

Program

Tuesday, 1 December 2009

Registration

10:00 AM - 6:30 PM

Lobby

Welcome

11:10 AM - 11:20 AM

Waldorf Theatre

Keynote

11:20 AM - 12:00 PM

Waldorf Theatre

Session sponsored by Victorian Government

Moshe Szyf

The epigenome linking the social and physical environment and the genome

abs#001



Lunch

12:00 PM - 1:30 PM

Exhibition Hall

Industry Workshop 1 - RIP - emerging technique for gene regulation study

12:45 PM - 1:15 PM

Waldorf Theatre

Session sponsored by Millipore Australia Pty Ltd

Presenter: Chee Wai Fong, Millipore Singapore



Epigenetics & Cancer I

1:30 PM - 3:00 PM

Waldorf Theatre

Session sponsored by The Royal College of Pathologists of Australasia

Chair: Hamish Scott

1:30pm

Jingde Zhu

Fundamental and translational perspectives of DNA methylation in cancer

abs#002

2:10pm

Susan Clark

Epigenetic Deregulation in Cancer

abs#003

2:40pm

Zdenko Herceg

Epigenetic changes in cancer as fingerprints of exposure and clinical predictors

abs#004



Afternoon Tea

3:00 PM - 3:30 PM

Exhibition Hall

Epigenetics & the Environment

3:30 PM - 5:00 PM

Waldorf Theatre
Session sponsored by NGED



Chair: Jean Finnegan

3:30pm

Peter Gluckman

Developmental plasticity, epigenetics and human health *abs#005*

4:10pm

Elizabeth Finnegan

Epigenetic regulation of an environmental response *abs#006*

4:40pm

Jun Okabe

Biochemical Characterization of the SET7/9 Histone Methyltransferase in Models of Hyperglycemic Variability *abs#007*

Welcome Function

5:00 PM - 6:30 PM

Exhibition Hall

Wednesday, 2 December 2009

Registration

8:00 AM - 5:45 PM

Lobby

Epigenetics & Disease

8:30 AM - 10:00 AM

Waldorf Theatre

Session sponsored by MCRI



Chair: Sam El Osta

8:30am

Art Petronis

Epigenomics of Major Psychiatric Disease *abs#008*

9:10am

Catherine Suter

Environment and selection lead to stabilisation of a germline epigenetic state *abs#009*

9:40am

Fatemeh Haghighi

Whole Genome DNA Methylation Profiling of Neuropsychiatric Disorders with Focus on Depression and Schizophrenia *abs#010*

Morning Tea

10:00 AM - 10:30 AM

Exhibition Hall

Epigenetics & Cancer II

10:30 AM - 12:00 PM

Waldorf Theatre

Session sponsored by The University of Melbourne



Chair: Alex Dobrovic

10:30am

Peter Jones

Cancer Epigenomics *abs#011*

11:10am

Sung Hee Baek

Roles of Methylation of a Chromatin-Remodeling Complex in Breast Cancer *abs#012*

11:40am

Alexander Dobrovic

Epigenetic and Genetic Origins of Human cancer *abs#013*

Lunch

12:00 PM - 1:30 PM

Exhibition Hall

Industry Workshop 2 - Epigenetic Solutions from Illumina - From Sequencing to Arrays

12:45 PM - 1:15 PM

Waldorf Theatre

Session sponsored by Illumina

Presented by Dr Arjuna Kumarasuriyar, Illumina Singapore



Epigenetics & Development

1:30 PM - 3:00 PM

Waldorf Theatre
Session sponsored by CSIRO



Chair: David Ravine

1:30pm

Richard Poethig

A miRNA-regulated pathway for vegetative phase change *abs#014*

2:10pm

Suyinn Chong

Epigenetics and the Determination of Phenotype *abs#015*

2:40pm

Haruhiko Koseki

HP1g links histone H3K9 methylation to homologous chromosome pairing during meiotic prophase *abs#016*

Afternoon Tea

3:00 PM - 3:30 PM

Exhibition Hall

Poster Session I

**Please note that only ODD numbered abstracts will be presented in Poster Session I and EVEN numbered abstracts will be presented in Poster Session II.*

3:30 PM - 5:30 PM

Exhibition Hall

Session sponsored by Victorian Government



Gavin Meredith

DNA methylome sequencing: Methylated DNA enrichment followed by high-throughput sequencing by ligation (SOLiD™) *abs#101*

