





Sunday 29 October 2017	
<b>PRE-CONFERENCE PROGRAM</b>	
1100 - 1600	<b>Technical Solutions to Single Cell Problems (Workshop)</b>
1200 - 1540	<b>Can Genome Editing Fulfil Its Promise in the Clinic and the Field? (Symposium)</b>
1400 - 1800	Conference Registration Open
<b>OPENING ORATION</b>	
1700 - 1715	<b>Welcome to Country – Kartanya Maynard</b>
1715 - 1800	<b>Opening Oration</b> <b>Dr Deanna Church, 10X Genomics</b> Technology impact on our view of technology
1800 - 2000	Welcome Reception & Trade Exhibition – Federation Ballroom, Hotel Grand Chancellor
Monday 30 October 2017	
0730 - 1730	Registration Desk Open
0800 - 1730	Trade Exhibition Open
0845 - 0900	<b>Official Welcome and Conference Opening</b>
<b>SESSION 1: Complex Trait Genomics</b>	
0900 - 0945	<b>Keynote Speaker</b> <b>Dr Elinor Karlsson, University of Massachusetts Medical School</b> Pet Dogs, Citizen Science and the Genomics of Behaviour
	
0945 - 1000	<b>Invited Abstract</b> <b>Dr John Blangero, UTRGV-South Texas Diabetes &amp; Obesity Institute</b> Environmental Signal Maximization in Human Complex Diseases Using Genetic Correction
1000 - 1015	<b>Invited Abstract</b> <b>Dr Kiyomet Bozaoglu, Murdoch Childrens Research Institute</b> Identification of Novel Genes in Large Families with Autism Spectrum Disorder
1015 - 1030	<b>Invited Abstract (Student)</b> <b>Mrs Patricia Graham, University of Tasmania</b> Whole exome sequencing and linkage analysis of extended pedigrees to identify glaucoma susceptibility genes
1030 - 1100	<b>Morning Refreshments &amp; Trade Exhibition</b>
<b>SESSION 2: Population Genetics and Evolution</b>	
1100 - 1130	<b>National Invited Speaker</b> <b>Professor Vanessa Hayes, Garvan Institute of Medical Research</b> Using genomics to decipher our modern human history
	
1130 - 1145	<b>Invited Abstract (ECR)</b> <b>Dr Mark Pinese, The Kinghorn Cancer Centre</b> The Medical Genome Reference Bank – Genomics of a disease-depleted, elderly Australian cohort
1145 - 1200	<b>Invited Abstract (ECR)</b> <b>Dr Nicholas Blackburn, UTRGV-South Texas Diabetes &amp; Obesity Institute</b> Untangling lipids – a pedigree based study of the plasma lipidome through whole genome sequencing to assess rare deleterious variants in 1,025 Mexican Americans.
1200 - 1215	<b>Invited Abstract</b> <b>Dr Michael Rhodes, Nanostring Technologies</b>

	Library-free, Targeted Sequencing of Native Genomic DNA and RNA from FFPE Samples Using Hyb & SeqTM technology – the Hybridization-based Single Molecule Sequencing System
1215 - 1315	<b>Lunch &amp; Trade Exhibition</b>
<b>SESSION 3: Computational Biology</b>	
1315 - 1400	<p><b>Keynote Speaker</b></p> <p><b>Dr Kimberly Reynolds, University of Texas Southwestern Medical Center</b></p> <p>Using genomic data to map functional interactions in cellular systems</p> 
1400 - 1415	<p><b>Invited Abstract (ECR)</b></p> <p><b>Dr Devika Ganesamoorthy, The University of Queensland</b></p> <p>Genotyping repeats with Nanopore Sequencing</p>
1415 - 1430	<p><b>Invited Abstract</b></p> <p><b>Dr Traude Beilharz, Monash University</b></p> <p>Building transcriptional landscapes using t-SNE based dimensionality reduction of public data</p>
1430 - 1445	<p><b>Invited Abstract (ECR)</b></p> <p><b>Dr Bennet McComish, University of Tasmania</b></p> <p>Genetic risk factors in a vulvar cancer cluster among young Indigenous women in Arnhem Land, Australia</p>
1445 - 1545	<b>Poster Session 1 &amp; Afternoon Refreshments</b>
<b>SESSION 4: Functional Genomics</b>	
1545 - 1615	<p><b>National Invited Speaker</b></p> <p><b>Associate Professor Greg Neely, The University of Sydney</b></p> <p>A genome-wide CRISPR-Cas9 knockout screen identifies novel anti-cancer drug resistant genes</p>
1615 - 1630	<p><b>Invited Abstract (ECR)</b></p> <p><b>Dr Brian Gloss, Garvan Institute of Medical Research</b></p> <p>High resolution temporal transcriptomics of mouse embryoid body development reveals complex expression dynamics of coding and noncoding loci</p>
1630 - 1645	<p><b>Invited Abstract</b></p> <p><b>Dr Anthony Borneman, The Australian Wine Research Institute</b></p> <p>Survival of the Fittest: The Fight For Dominance In Wine Fermentation And The Genomic Adaptations That Underpin Yeast Strain Performance</p>
1645 - 1700	<p><b>Invited Abstract (Student)</b></p> <p><b>Mr Mainul Hasan, University of Tasmania</b></p> <p>Genetic and molecular analysis of two new loci controlling flowering in garden pea, Pisum sativum.</p>
1800 - 2300	<b>Conference Dinner – Museum of Old and New Art (Mona)</b>

