

## 11th February 2018

### Conference Welcome

2:00PM - 2:10PM Auditorium

### Opening Lecture

2:10PM - 3:00PM Auditorium

Chair: Traude Beilharz

2:10 PM **Jennifer Doudna**

CRISPR-Cas Gene Editing: Biology, Technology and Ethics *abs# 1*

### Afternoon Tea

3:00PM - 4:00PM Exhibition Hall

### Session 1: Nuclear Organization and Chromosome Structure

4:00PM - 6:30PM Auditorium

Chairs: Tanya Soboleva & Rhys Allan

4:00 PM **Ali Shilatifard**

Principles of epigenetics and chromatin in development and human disease *abs# 2*

4:35 PM **Ian D Hickson**

Defining how problematic DNA replication impacts on chromosome segregation *abs# 3*

5:10 PM **Elizabeth Hinde**

Imaging chromatin dynamics during the DNA damage response by FLIM-FRET microscopy *abs# 4*

5:35 PM **Anthony J Cesare**

Actin polymerization alters nuclear architecture in response to DNA replication stress to maintain genome stability *abs# 5*

5:55 PM **Ulrike Schumann**

Investigating the function of 5-methylcytosine in mRNA biology *abs# 101*

5:58 PM **Katherine A Giles**

BRG1 maintains chromatin at active enhancers and the expression of proliferation genes in prostate cancer *abs# 102*

6:01 PM **Matthew E Ritchie**

Tools for preprocessing and benchmarking single cell RNA-sequencing data *abs# 103*

6:04 PM **Georgia R Kafer**

Sequential occupation of the nuclear periphery by H2A.Zac and H3K9me2 accompanies pluripotency loss in Human embryonic stem cells *abs# 104*

6:07 PM **Ulf Schmitz**

Intron retention redefines post-transcriptional gene regulation in vertebrate species *abs# 105*

**Welcome BBQ**

6:30PM - 8:30PM Lorne Surf Club

**Poster Session 1**

8:30PM - 10:30PM Louttit Bay Room

**Waruni Abeysekera**

Identifying Hepatitis B virus integration events on Mouse genome *abs# 107*

**Casey Ah-Cann**

Developing a novel embryonic lung progenitor culture system: technique and applications *abs# 108*

**Tanveer Ahmad**

RNA processing is critical for the generation of mature megakaryocytes capable of producing platelets *abs# 109*

**Joshua AM Allen**

Visualisation of telomeres by telomere fibre-FISH *abs# 110*

**Joshua Anderson**

Characterisation of NHL-2 in small RNA pathways of *Caenorhabditis elegans*. *abs# 111*

**Alyson Ashe**

Small RNA profiling of the reproductive tissues of the honeybee *Apis mellifera* *abs# 112*

**Vinod Benjamin**

The phosphorylation of H3.3 Serine 31 and its role in heterochromatin formation *abs# 113*

**Maina Bitar**

Genes with human-specific features, ncRNAs and innovations in genetic and epigenetic mechanisms cooperate to brain evolution *abs# 114*

**Jimmy Breen**

*msgbsR*: An R package for analysing methylation-sensitive restriction enzyme sequencing data *abs# 115*

**Christopher M Brown**

Viral genome analysis: bioinformatic analysis of RNA elements essential for replication *abs# 116*

**Tracy M Bryan**

Links between DNA replication stress and telomere extension in cancer cells *abs# 117*

**Emily L Button**

Analysis of functionally deficient variants of transcription factor *SIM2* present in patients with intellectual disabilities *abs# 118*

**Jessica Cale**

Antisense oligonucleotide-mediated exon skipping: a potential therapeutic strategy for Marfan syndrome *abs# 119*

**Michel Cannieux**

Efficient homology-directed repair using single-stranded DNA templates *abs# 120*

**Wing Fuk Chan**

Disrupting promoter-enhancer interaction of *Bcl11b* in T cell by CRISPR/Cas9 *abs# 121*

**Yunshun Chen**

Differential methylation analysis of reduced representation bisulfite sequencing experiments *abs# 122*

**Eugene Choi**

Identification of ALT phenotypes in telomerase positive cancers *abs# 123*

**Daria A. Chudakova**

Non-coding transcription and mitotic recombination of the ribosomal RNA gene repeats in cancer *abs# 124*

**Vignesh Kartik Chundru**

Fine-mapping reveals complex genetic architecture underlying DNA methylation *abs# 125*

