - 12:11 PM

Speaker: James Temple

**AGTA Ads: South Australian Genomics Centre (SAGC)**

12:11 PM - 12:13 PM

**A Comparative Evaluation Of 10x, BD Rhapsody, And DEFNDseq Multiome Workflows**

12:13 PM - 12:16 PM

Speaker: Chris O'Keeffe

**Transforming Genome Assembly in Complex Plants with Nuclei-Enriched Omni-C**

12:16 PM - 12:19 PM

Speaker: Dhanya Sooraj

**AGTA Ads: Revvity**

12:19 PM - 12:21 PM

**Benchmarking quantification tools for TP53 isoforms using simulated long-read RNA sequencing data**

12:21 PM - 12:24 PM

Speaker: Jonathan Fu

**AVIT124: High-Quality Short-Read Sequencing and Spatial Multi-Omics Capabilities from a Single, Cost-Effective Instrument**

12:24 PM - 12:27 PM

Speaker: Rabia Chaudhry

**AGTA Ads: Oxford Nanopore Technologies**

12:27 PM - 12:29 PM

**Decoding disease risk: A framework from discovery to functional characterisation of novel risk-associated protein-coding and lncRNA genes**

12:29 PM - 12:32 PM

Speaker: Isabela Almeida

**Advancing Non-Invasive Diagnostics: Development of a Human Kidney Injury Assay Using Methylated Cell-Free DNA**

12:32 PM - 12:35 PM

Speaker: Shanon Ranjit

12:35 PM - 2:00 PM

**Lunch & Poster Session**

Location: Exhibitor lounge & Upstairs atrium

**Poster Session II**

12:35 PM - 2:00 PM

Location: Upstairs Atrium

1:00 PM - 2:00 PM

**Sponsor/Tech Showcase**

2:00 PM - 3:30 PM

**Microbial, Agricultural & Environmental Genomics**

Location: Main Stage

Moderator: Elizabeth Ross

**Thermo Fisher Scientific**

2:00 PM - 2:05 PM

Location: Main Stage

**RNAi in Plants (Mechanistic dissection and functional assessment of exogenous RNAi by active siRNA sequencing)**

2:05 PM - 2:25 PM

Speaker: Chris Brosnan

**Genomic surveillance to inform anti-Klebsiella pneumoniae vaccines**

2:25 PM - 2:45 PM

Speaker: Kelly Wyres

**Evaluating genotyping accuracy of structural variants (SV) and SNP at population-scale for the Bovine Long Read Consortium**

2:45 PM - 2:55 PM

Speaker: Tuan Nguyen

**Streamlining Nanopore direct RNA sequencing for bacteria: are we there yet?**

2:55 PM - 3:05 PM

Location: Main Stage

Speaker: Miranda Pitt

**Growth condition specific DNA methylation patterns in the Escherichia coli genome**

3:05 PM - 3:10 PM

Speaker: Ziming Chen

**Q&A Panel**

3:10 PM - 3:30 PM

Speakers: Chris Brosnan, Kelly Wyres, Ziming Chen, Tuan Nguyen, Miranda Pitt

3:30 PM - 4:00 PM

**Afternoon Tea**

4:00 PM - 5:00 PM

**Keynote: Alison Van Eenennaam**

Location: Main Stage

Speaker: Alison Van Eenennaam ; Moderator: Sandra Fitzgerald

5:10 PM - 6:00 PM

**AGTA: Annual General Meeting**

Speaker: Mark Cowley

6:30 PM - 11:00 PM

**Conference Dinner & Entertainment**

Location: The Beresford, 354 Bourke Street, Surry Hills

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**Wednesday, October 15, 2025**

9:30 AM - 11:00 AM

## Innovative & Emerging Technologies II

Location: Main Stage

Moderator: Nadia Davidson

### Decode Sciences Introduction

9:30 AM - 9:35 AM

Location: Main Stage

### Dysregulated germinal centre: Increased splenic regulatory Tfh and atypical memory B cells in chronic malaria

9:35 AM - 9:55 AM

Speaker: Damian Oyong

### T helper (Th) cell epigenome dynamics in chronic inflammation

9:55 AM - 10:15 AM

Speaker: Chloe Goldsmith

### Combining Xenium spatial transcriptomics and imaging mass cytometry on a single tissue section

10:15 AM - 10:35 AM

Speaker: Ellis Patrick

### CONCERT-DR: A Context-Aware Transcriptomic Framework for Drug Repositioning

10:35 AM - 10:45 AM

Speaker: Hengxin Pan

### Short-read structural variant detection in the long-read sequencing era

10:45 AM - 10:50 AM

Speaker: James Slimmer

### Q&A Panel

10:50 AM - 11:00 AM

Speakers: Chloe Goldsmith, Ellis Patrick, Hengxin Pan, James Slimmer, Nadia Davidson

11:00 AM - 11:30 AM

## Morning Tea

11:30 AM - 12:30 PM

## Keynote: Translating Large-scale Genomics to Precision Oncology

Speaker: Edwin Cuppen ; Moderator: Mark Cowley

12:30 PM - 1:30 PM

## Lunch & Demos

1:30 PM - 3:00 PM

## Microbial, Agricultural & Environmental Genomics II

Location: Main Stage

Moderator: Miranda Pitt

### Multi-Omics for Predictive Modelling (A Grapevine Case Study)

1:35 PM - 1:55 PM

Location: Main Stage

Speaker: Hannah Robinson

### Genomics informed diagnostics for infectious diseases in wildlife

1:55 PM - 2:15 PM

Location: Main Stage

Speaker: Jemma Geoghegan

### Addressing Chimeric Gene Mis-Annotations in Non-Model Organisms Using Machine Learning Approaches

2:15 PM - 2:25 PM

Speaker: Andreas Bachler

### Mapping Cas13 Guide Pressure on Avian Influenza Evolution

2:25 PM - 2:35 PM

Speaker: Emiliana Weiss

### Evaluating Cross-Species Cell Type Annotation in Single-cell RNA-sequencing Data

2:35 PM - 2:40 PM

Speaker: Steven Morgan

### Q&A Panel

2:40 PM - 3:00 PM

Location: Main Stage

Speakers: Hannah Robinson, Jemma Geoghegan, Andreas Bachler, Miranda Pitt, Emiliana Weiss, Steven Morgan, Elizabeth Ross

3:00 PM - 3:30 PM

## Closing Remarks & Awards

Location: Main Stage

Speakers: Mark Cowley, Sandra Fitzgerald, Martin Smith