Human Genome Meeting 2016
28th of February – 2nd of March 2016
Hilton Americas, Houston, USA

FINAL PROGRAMME & ABSTRACT BOOK

“Translational Genomics”

Human Genome Organisation
20 Bendemeer Road
#04-02 BS Bendemeer Centre
Singapore 339914
Tel: +65 6411 6631 - Fax: +65 6496 5599
Email: admin@hugo-international.org
Website: www.hugo-international.org
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WELCOME MESSAGE FROM THE ORGANISING COMMITTEE

On behalf of the local organizing committee and HUGO, we are delighted to welcome you in Houston for the HGM2016. This is the first time the HGM meeting is held in the US – and we are proud and excited for the opportunity to bring science from across the globe here to Texas.

This meeting has a unifying theme of translation as its core, focusing on the current state and future direction of implementing genomics driven approaches in diagnosis/treatment/management of cancer and genetic disease, with a specific focus on strategies and technologies for implementation.

Drawing on expertise from the Texas Medical Center’s constituent institutions and a truly broad-reaching, international line up of experts, the meeting promises to be both a dynamic forum for scientific exchange and a unique opportunity to bring together global expertise all focused on the understanding of the impact of that most fundamental variable, that encoded in our genomes, in the context of health and disease.

We wish you a successful and fruitfull meeting!

Prof. Stylianos E. Antonarakis
President of HUGO
University of Geneva Medical School

Prof. Andy Futreal
Chair of the Local Organising Committee
University of Texas MD Anderson Cancer Centre

LOCAL ORGANISING COMMITTEE

Andy Futreal (CHAIR)
Ad Interim Chair/Professor
Robert A Welch Distinguished University Chair
Director – Center for Survivorship Genomics
University of Texas MD Anderson Cancer Center and
Honorary Faculty, Wellcome Trust Sanger Institute

Eric Boerwinkle, Kozmetsky Family Chair in Human
Genetics
Professor and Chair, Human Genetics Center and Dept. of Epidemiology
Associate Director, Human Genome Sequencing Center at BCM
UT Health Science Center at Houston

INTERNATIONAL PROGRAMME COMMITTEE

Stylianos E. Antonarakis (CHAIR) (CH)
Professor, Department of Genetic Medicine and Development
University of Geneva Medical School

Charles Lee (US)
Scientific Director
The Jackson Laboratory for Genomic Medicine

Michael Snyder (US)
Professor and Chair of Genetics
Director, Stanford Center for Genomics and Personalized Medicine
Stanford University School of Medicine

Gerardo Jimenez-Sanchez, Adjunct Professor of Epidemiology, Harvard T.H. Chan School of Public Health
Executive President, Global Biotech Consulting Group

Richard Gibbs, Director and Wofford Cain Endowed Chair
BCM Human Genome Sequencing Center
Department of Molecular and Human Genetics

Robert C. Robbins, President and CEO
Texas Medical Center

Alfredo Hidalgo Miranda, Researcher, Cancer Genomics Lab Instituto Nacional de Medicina Genómica (INMEGEN)

Edison Liu (US)
President and CEO
The Jackson Laboratory

Ruth Chadwick (UK)
Professor of Bioethics
University of Manchester

Ada Hamosh (US)
Professor, Department of Pediatrics and Institute of Genetic Medicine
Professor, Department of Epidemiology, Bloomberg School of Public Health
Johns Hopkins University School of Medicine
Institute of Genetic Medicine
HUGO COUNCIL MEMBERS

Stylianos E. Antonarakis, Switzerland, President
Edison Liu, United States, President Emeritus
Karen B. Avraham, Israel
Piero Carninci, Japan
Ruth Chadwick, United Kingdom
Aravinda Chakravarti, United States
Eva Cutiongco De La Paz, Philippines
Kartiki Desai, India
Ada Hamosh, United States
Alfredo Hidalgo Miranda, Mexico
Charles Lee, United States
Klaus Linpaintner, United States
Partha Majumder, India
Julie Makani, Tanzania
John Mattick, Australia
Stefan Mundlos, Germany
Carmencita Padilla, Philippines
Heidi Rehm, United States
Juergen Reichardt, Australia
Michael Snyder, United States
Himla Soodyall, South Africa
Yik-Ying Teo, Singapore
Ambroise Wonkam, South Africa
Charles Rotimi, United States
MEETING INFORMATION

BADGE & MEETING DOCUMENTS
The meeting documents (including name badges) should be collected on-site, during the official opening hours, from the registration desk at the meeting hotel, the Hilton Americas. Your name badges must be visible at all times in the HGM 2016 meeting area at the Hilton Americas.