**Michael B Clark**

Long-read sequencing reveals the splicing profile of the neuropsychiatric disease gene *CACNA1C* in human brain *abs# 126*

**Scott Cohen**

Electron microscopy of human telomerase *abs# 127*

**Lachlan Coin**

Chiron: Translating nanopore raw signal directly into nucleotide sequence using deep learning *abs# 128*

**Rhys N Colson**

Structural and functional analysis of the *C. elegans* TRIM protein NHL-2 *abs# 129*

**Caitlin Coombes**

Mutation Analysis and Effect on Prognosis of Direct Antiglobulin Test Positivity in Diffuse Large B-Cell Lymphoma *abs# 130*

**Jack A L Cooper**

Four gene regulatory functions of oncogenic potential for NONO protein in neuroblastoma *abs# 131*

**Vincent Corbin**

Detecting RNA Structure Heterogeneity in Cells *abs# 132*

**Brittany Croft**

FGF9 homodimerization is required for male sex determination *abs# 133*

**Emelyne Cunnington**

Can genomic and phenotypic analyses unravel how the yeast *Saccharomyces cerevisiae* evolves in emulsion culture? *abs# 134*

**Chen Davidovich**

Mechanism for RNA-mediated regulation of the histone methyltransferase Polycomb repressive complex 2 (PRC2) *abs# 135*

**Ruby Dawson**

Using *in utero* electroporation to model a second-hit mechanism for GATOR1-related focal epilepsy in mice *abs# 136*

**Andrew J Deans**

*FANCM* protein maintains genome stability by removing co-transcriptional R-loops *abs# 137*

**Donna Denton**

Hormone-mediated autophagy-dependent cell death in *Drosophila* *abs# 138*

**Ira Deveson**

Representing the human genome with chiral DNA reference standards *abs# 139*

**Renaë Domaschenz**

The Histone Variant H2A.Z is a Master Regulator of the Epithelial-Mesenchymal Transition *abs# 140*

**Deepti Domingo**

VISUALISING THE NONSENSE: Fluorescent quantitation of the nonsense mediated mRNA decay pathway during brain development *abs# 141*

**Richard J Edwards**

Genome-guided characterisation of evolved xylose metabolism in *Saccharomyces cerevisiae* *abs# 142*

**Tansel Ersavas**

MitoWisdom: An Unsupervised Mitochondrial Genome Analyser Using Deep Learning *abs# 143*

**James M Ferguson**

Unsupervised demultiplexing of single-cell barcodes from raw nanopore sequencing data *abs# 144*

**Matt Field**

Comparison of predicted and actual consequences of missense mutations *abs# 145*

**Elizabeth A Ford**

The Role of Twist in Glutamate Stimulated Neuronal Apoptosis *abs# 146*

**Alexandra L Garnham**

Analysis of ATAC sequencing data *abs# 147*

**Jozef Gecz**

Understanding the role of cellular mosaicism in PCDH19 epilepsy and intellectual disability. *abs# 148*

**Alexis G Gerassimou**

Mechanisms of regulation of the transcription factor Single-Minded 1 in obesity *abs# 149*

**Kevin R Gillinder**

Expanding the repertoire of Transcription Factor Motifs *abs# 150*

**Brian S Gloss**

Modelling Breast Cancer Progression Using Single-cell RNA-seq *abs# 151*

**Akira Gokoolparsadh**

The Landscape Of Circular RNA Expression In The Human Brain *abs# 152*

**Quentin Gouil**

Using long-read sequencing to detect haplotype-specific differential methylation *abs# 153*

**Hayley Goullée**

The Human "Muscle-ome": Studying the skeletal muscle transcriptome to understand normal muscle biology and disease *abs# 154*

**Taylin E Gourley**

*atz-1* promotes meiosis to maintain germline chromosomal integrity *abs# 155*

**Janya Grainok**

Development of Molecular Therapies for *PRPF31*-associated Retinitis Pigmentosa Using Splice-switching Antisense Oligonucleotides *abs# 156*

**Zoe L Grant**

Investigating the role of histone acetylation in angiogenesis *abs# 157*

**David Grasso**

Improved Chemistry for NGS Library Cleanup and Size Selection *abs# 158*

**Kristina Handler**

Optimisation of massively parallel single cell RNA-seq method (Drop-seq) in tumour tissues *abs# 159*