Michelle Newman

Quantitation of global DNA methylation levels in response to low dose radiation exposure using high resolution melt curve analysis *abs#102*

Pei-Ming Yang

Abstract withdrawn *abs#103*

Karen Chiam

GSTP1 is a marker of treatment response to DNMT inhibitors in prostate cancer *abs#104*

Joice Kuroiwa-Trzmielina

Germline epimutation of *BRCA1&BRCA2* genes: a rare event in familial breast cancer *abs#105*

Chau-To Kwok

Lynch syndrome cases with a germline *MLH1* epimutation display allele-specific histone motifs at the *MLH1* promoter *abs#106*

Soung Min KIM

Metastatic leiomyosarcoma in the oral cavity: Case report with protein expression profiles *abs#107*

Yasser Riazalhosseini

Genome-wide DNA methylation screening in breast cancer revealed new candidate loci potentially involved in field defect *abs#109*

Li-Jeen Mah

γ H2AX as an epigenetic marker of DNA damage and disease *abs#110*

Katie Huang

Aberrant DNA methylation of the HIF-1 α inhibitor gene *CITED4* in breast cancer *abs#111*

Rebecca Hinshelwood

Aberrant de novo methylation of the p16^{INK4A} CpG island is initiated post gene silencing in association with chromatin remodeling and mimics nucleosome positioning *abs#112*

Thomas Mikeska

MethMarker: Design of DNA methylation assays and optimisation for use as clinical biomarkers *abs#113*

Jia (Jenny) Liu

Differences in folate distribution and global DNA methylation in the normal colonic mucosa and peripheral blood of colorectal cancer patients *abs#114*

Horace Drew

Bisulphite-tagging: a new high resolution approach to the analysis of whole-genome DNA methylation *abs#115*

Mari Kondo

Effect of *Mecp2* mutation on BDNF expression and rescue of autistic spectrum disorder endophenotypes by environmental modulation in Rett syndrome mice *abs#116*

Christopher Cazzonelli

Regulation of carotenoid composition and plant development by a chromatin modifying histone methyltransferase, *sdg8* *abs#117*

Romain BARRES

Increased non-CpG methylation in type 2 diabetes: a possible role of saturated fatty acids *abs#118*

Ji-Hoon Joo

Evaluation of Gene Expression Discordance in Monozygotic Twins at Birth *abs#119*

YoungJoo Lee

Hypoxia induces estrogen receptor mRNA repression in MCF-7 human breast cancer cells *abs#120*

Kristina Warton

Optimising the detection of methylation patterns in circulating DNA from ovarian cancer patients using headloop suppression PCR *abs#121*

Annabel Short

Regulation of the ITGA2 Gene by Methylation in Prostate Cancer *abs#124*

Pei Woon Ang

Comprehensive profiling of DNA methylation in colorectal cancer reveals three subgroups with distinct clinicopathological and molecular features *abs#125*

Izhak Haviv

Environmental Epigenetics analysis using next generation sequencing *abs#126*

Ida Candiloro

DNA methylation at the MGMT promoter is associated with the T allele of the rs16906252 SNP in peripheral blood of normal individuals *abs#127*

Sebastian Lunke

The standardization and exemplification of soluble MeCP2 chromatin immunopurification *abs#128*

Timothy Bredy

How the epigenome contributes to long-term memory *abs#129*

Victoria Louise Haley

Functional genetic interactions between IGF2 and p53 during development and tumour formation *abs#130*

Ralf Moser

Epigenetic target identification *abs#132*

Neil Youngson

Searching for subtle epigenetic abnormalities in the male mouse germ line *abs#133*

Eric Smith

Two variants of esophageal adenocarcinoma distinguished by their methylation profile *abs#134*

Vanisri Raviraj

Inhibition of histone deacetylase reduces the expression of metastasis promoter genes including ROCK1 in high-density (HD) collagen matrix *abs#135*

Tennille Sibbritt

Epigenetic deregulation of miRNA expression in prostate cancer *abs#136*

Samantha Lupton

Age and Gender Differences in the Expression of Cardiovascular Relevant Genes *abs#137*

Lucy Apps

Epigenetic regulation of the gm-csf promoter in immune cells *abs#138*

Tina Bianco-Miotto

H3K18Ac and H3K4diMe are independent predictors of relapse in prostate cancer *abs#139*

Huei San Leong

Investigating a potential role for the novel chromatin protein SmcHD1 in cancer *abs#140*