**Tuesday 31 October 2017**

0730 - 1730	Registration Desk Open
0800 - 1730	Trade Exhibition Open
0855 - 0900	Welcome to Day Two
<b>SESSION 5: Single Cell 'omics and Genome Assembly</b>	
0900 - 0945	<p><b>Keynote Speaker</b></p> <p><b>Dr Deanna Church, 10X Genomics</b></p> <p>High resolution biology using 10x</p> 
0945 - 1000	<p><b>Invited Abstract (ECR)</b></p> <p><b>Dr Seyhan Yazar, University of Edinburgh</b></p> <p>De novo Genome and Transcriptome Assemblies of the Bare-nosed Wombat</p>
1000 - 1015	<p><b>Invited Abstract</b></p> <p><b>Dr David Gallego-Ortega, Garvan Institute of Medical Research</b></p> <p>Modelling Breast Cancer Progression Using Massively Parallel Single-Cell RNA-seq Technology.</p>
1015 - 1030	<p><b>Invited Abstract (Student)</b></p> <p><b>Mrs Nona Farbehi, University of New South Wales</b></p>

	Single cell RNA-Seq of cardiac interstitial cells reveals novel populations in healthy and diseased heart
030 - 1100	<b>Morning Refreshments &amp; Trade Exhibition</b>
<b>SESSION 6: Synthetic Biology and Novel Technologies</b>	
1100 - 1130	<b>National Invited Speaker</b> <b>Professor Ian Paulsen, Macquarie University</b> Yeast 2.0 and beyond: Building the world's first synthetic eukaryote
1130 - 1145	<b>Invited Abstract (ECR)</b> <b>Dr Martin Smith, Garvan Institute of Medical Research</b> Big data from a small device: real time genomics with nanopore sequencing
1145 - 1200	<b>Invited Abstract</b> <b>Dr Longqi Liu, BGI</b> Parallel assay of single-cell chromatin accessibility and transcriptome
1200 - 1215	<b>Invited Abstract (Student)</b> <b>Mr Haojing Shao, The University of Queensland</b> Ongoing human chromosome end extension driven by a primate ancestral genomic region revealed by analysis of BioNano and Nanopore genomics data
1215 - 1315	<b>Lunch &amp; Trade Exhibition</b>
<b>SESSION 7: Bioinformatics and Data Analytics</b>	
1315 - 1400	<b>Keynote Speaker</b> <b>Dr Pauline Ng, Genome Institute of Singapore</b> Mutations that Matter
1400 - 1415	<b>Invited Abstract</b> <b>Dr Thom Quinn, Deakin University</b> A Compositionally Valid Pipeline for any-omics Data
1415 - 1430	<b>Invited Abstract (ECR)</b> <b>Dr Laurence Wilson, CSIRO</b> Using Machine Learning to understand CRISPR-Cas9 activity"
1430 - 1445	<b>Invited Abstract</b> <b>Dr Susan Corley, University of New South Wales</b> Functional insights from RNA-Seq are affected by decisions made early in the experimental design, library preparation and sequencing protocol
1445 - 1545	<b>Poster Session 2 &amp; Afternoon Refreshments</b>
<b>SESSION 8: Epigenetics and Transcriptomics</b>	
1545 - 1615	<b>National Invited Speaker</b> <b>Dr Paul Waters, University of New South Wales</b> Sex specific landscapes of DNA methylation on the marsupial X chromosome: the shape of silencing
1615 - 1630	<b>Invited Abstract</b> <b>Dr Oscar Luo, CSIRO</b> RNA-Chromatin Interactome Reveals ncRNA Functions for Transcription Regulation and Genome Organization
1630 - 1645	<b>Invited Abstract (Student)</b> <b>Mr Simon Hardwick, Garvan Institute of Medical Research</b> Spliced synthetic genes as internal controls in RNA-seq experiments
1645 - 1700	<b>Invited Abstract</b> <b>Dr Irene Gallego Romero, The University of Melbourne</b> Dynamics of chromatin accessibility and transcription factor binding in human and chimpanzee pluripotent stem cells
1715 - 1745	<b>AGTA Annual General Meeting</b>
	<b>Student Function</b>