**Simon A Hardwick**

Transcriptional complexity of non-coding genomic regions associated with cognitive function *abs# 160*

**Vincent Harley**

RNA splicing in mammalian sex determination *abs# 161*

**Vincent Harley**

SRY and male sex bias in Parkinson's disease *abs# 162*

**Paul F Harrison**

Confident effect sizes controlling FDR provide an ideal ranking of differentially expressed genes *abs# 163*

**Rippe Hayashi**

A highly selective mechanism to discriminate transposon RNA from self-RNA in *Drosophila ovaries abs# 164*

**Jacki E Heraud-Farlow**

Protein recoding by ADAR1-mediated RNA editing is not essential for normal development and homeostasis *abs# 165*

**Erin E Heyer**

Transcriptional Consequences of Cancer Fusion Genes *abs# 166*

**Di Huang**

Therapeutic potential of antisense oligonucleotide-mediated exon inclusion for Stargardt disease *abs# 167*

**Yoshika Janapala**

Genome-wide discovery of translation control mechanisms *abs# 168*

**Natasha Jansz**

The role of Smchd1 in mediating higher order chromatin conformation *abs# 169*

**Johanna L Jones**

Whole genome sequencing is improving the identification of genetic causes of paediatric cataracts, including novel cataract genes. *abs# 170*

**Paul Kalitsis**

Loss of topoisomerase III beta is associated with hallmarks of genome instability *abs# 171*

**Thaksaon Kittipassorn**

Metabolic and transcriptomic analyses of Müller glial cells of the retina *abs# 172*

**Alexander Knights**

Regulation of novel 'eosinokines' in the development of beige fat *abs# 173*

**Andrew Kueh**

Investigating the role of mutant DNMT3A in Acute Myeloid Leukaemia and other cancers *abs# 174*

**Kristen Laricchia**

Mitochondrial variant calling in 15,496 individuals in the Genome Aggregation Database (gnomAD) *abs# 175*

**Timo Lassmann**

Personalized analytics to improve diagnostic rates in clinical sequencing. *abs# 176*

**Michael Lee**

Elucidating the molecular signatures underlying ALT activity in tumours *abs# 177*

**Jasmine Li**

Stepwise engagement of the Killer T cell function is underscored by H3K27 demethylation *abs# 178*

**Chun Shen Lim**

A Cross Species and Multi-omic Analysis Indicates the Exon/Intron Structure Preceding Initiation Codons Predicts their Translation Efficiency *abs# 179*

**Jonathan WC Lim**

Nuclear factor one transcription factors regulate developmental enhancers during brain development: insights from motif discovery *abs# 180*

**Ning Liu**

Investigating computational analysis pipelines and genomic proximity interactions in T lymphocytes *abs# 181*

**Jieqiong Lou**

Quantifying chromatin structure at the level of nucleosomes by correlative live cell FLIM-FRET microscopy and fixed cell single molecule localization microscopy. *abs# 182*

## 12th February 2018

### Breakfast Workshop - Implementing CRISPR CAS9

7:30AM - 8:30AM Auditorium

Chair: Paul Thomas

### Micro Break

8:30AM - 8:40AM Auditorium Foyer

### Session 2: Computational Biology

8:40AM - 10:10AM Auditorium

Chairs: Alicia Oshlack & Gaetan Burgio

8:40 AM **Kevin Esvelt**

Editing wild populations: local gene drive, evolutionary stability, and community guidance *abs# 11*

9:15 AM **Sara Ballouz**

Conservation of transcriptional variation across human, mouse and ... armadillo?! *abs# 12*

9:35 AM **Rafael Irizarry**

Accounting for systematic bias in bulk and single cell RNA-Seq data *abs# 13*

### Morning Tea

10:10AM - 11:00AM Exhibition Hall

### Session 3: Gene Regulation

11:00AM - 12:30PM Auditorium

Chairs: Alistair Forrest & Leonie Quinn

11:00 AM **Shyam Prabhakar**

Single-cell tumor transcriptomics: algorithms and applications *abs# 14*

11:35 AM **Julie Secombe**

Transcriptional regulation of neuronal function by the histone demethylase KDM5 *abs# 15*

12:10 PM **Rachel Woodhouse**

Chromatin modifiers SET-32 and SET-25 establish a transgenerational silencing signal in *Caenorhabditis elegans* *abs# 16*