Kevin Knowler

Investigating the epigenetic regulation of intratumoral oestrogen production in human breast cancer *abs#141*

Ashwin Kelkar

A novel method of methylation detection using a monoclonal antibody and a microarray approach *abs#142*

Pia Larsson

The Epigenetic Modifier Valproic Acid Stimulates Tissue-type Plasminogen Activator Expression in Human Endothelial Cells *abs#143*

Amity Roberts

Haploinsufficiency for DNA methyltransferase 1 is associated with increased risk of mouse embryonic death *abs#144*

Elaine Sanij

The upstream binding factor ubf regulates the epigenetic state of ribosomal chromatin and general heterochromatin *abs#145*

Phillippa Taberlay

Distinct chromatin signatures at the enhancer define the different activation states of a Polycomb target gene *abs#146*

Ee Ming Wong

Constitutional methylation of the *brca1* promoter region is associated with risk of early-onset '*brca1*-like' breast cancer *abs#147*

Nina Kaminen-Ahola

Maternal Ethanol Consumption Alters the Epigenotype and the Phenotype of Offspring in a Mouse Model *abs#148*

Brian Gloss

Integrated genome analysis of DNA methylation and pharmacological induced epigenetic re-expression reveal potential biomarkers for ovarian cancer *abs#149*

Kevin Dudley

Offspring of mothers fed a high fat diet during pregnancy and lactation display hepatic cell-cycle inhibition and associated changes in gene expression and DNA methylation *abs#150*

Suyinn Chong

The role of modifiers of epigenetic reprogramming in genome stability in the mouse *abs#151*

Warwick Locke

Modelling Early Epigenetic Changes in Breast Cancer *abs#152*

Ganesan Gopalan

Downregulation of Ras-related Estrogen-regulated Growth Inhibitor (RERG) prevents differentiation of breast cancer cells *in vitro* *abs#153*

Stephen Jane

Identification of a prmt5-dependent repressor complex linked to silencing of human fetal globin gene expression *abs#154*

Mark Cruickshank

Cell-specific epigenetic regulators: *Complement Receptor 2 (CR2/CD21)* transcriptional control via a novel repressor protein (RP58), E2A and localised chromatin accessibility *abs#155*

Bilal Sheikh

The Histone Acetyltransferase Querkopf is a key Regulator and Marker of Stemness - the Self-renewal ability and Multipotency of Adult Neural Stem Cells *abs#156*

Masumi Robertson

The H3K27me3 mark and gene transcription in plants *abs#157*

Marjan Askarian-Amiri

Characterization of long noncoding RNAs associated with mouse mammary gland development *abs#158*

Trevelyan Menheniott

STAT3 mediated transcriptional and epigenetic silencing at a tumour suppressor gene cluster in gastric cancer *abs#159*

Hitomi Matsuzaki

Post-fertilization methylation imprinting in the randomly integrated transgenic H19-ICR fragment *abs#160*

Candice Sheldon

Epigenetic repression and reprogramming of the *FLOWERING LOCUS C*-clade of genes *abs#161*

Nadia Whitelaw

A role for trim28 in metabolic syndrome and infertility *abs#162*

Keiji Tanimoto

Possible role of CTCF binding in the post-fertilization methylation imprinting at the transgenic H19-ICR in *beta-globin* YAC *abs#163*

Björn Oback

Reduced histone 3 lysine 9 trimethylation in embryonic stem cells improves their reprogramming into cloned mouse embryos *abs#164*

Prabhu Mathiyalagan

Cardiac ventricular chambers are epigenetically distinguishable *abs#165*

Gina Oliver

Alterations in gene expression in the uterine environment and embryos derived from feed restricted sows *abs#166*

Miina Ollikainen

Does epigenetics make the difference? -A study of imprinted genes in multiple tissues of newborn MZ twins *abs#168*

Anderly Chueh

HDAC inhibitor induced apoptosis in colon cancer cells is linked to transactivation of the Sp3 transcription factor *abs#169*

Qiao Li

The function of transcriptional coactivator p300 and cell differentiation *abs#170*

Fatima Valdes-Mora

Transcriptional deregulation and epigenetic remodelling in prostate cancer is associated with re-organisation of the H2A.Z histone variant at gene promoters *abs#171*

Sung Lee

Functional analysis of L1 retrotransposable elements in mouse genome *abs#172*

Ross Tellam

High resolution mapping of nucleosomes and histone 3 lysine 27 trimethylation in the ovine genome during skeletal muscle development *abs#173*