CERTIFICATE OF ATTENDANCE
The meeting participants will receive their E-certificate of attendance by email after the meeting.

DISCLAIMER
HUGO and MCI Suisse SA, as the meeting organisers, claim no liability for the act of any supplier to this meeting, nor liability for personal injury, the safety of any attendee while in transit to or from this event, for any loss or damage, for delays in transport by air, sea, rail, road, weather, in case of strikes, sickness, war or other causes.

EXHIBITION INFORMATION
The HGM 2016 exhibition, featuring commercial displays of International Organisations, Life Science Companies, Media Publishers and Scientific Societies, is located in Ballroom D-F, level 4 of the Hilton Americas. Coffee breaks will be distributed within and around the exhibition.

EXHIBITION SCHEDULE

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<thead>
<tr>
<th>Day</th>
<th>Date</th>
<th>Opening hours</th>
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<tbody>
<tr>
<td>Sunday</td>
<td>28 February 2016</td>
<td>12:00 - 18:30</td>
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<tr>
<td>Monday</td>
<td>29 February 2016</td>
<td>10:00 - 17:00</td>
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<tr>
<td>Tuesday</td>
<td>1 March 2016</td>
<td>09:30 - 16:30</td>
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<tr>
<td>Wednesday</td>
<td>2 March 2016</td>
<td>09:00 - 10:30</td>
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</table>

FOOD & BEVERAGE
Coffee/tea during official breaks is included in the registration fees and will be served within the exhibition area.

LANGUAGES/OFFICIAL LANGUAGE
The official meeting language is English. No simultaneous translation is provided.

INSURANCE AND LIABILITY
It is recommended that participants obtain adequate cover for travel, health and accident insurance before they depart from their countries. HUGO and MCI as organisers cannot accept responsibility for personal injuries, or loss of, or damage to, private property belonging to the Meeting participants.

LOST AND FOUND
A lost-and-found service is available at the registration desk.

MOBILE DEVICES
Delegates are kindly requested to keep their mobile phones in silent mode in meeting area.

REGISTRATION DESK
The desk for registration, information and distribution of documents will be open as follows:

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<tr>
<th>Day</th>
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<tr>
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<td>28 February 2016</td>
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<td>Monday</td>
<td>29 February 2016</td>
<td>07:30 - 18:30</td>
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<tr>
<td>Tuesday</td>
<td>1 March 2016</td>
<td>08:30 - 16:30</td>
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<tr>
<td>Wednesday</td>
<td>2 March 2016</td>
<td>07:30 - 11:30</td>
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SMOKING POLICY
The HGM 2016 is a non-smoking event. It is forbidden to smoke in the meeting area, including the exhibition & posters area.

SCIENTIFIC INFORMATION

POSTER SESSIONS
Posters sessions will take place in the exhibition area. Please go to the registration desk for any information and to collect necessary hanging material. The author must be present in front of his/her poster during poster viewing for free discussion.

SPEAKER’S PREVIEW ROOM
The Speakers’ Preview Room is located in Room 430, level 4. Speakers are kindly requested to provide their PC formatted USB keys (PowerPoint presentations) to the Speaker’s Preview Room centre at least two hours before their session. All conference rooms contain state-of-the-art technical equipment.

The Speakers’ Preview Room will be opened as follows:

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<tr>
<th>Day</th>
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<tr>
<td>Wednesday</td>
<td>2 March 2016</td>
<td>08:00 - 11:30</td>
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HUGO CORPORATE SOCIAL RESPONSIBILITY STATEMENT
HUGO is aware of the environmental, economic and social impact of holding a large meeting, and is working closely with its partners to ensure that environmentally, economically and socially friendly policies are in place. For the Houston Meeting, HUGO has made the following sustainable arrangements:

HEALTHY FOOD
All catering provided offer healthy options and local products have been prioritized

PRINTING
HUGO is committed to ensuring that printing is kept to a minimum to reduce the amount of waste paper. Abstracts are published in the HUGO journal and the final programme is available on the HGM meeting website. Both documents are available online, saving the printing of thousands of pages.