12:22 PM **Qian Du**

DNA replication timing shapes the cancer epigenome *abs# 17*

### **Lunch**

12:30PM - 1:15PM Exhibition Hall

### **Micro Break**

2:45PM - 3:00PM Auditorium Foyer

### **Afternoon Break/High-content functional genomics workshop**

1:15PM - 2:45PM Horizons Room

Chair: Kaylene Simpson

### **Session 4A: Regulation of Gene Expression**

3:00PM - 4:00PM Auditorium

Chairs: Alyson Ashe & Greg Neely

3:00 PM **Belinda J Goldie**

3'-deoxyadenosine induces bulk transcript lengthening via alternative polyadenylation *abs# 18*

3:15 PM **Justin JL Wong**

Intron retention: A widespread and conserved mechanism of gene expression control regulated by epigenetic changes *abs# 19*

3:30 PM **Kate GR Quinlan**

Understanding the role of eosinophils in adipose tissue energy expenditure *abs# 20*

3:45 PM **David Gallego Ortega**

Modelling breast cancer progression using massively-parallel single-cell RNAseq technology. *abs# 21*

### **Session 4B: Disease & Development**

3:00PM - 4:00PM Horizons Room

Chairs: Andrew Perkins & Julia Horsfield

3:00 PM **Paul Lacaze**

Genome sequencing of 15,000 healthy elderly Australians *abs# 22*

3:15 PM **Jayne A Barbour**

Identifying the cause and function of T>G mutations in oesophagus and gastric cancer genomes *abs# 23*

3:30 PM **Nathan Palpant**

Cardiac directed differentiation using small molecule Wnt modulation at single-cell resolution *abs# 24*

3:45 PM **Karen Doggett**

Essential roles for minor class splicing in development and cancer *abs# 25*

### **Mini Break**

4:00PM - 4:30PM Auditorium Foyer

### **Session 5: Julian Wells Medal/Noncoding RNA and RNA Regulation**

4:30PM - 6:30PM Auditorium

Chairs: Vincent Harley & Timothy Mercer

4:30 PM **Greg Goodall**

MicroRNAs act on and within regulatory networks *abs# 26*

5:05 PM **Karla Neugebauer**

Coordination of RNA Processing events in vivo *abs# 27*

5:40 PM **Archa Fox**

Enhancing the spatiotemporal sub-nuclear sequestration of RNA binding proteins by manipulating paraspeckle size *abs# 28*

6:05 PM **Gabriella E Martyn**

Elevated foetal globin caused by natural regulatory mutations that disrupt foetal repressor binding *abs# 201*

6:08 PM **Mathew G. Lewsey**

Cross-regulation between the ethylene and abscisic acid hormone signalling pathways is regulated by EDF transcription factors *abs# 202*

6:11 PM **Sureshkumar Balasubramanian**

RNA-dependent epigenetic silencing directs transcriptional down regulation caused by intronic repeat expansions *abs# 203*

6:14 PM **Brittany Croft**

Duplication and deletion of key *SOX9* enhancers causes sex reversal in humans *abs# 204*

6:17 PM **Ewa M Michalak**

Canonical PRC2 function is essential for mammary gland development and affects chromatin compaction in mammary organoids *abs# 205*

6:20 PM **Martin Smith**

Welcome to the macrogenomics era: a long read revolution *abs# 206*

## **Dinner Break**

6:30PM - 8:30PM

## **Poster Session 2**

8:30PM - 10:30PM Louttit Bay Room

### **Lithin Louis**

Molecular and cellular role of RNA-binding proteins in cardiac biology and disease *abs# 207*

### **Robert Lu**

FANCM protects telomeres from aberrant replication fork processing in cancers engaging in Alternative Lengthening of Telomeres (ALT) *abs# 208*

### **Lana C Ly**

Investigating the role of ZBTB7A homodimerisation in adult erythroid cells *abs# 209*

### **Graham W Magor**

KLF1 is a pioneer transcription factor for erythroid cells *abs# 210*

### **John Manion**

Restoring Central Inhibition Relieves Chronic Neuropathic Pain *abs# 211*

### **Owen J Marshall**

When is a global repressor not a repressor? Genome-wide profiling of the Snail family transcription factor Worniu in neural stem cells *abs# 212*

### **Elizabeth A Mason**

Modelling transcriptional variability in single cell RNA-seq data during human embryogenesis captures changes in the regulation of critical developmental genes *abs# 213*