Ryo Fujimoto

Control of *FWA* gene silencing in the genus *Arabidopsis* *abs#174*

Ji Hun Kim

Creating a genome-wide map of condensin in vertebrate cells *abs#175*

Boris Novakovic

Unique profile of DNA methyltransferase promoter methylation in human placental tissue and purified trophoblasts *abs#176*

Wei-Chien Huang

Akt facilitates the nuclear translocation of IKK α *abs#177*

Emilie Bard-Chapeau

Role of Evi1 oncogene in transcription regulation *abs#178*

Fathima Gani

MeCP2 in Arginine methylation and its impact on Fragile X Syndrome *abs#179*

Lucia Daxinger

A saturation screen for modifiers of epigenetic reprogramming in the mouse *abs#180*

Jenny Ooi

Epigenetic modifications and the role of the chromatin modifying determinants in the hypertrophied heart *abs#181*

Hugh Morgan

Reassessment of Epigenetic Reprogramming in the Early Embryo *abs#182*

Melanie Morris

Epigenetic regulation of the microRNA-200 family during Epithelial-Mesenchymal Transition *abs#183*

Li-Jeen Mah

γ H2AX: DNA damage in epidermal stem cells *abs#184*

Jeena Gupta

Genome wide analysis of insulin induced histone modifications regulated genes under hyperglycemic condition in 3T3 adipocytes *abs#185*

Fiona Poke

Re-establishing the epigenetic signature of the GM-CSF promoter following gene activation *abs#186*

Christopher Slape

HoxA9 overexpression in myelodysplastic syndrome is associated with H3K4 trimethylation *abs#187*

Yoon Pin Lim

Cep68 expression in Breast Cancer *abs#188*

Lee Wong

Histone variant H3.3 and ATRX are key chromatin assembly regulators at the telomeres in embryonic stem cells *abs#189*

Richard Bayles

Transcriptional inhibition of the noradrenaline transporter gene *Slc6a2* *abs#190*

Marguerite Evans-Galea

What role does epigenetic modification of the FXN gene play in Friedreich ataxia? *abs#191*

Chris Helliwell

The polycomb repression system in Arabidopsis and its role in regulation of the flowering repressor FLC *abs#192*

Jason Lee

Methylation of a chromatin remodelling factor, represses by G9a links hypoxia target gene expression and tumorigenesis *abs#193*

Boris Novakovic

Characterising the Methylome of First Trimester Human Placenta *abs#194*

Yan Li

Epigenetic control of inducible gene expression in the immune system *abs#195*

Keith Rand

Helper-Dependent PCR (HDCR) for improved detection of hypermethylated CpG islands *abs#196*

Shing-Ling Tsai

Lapatinib enhances cell migration of breast cancer cells via down-regulating miR-7 *abs#197*

Ming Luo

Characterisation of genomic imprinting in rice endosperm by transcriptome sequencing *abs#198*

Traute Flatscher-Bader

Effect of advanced paternal age on copy number variation in the next generation *abs#199*

Ikhide Imumorin

Epigenetic Studies in Cattle: DNA Methylation, Gene Expression and Imprinting Analysis of some Placental Genes in Cow *abs#200*

Alice Wang

The C-terminus of histone variant H2A.Z is important for its deposition and function *abs#202*

Zena Kassir

Epigenetic Control of the Metallothionein Genes in Cancer Cells Controls Zinc Induction *abs#203*

Nancy Levesque

Shared function between the NuA4 and SWR1 complexes *abs#204*

Michaela Petter

The role of alternative histone variants in gene regulation of the malaria parasite *Plasmodium falciparum* *abs#205*

Pek Lim

The chromatin state of inducible genes determines their expression kinetics in T cells *abs#206*

Yun-Ju Chen

Nuclear EGFR-mediated BCRP expression confers gefitinib resistance *abs#207*

Li-Jeen Mah

Temporal and spatial distribution of a molecular marker of DNA damage *abs#208*

Kristine Hardy

Defining the chromatin signature of inducible genes in T cells *abs#209*

Shunsuke Suzuki

Characterization of the Marsupial PHLDA2 Reveals Eutherian Specific Acquisition of Imprinting *abs#210*

Jessica Stringer

The imprint status and expression of INS in the marsupial mammary gland *abs#211*