LOCAL SUPPLIERS
HUGO wishes to have a positive local impact. When sourcing materials and supplies, HUGO considers local partners in priority to avoid associated impacts of transportation and to positively impact the local economy.

SERVICES FOR THE DISABLED
HUGO wishes to make the meeting experience comfortable for all attendees. All the rooms and areas at the meeting venue are fully accessible to participants with disabilities.
NETWORKING EVENTS

HGM 2016 provides delegates with numerous opportunities to network with colleagues and other professionals in the field of human genomics. The meeting organizers are pleased to invite you to the following events:

HGM 2016 WELCOME RECEPTION
Sunday 28 February 2016, 17:45 - 18:30
With the kind support of The Jackson Laboratory

HGM 2016 will organize a networking reception on the first day of the conference to welcome delegates and colleagues coming from all over the world. This reception is held in the exhibition area of the venue.

- **Venue:** Hilton Americas – Ballroom D-F, Level 4
- **Dress code:** Business casual
- **Rate:** Included in the registration fee

HGM 2016 NETWORKING DINNER
Tuesday 1 March 2016, 19:00 – 22:00

Join us for a networking dinner with the faculty and peers.

- **Venue:** Hilton Americas, Ballroom J, level 4
- **Dress code:** Business casual
- **Rate:** Limited tickets can still be purchased at the registration area for USD 220.00
Karger Publications in Genetics

Cytogenetic and Genome Research
Editor-in-Chief: M. Schmid (Würzburg)
A leading journal on chromosome and genome research

Human Heredity
Editor-in-Chief: F. Clerget-Darpoux (Paris)
An excellent source of methodological and applied genetic research

Molecular Syndromology
Editors-in-Chief: L.G. Shaffer (Spokane, Wash.)
M. Schmid (Würzburg)
Focusing on research on common and rare genetic syndromes

Public Health Genomics
Editor-in-Chief: A.M. Brand (Maastricht)
From genome-based sciences to public health

Sexual Development
Editors-in-Chief: M. Schmid (Würzburg)
P. Koopman (Brisbane, Qld.)
M. Schurtl (Würzburg)
A unique forum for research on sexual development

ISCN 2013
Editors: L.G. Shaffer (Spokane, Wash.)
J. McGowan-Jordan (Ottawa, Ont.)
M. Schmid (Würzburg)
New edition coming in 2016

Find detailed information on each publication’s website!
# Programme Overview – Sunday, 28 February 2016

<table>
<thead>
<tr>
<th>Time</th>
<th>Room</th>
<th>Grand Ballroom D-F</th>
<th>Grand Ballroom A + B</th>
<th>Grand Ballroom C</th>
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<tbody>
<tr>
<td>12:00 – 13:00</td>
<td></td>
<td>Registration</td>
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<td>13:00 – 13:15</td>
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<tr>
<td>13:15 – 14:15</td>
<td></td>
<td>Opening Ceremony</td>
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<tr>
<td>14:15 – 15:45</td>
<td></td>
<td>S1 – Genetics 1: Common Diseases I</td>
<td>W1 – Interpreting Clinical Genomes</td>
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<tr>
<td>15:45 – 16:15</td>
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<td>Coffee Break</td>
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<td>With the kind support of IBM</td>
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<tr>
<td>16:15 – 17:45</td>
<td></td>
<td>W2 – Interpreting Cancer Genomes</td>
<td>W3 – Functional Genomics</td>
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<tr>
<td>17:45 – 18:30</td>
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<td>Welcome Reception</td>
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<td>With the kind support of The Jackson Laboratory</td>
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# Programme Overview – Monday, 29 February 2016