### **Stephen Mieruszynski**

Coordinated up-regulation of splicing machinery components in a zebrafish intestinal development mutant harbouring a mutation in *gtf2h4*, a component of the general transcription factor complex, TFIIH *abs# 214*

### **Katrina A Mitchell**

Identification of Hippo pathway target genes important for tissue growth. *abs# 215*

### **Kimberly Morgan**

Genetic and chemical approaches to inhibiting hyperplasia in a zebrafish model of hepatocellular carcinoma *abs# 216*

### **Zeynep MUTLU**

NEAT1 changes imatinib response and contributes to tyrosine kinase inhibitor-based resistance in a chronic myeloid leukemia cell line *abs# 217*

### **Greg Neely**

Whole genome dissection of the box jellyfish venom death pathway *abs# 218*

### **Christopher B Nelson**

The Tumor Suppressor EYA4 Functions in DNA Double Strand Break Repair *abs# 219*

**Christian Friberg F Nielsen**

Topoisomerase 2A is essential for maintenance of mitotic chromosome structure *abs# 220*

**Andy R Nilsen**

Investigating the evolution of truffle-like fungi *abs# 221*

**Katia Nones**

Mutational Landscape of Familial Breast Cancers *abs# 222*

**Bhupinder Pal**

Single-cell RNA profiling reveals developmental lineage relationships between the mouse mammary epithelial cells *abs# 223*

**Ann-Marie Patch**

Genomics of malignant pleural mesothelioma *abs# 224*

**Deepali Pathak**

Human *SRY* regulates haploid specific Protamine (*PRM1*) promoter activity *abs# 225*

**Andrew Pattison**

Predicting the outcome of breast cancer using novel RNA-Seq analysis *abs# 226*

**Jonas Paulsen**

Computational modeling reveals 4D genome reorganization during stem cell differentiation *abs# 227*

**Jodie Pearlman**

A Functional Genomic Approach to Identifying New Motor Neuron Disease Genes and Drug Targets *abs# 228*

**Timothy J Peters**

A general framework for evaluating cross-platform concordance in genomic studies *abs# 229*

**Chandran Pfitzner**

Developing CRISPR-Cas9 Based Gene Drives in *Mus musculus* *abs# 230*

**Chikako Ragan**

Insights into the biogenesis and possible functions of exonic circular RNA *abs# 231*

**Kelsie Raspin**

The identification of rare variants in Tasmanian prostate cancer pedigrees using whole-genome sequencing *abs# 232*

**Madara Ratnadiwakara**

Splicing factors as novel regulators of oncogenic miRNAs *abs# 233*

**Louise Robertson**

Expanding the RNA-guided endonuclease toolkit for mouse genome editing. *abs# 234*

**Jessica Robinson**

The A/HeJ Mouse: Dysfunction in Sex Development *abs# 235*

**Samuel Rogers**

MASTL overexpression promotes chromosome instability and metastasis in breast cancer *abs# 236*

**Joseph Rosenbluh**

Overcoming off target effects in CRISPR and RNAi loss of function screens *abs# 237*

**Joseph J Rossi**

Characterising Human Variants of the Transcription Factors NPAS3 and NPAS4 Identified in Patients with Mental Illness *abs# 238*

**Brendan Russ**

Modulation of higher order chromatin structures associated with virus-specific killer T cell differentiation *abs# 239*

**Jafar S. Jabbari**

Highly Parallel Concurrent Gene Expression and Iso-Seq Analysis of Single Cells *abs# 240*

**Agus Salim**

DECENT: Differential Expression with Capture Efficiency adjustmeNT for Single-Cell RNA-seq Data *abs# 241*

**Jack Scanlan**

Comparative phylogenomic evidence for a novel detoxification gene family in insects *abs# 242*

**Colin A Semple**

Breaking point: computational interrogation of structural variation in cancer *abs# 243*

**Manan Shah**

Investigating the role of R-loops in erythroid differentiation *abs# 244*

**Diksha Sharma**

Developing a bioinformatics pipeline to measure changes in ribosomal RNA genes copy number in cancer *abs# 245*

**Nikolay Shirokikh**

*In vivo* targets and mechanisms of gene control during protein synthesis *abs# 246*