Sarah Kinkel

Investigating the role of Dnmt3L in medullary thymic epithelial cells *abs#212*

Thursday, 3 December 2009

Registration

8:00 AM - 6:00 PM

Lobby

Young Investigator Session

8:30 AM - 10:00 AM

Waldorf Theatre

Session sponsored by Diagenode



Chair: Richard Saffery

- 8:30am **Ryan Taft**
Nuclear localized tiny RNAs are associated with transcription starts sites in animals *abs#017*
- 8:45am **Cheryl Li**
Epigenetic programming in response to maternal nutrition *abs#018*
- 9:00am **David Mossman**
Prolonged transcriptional reactivation of epigenetically silenced genes requires hypomethylated CpG sites and histone acetylation *abs#019*
- 9:15am **Mark Robinson**
Critical assessment of genome analyses for DNA methylation *abs#020*
- 9:30am **Luciano Pirola**
Correlation between histone acetylation, histone variant H2A.Z deposition and transcript levels in insulin-modulated genes. A possible epigenetic link to insulin-dependent transcription *abs#021*
- 9:45am **Nicholas Wong**
The DNA methylation signature of paediatric B-cell precursor acute lymphoblastic leukaemia *abs#022*

Morning Tea

10:00 AM - 10:30 AM

Exhibition Hall

Epigenetic Mechanisms

10:30 AM - 12:00 PM

Waldorf Theatre

Chair: Adele Holloway

- 10:30am **Wendy Bickmore**
Regulation of gene expression in nuclear space *abs#023*
- 11:05am **David Tremethick**
Remodeling of chromatin by histone variants during mammalian differentiation *abs#024*
- 11:25am **Francis Stewart**
Epigenetic aspects of Pol II promoters *abs#025*
- 11:45am **Anne Kathrin Voss**
The role of the Moz histone acetyltransferase in development *abs#026*

Lunch

12:00 PM - 1:30 PM

Exhibition Hall

Industry Workshop 3 - Analyzing epigenetic changes in cancer: tools of the trade

12:45 PM - 1:15 PM

Waldorf Theatre

Session sponsored by Life Technologies

Presented by Gavin Meredith, Live Technologies, Inc.



Epigenetic Technologies

1:30 PM - 3:00 PM

Waldorf Theatre

Chair: John Mattick

1:30pm

Thomas Down

Deconvolving the epigenome: analysis strategies for genome-wide studies *abs#027*

2:10pm

Toshikazu Ushijima

Instructive induction of aberrant DNA methylation, and epigenomic analysis of its underlying mechanisms *abs#028*

2:40pm

John Mariadason

An integrated genome-wide profiling strategy for the identification of novel epigenetically regulated loci in colon cancer *abs#029*

Afternoon Tea

3:00 PM - 3:30 PM

Exhibition Hall

Special Lecture

3:30 PM - 4:00 PM

Waldorf Theatre

Chair: Jeff Craig

Mukesh Verma

Research opportunities at NIH in cancer epidemiology and epigenetics *abs#030*

Poster Session II

**Please note only EVEN numbered abstracts will be presented in Poster Session II.*

4:00 PM - 6:00 PM

Exhibition Hall

Conference Dinner

7:00 PM - 11:00 PM

State Ballroom

Session sponsored by Illumina Australia



Friday, 4 December 2009

Registration

8:00 AM - 1:00 PM

Lobby

Non-coding RNAs

8:30 AM - 10:00 AM

Waldorf Theatre

Chair: Sue Clark

8:30am

Mario Arteaga-Vazquez

Interchromosomal Transfer of Epigenetic Information *abs#031*

9:10am

John Mattick

RNA regulation of the epigenome *abs#032*

9:40am

Bernard Carroll

Mechanisms of transgene silencing in Arabidopsis *abs#033*

Morning Tea

10:00 AM - 10:30 AM

Exhibition Hall

Imprinting

10:30 AM - 12:00 PM

Waldorf Theatre

Chair: David Tremethick

10:30am

Benjamin Tycko

DNA methylation and genetic-epigenetic connections in normal and diseased human tissues *abs#034*

11:10am

Marilyn Renfree

Evolution of genomic imprinting: a marsupial perspective *abs#035*

11:40am

Julie Demars

Analysis of the IGF2/H19 imprinting control region uncovers new genetic defects, including mutations of Oct-binding sequences, in patients with 11p15 fetal growth disorders *abs#036*

Closing Remarks

12:00 PM - 12:10 PM

Waldorf Theatre

Chair: Jeff Craig

Lunch

12:10 PM - 1:30 PM

Exhibition Hall