	<b>VIP Function</b>
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<b>Wednesday 1 November 2017</b>	
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0800 - 1730	Registration Desk Open
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0800 - 1200	Trade Exhibition Open
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0855 - 0900	Welcome to Day Three
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<b>SESSION 9: Comparative Genomics</b>	
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0900 - 0930	<b>National Invited Speaker</b> <b>Dr Austen Ganley, University of Auckland</b> Repetitive DNA: evolving safely in numbers
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0930 - 0945	<b>Invited Abstract</b> <b>Dr Anna MacDonald, Australian National University</b> The Oz Mammals Genomics initiative: mammal genomics, evolution and conservation at a continental scale
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0945 - 1000	<b>Invited Abstract</b> <b>Professor Justin Borevitz, Australian National University</b> Population structure of the Brachypodium species complex and genome wide dissection of agronomic traits in response to climate.
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1000 - 1015	<b>Invited Abstract (ECR)</b> <b>Dr Weerachai Jaratlerdsiri, Garvan Institute of Medical Research</b> Identifying Racial Differences in the Mutational Landscape of Aggressive Prostate Cancer
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1015 - 1045	<b>Morning Refreshments &amp; Trade Exhibition</b>
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<b>SESSION 10: Gene Editing and Gene Regulation</b>	
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1045 - 1115	<b>National Invited Speaker</b> <b>Associate Professor Alice Pebay, The University of Melbourne</b> Automated culture system for large scale disease modelling
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1115 - 1130	<b>Invited Abstract (ECR)</b> <b>Dr Quentin Gouil, Walter and Eliza Hall Institute of Medical Research</b> Extensive transcriptomic and epigenomic remodeling during Arabidopsis thaliana germination
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1130 - 1145	<b>Invited Abstract</b> <b>Mr Aidan O'Brien, Australian National University</b> Predicting the HDR Efficiency of CRISPR-Cas
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1145 - 1200	<b>Invited Abstract</b> <b>Dr Joseph Powell, The University of Queensland</b> Single cell sequencing reveals changes in the genetic control of gene expression through reprogramming of induced pluripotent stem cells from fibroblasts
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1200 - 1300	<b>Lunch &amp; Trade Exhibition</b>
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<b>SESSION 11: Medical and Cancer Genomics</b>	
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1300 - 1330	<b>National Invited Speaker</b> <b>Associate Professor Alicia Oshlack, Murdoch Childrens Research Institute</b> Single-cell RNA-seq: Analysis, simulation and kidneys in a dish
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1330 - 1345	<b>Invited Abstract (Student)</b> <b>Ms Johanna Jones, University of Tasmania</b> Whole genome sequencing is improving the identification of genetic causes of paediatric cataracts
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1345 - 1400	<b>Invited Abstract</b> <b>Dr Daniel Roden, Garvan Institute of Medical Research</b> Single-cell transcriptomics reveals functional heterogeneity in breast cancer cells
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1400 - 1415	<b>Invited Abstract</b> <b>Dr Eva Chan, Garvan Institute of Medical Research</b> Genome mapping illuminates architecture of chained fusions in cancer
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1415 - 1445	<b>National Invited Speaker</b> <b>Professor Sean Grimmond, The University of Melbourne</b> The Genomic Pathology of Pancreatic Cancers
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The 2017 AGTA Conference reserves the right to amend or alter any advertised details relating to dates, program and speakers if necessary and without notice, as a result of circumstances beyond their control. All attempts will be made to keep any changes to an absolute minimum.