**Alexander P. Sobinoff**

Targeting telomeric repeat-binding factor 2 (TRF2) with small molecule inhibitors to prevent cancer cell growth *abs# 247*

**Tanya Soboleva**

Gene editing of the multi-copy H2A.B.3 gene family by a single pair of TALENs *abs# 248*

**Huma Sohail**

Investigating the role of *MYD88* mutations in lymphoma. *abs# 249*

**Jirawas Sornkom**

BET bromodomain inhibition sensitises ribosomal DNA to localised damage and provides a robust synergistic therapeutic strategy for treating AML *abs# 250*

**Laura Sourdin**

Nuclear microRNAs as Direct Regulators of Transcription *abs# 251*

**Elizabeth S Stout**

The Search for Disease Severity Modifiers in Patients Suffering from Blood Disorders *abs# 253*

**Medha Suman**

Invasive Lobular Breast Cancer: Using tumour genome-wide DNA methylation to further subtype and aid in the identification of susceptibility genes. *abs# 254*

**Stephanie Sun**

Integrated profiling of single-cell chromatin accessibility and transcriptome reveals regulatory heterogeneity *abs# 255*

**Tessa Swain**

Exploring the combinatorial effects of epigenetic modifiers upon the mammalian genome using CRISPR-dCas9 *abs# 256*

**Aleisha Symon**

Identifying Novel Testis-Determining Genes from Integrated RNAseq and ChIPseq Data *abs# 257*

**Andres ATdF Tapia del Fierro**

Investigating the role of Cis and Trans acting regulators in the process of X inactivation *abs# 258*

**Daniel Thomson**

Investigating DNA transposition as a cause of genomic instability and therapy-resistance in Chronic Myeloid Leukaemia *abs# 259*

**KANUPRIYA TIWARI**

Bayesian neural network based modelling of steady-state splicing mechanism. *abs# 260*

**James R Torpy**

Repetitive RNA and genomic instability in high-grade serous ovarian cancer progression and development *abs# 261*

**Rachael E Turner**

Investigation into the mechanisms of alternative 3'UTRs in the control of gene expression *abs# 262*

**Sonika Tyagi**

Pre-miRNA Folding Through Context-Free Grammar Parsing and the Identification of miRNA Using a Feedforward Neural Network *abs# 263*

**Dean S. Tyler**

Click chemistry enables preclinical evaluation of targeted epigenetic therapies *abs# 264*

**Sasiwimon Utama**

Characterization of *COL3A1* mutations causing Ehler-Danlos Syndrome type IV: the first step in designing molecular therapies *abs# 265*

**Jim Vadolas**

shRNA screen for novel epigenetic regulations of  $\gamma$ -globin silencing *abs# 266*

**Fatima Valdes Mora**

Novel contribution of acetylated histone variant H2A.Z in activation of neo-enhancers in prostate cancer. *abs# 267*

**Dulce Vargas Landin**

Transcriptional characterization of low input frozen brain samples at single-nucleus resolution using 10x Genomics Chromium microfluidics *abs# 268*

**Sarah Voisin**

Racing against the (epigenetic) clock: physical activity reverses age-related epigenetic drift in human skeletal muscle *abs# 269*

**Susan Wagner**

Dissecting the roles of eIF2 and eIF3 during translation using TCP-seq *abs# 270*

**Matthew Wakefield**

Molecular Dynamics Modelling of a Variant of Unknown Effect in RAD51D *abs# 271*

**Qi Wang**

Development and optimization of an efficient method for CRISPR/Cas correction of patient-specific iPSCs *abs# 272*

**Weiwen wang**

An optimal approach to assembling chloroplast genome *abs# 273*

**Iromi Wanigasuriya**

Characterizing the epigenetic modifier Smchd1 in X chromosome inactivation *abs# 274*

**Alex CH Wong**

NxtIRF: A novel computational approach to measure differential intron retention in cancer databases *abs# 275*

**Lee Wong**

Roles of histone variant H3.3 and ATRX in tumorigenesis *abs# 276*

**Hyun Goo Woo**

Systematic discovery of coding and noncoding transcriptomic variants in liver cancer *abs# 277*

**Lu Yang**

DNA methylation and transcription factor binding *abs# 278*

**Sile Fiona Yang**

ZNF827 - a molecular target for telomere maintenance in cancer *abs# 279*

**Chengzhong Ye**

Identification and characterization of novel cell populations using single-cell RNA-seq: an example on breast cancer T cell infiltrate *abs# 280*

**Olga Zaytseva**

The FUBP1 *Drosophila* ortholog Psi interacts with the Mediator Complex to regulate growth through modulating expression of *MYC* and RNA processing machinery *abs# 281*



## 13th February 2018

### Session 6: Disease and Disease Genomics

9:00AM - 10:30AM Auditorium

Chairs: Minna-Liisa Anko & Juliet French

9:00 AM **Marina Pajic**

Integrative analysis of *in vivo* models of pancreatic cancer reveals complex mechanisms behind treatment failure and provides new tools for effective targeting *abs# 35*

9:25 AM **Adrian Krainer**

Spinraza: The first approved treatment for spinal muscular atrophy *abs# 36*

10:00 AM **Steve Wilton**

Therapeutic alternative splicing: Making sense where there was none *abs# 37*

### Morning Tea

10:30AM - 11:00AM Exhibition Hall

### Session 7: Evolution and Population Genetics

11:00AM - 12:15PM Auditorium

Chairs: Kathryn Burdon & Richard Edwards

11:00 AM **Marylyn Ritchie**

PheWAS in Populations: Exploring the relationship between the genome and the phenome *abs# 38*

11:35 AM **Irene Gallego Romero**

Developing iPSCs as a model for primate evolutionary genomics *abs# 39*

12:00 PM **Robert Lanfear**

The genome-wide rate and spectrum of somatic mutation in individual plants *abs# 40*

### Student Lunch

12:15PM - 1:15PM Lorne Central

### Lunch

12:15PM - 1:15PM Exhibition Hall

### Lorne Genome AGM

1:15PM - 2:30PM Auditorium

**Session 8A: Computational Biology**

2:30PM - 3:30PM Auditorium

Chairs: Sonika Tyagi & Matthew Ritchie

2:30 PM **Gordon K Smyth**

Using scRNA-seq to construct developmental lineage relationships in the mouse mammary gland *abs# 41*

2:45 PM **Clare Puttick**

Whole Genome Sequencing for the Detection of Pathogenic Mitochondrial Mutations *abs# 42*

3:00 PM **Hamid Alinejad Rokny**

Recurrent regions of copy number variations in autism spectrum disorder are enriched for brain enriched coding and non-coding RNAs *abs# 44*

3:15 PM **Akanksha Srivastava**

Deep-Mpute: Imputation of missing methylation values using deep convolution neural networks *abs# 252*

**Session 8B: Epigenetics/genomics**

2:30PM - 3:30PM Horizons Room

Chairs: Lee Wong & Ryan Lister

2:30 PM **Philippe Collas**

TAD cliques shape the 4-dimensional human genome during lineage-specific differentiation *abs# 45*

2:45 PM **Christine R Keenan**

Loss of Suv39h1 and h2 histone methyltransferases results in disruption of chromatin organisation which leads to immune progeria *abs# 46*

3:00 PM **Timothy Johanson**

No kissing in the nucleus: Genome-wide analysis reveals no evidence of trans chromosomal regulation of mammalian immune development *abs# 47*

3:15 PM **Hsiao Voon**

Inhibition of a K9/K36 Demethylase by an H3.3 Point Mutation Found in Paediatric Glioblastoma *abs# 48*

**Mini Break**

3:30PM - 3:45PM Auditorium Foyer

## **Session 9: Chromatin and Epigenetics/Epigenomics**

3:45PM - 5:30PM Auditorium

Chairs: Anne Voss & Tamas Fischer

3:45 PM **Laszlo Tora**

The role of co-activator complexes in regulating RNA polymerase II transcription *abs# 50*

4:20 PM **Wendy Bickmore**

The remote control of gene expression *abs# 51*

4:55 PM **Kirsten R McEwen**

Interpreting transcriptional heterogeneity in pluripotent stem cells using concerted computational approaches *abs# 43*

### **Micro Break**

5:30PM - 5:45PM Auditorium Foyer

### **Closing Lecture**

5:45PM - 6:30PM Auditorium

Chairs: Peter Boag & Tracy Bryan

5:45 PM **Kenneth W Kinzler**

The expanding clinical utility of cancer genomes *abs# 52*

### **Announcement of Conference Awards & Conference Close**

6:30PM - 7:30PM Auditorium

### **Conference Dinner**

7:30PM - 11:59PM Grand Pacific Hotel Lorne