<table>
<thead>
<tr>
<th>Time</th>
<th>Room</th>
<th>Grand Ballroom D-F</th>
<th>Grand Ballroom A + B</th>
<th>Grand Ballroom C</th>
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<tbody>
<tr>
<td>08:00 – 09:00</td>
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<tr>
<td>09:00 – 10:30</td>
<td></td>
<td>PLENARY LECTURE 2 &amp; 3</td>
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<td>10:30 – 11:00</td>
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<td>Coffee Break</td>
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<tr>
<td>11:00 – 13:00</td>
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<td>S2 – Cancer 1: Cancer Genome Translation/Microbiome</td>
<td>S3 – Human Variome Project</td>
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<td>13:00 – 14:00</td>
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<tr>
<td>14:00 – 16:00</td>
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<td>ORAL PRESENTATIONS 1</td>
<td>ORAL PRESENTATIONS 2</td>
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<td>16:00 – 16:30</td>
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<td>Coffee Break</td>
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<tr>
<td>16:30 – 18:00</td>
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<td>ORAL PRESENTATIONS 3</td>
<td>ORAL PRESENTATIONS 4</td>
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## Program Overview – Tuesday, 1 March 2016

<table>
<thead>
<tr>
<th>Time</th>
<th>Room</th>
<th>Grand Ballroom D-F</th>
<th>Grand Ballroom A + B</th>
<th>Grand Ballroom C</th>
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<tbody>
<tr>
<td>09:00 – 10:00</td>
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<td></td>
<td><strong>PLenary Lecture 4</strong></td>
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<td>10:00 – 10:30</td>
<td><strong>Coffee Break</strong></td>
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<tr>
<td>10:30 – 12:30</td>
<td><strong>S4 – Genetics 2: Mendelian Genetics</strong></td>
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<td><strong>W4 – ELSI/International Data</strong></td>
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<tr>
<td>12:30 – 13:30</td>
<td><strong>Symposium PwC</strong></td>
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<tr>
<td>13:30 – 15:30</td>
<td><strong>S5 – Cancer 2: International Consortia Symposium (ICGC)</strong></td>
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<td><strong>Oral Presentations 5</strong></td>
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<tr>
<td>15:30 – 16:00</td>
<td><strong>Coffee Break</strong></td>
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<tr>
<td>16:00 – 17:00</td>
<td><strong>Hugo Members’ Meeting</strong></td>
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<td>19:00 – 22:00</td>
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<td><strong>Networking Dinner with Faculty</strong></td>
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## Program Overview – Wednesday, 2 March 2016

<table>
<thead>
<tr>
<th>Time</th>
<th>Room</th>
<th>Grand Ballroom D-F</th>
<th>Grand Ballroom A + B</th>
<th>Rooms 337A/B</th>
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<tbody>
<tr>
<td>08:00 – 09:00</td>
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<td></td>
<td><strong>Meet the Professors</strong></td>
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<td>09:00 – 09:45</td>
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<td><strong>Plenary Lecture 5</strong></td>
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<td>09:45 – 10:15</td>
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<td><strong>Coffee Break</strong></td>
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<tr>
<td>10:15 – 11:15</td>
<td><strong>S6 – Genomic Medicine: Medical Translation</strong></td>
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<td><strong>Chen Award &amp; Hugo-African Prize Award Lectures</strong></td>
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<tr>
<td>11:15 – 13:00</td>
<td><strong>Chen Award &amp; Hugo-African Prize Award Lectures</strong></td>
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<td><strong>Awards Presentation &amp; Closing Ceremony</strong></td>
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<td>13:00 – 18:00</td>
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<td><strong>Space Center Visit</strong></td>
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<td>Time</td>
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<tr>
<td>13:00-13:15</td>
<td>OPENING CEREMONY</td>
<td>BALLROOM A+B</td>
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<tr>
<td>13:00-13:05</td>
<td>Stylianos Antonarakis (CH)</td>
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<td>13:05-13:10</td>
<td>Andy Futreal (US)</td>
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<td>13:10-13:15</td>
<td>Guest of honor, Bobby Robbins (US)</td>
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<td>13:15-14:15</td>
<td>OPENING PLENARY LECTURE</td>
<td>BALLROOM A+B</td>
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<tr>
<td>13:20-14:15</td>
<td>I25 - AT 30, GENOMICS COMES OF AGE</td>
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<tr>
<td>14:15-15:45</td>
<td>S1 – GENETICS 1: COMMON DISEASES I</td>
<td>BALLROOM A+B</td>
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<tr>
<td>14:20-14:45</td>
<td>GENOME EDITING USING CRISPR-CAS SYSTEMS</td>
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<td>14:45-15:10</td>
<td>DISSECTING DIABETES: FROM GENETICS AND GENOMICS TO BIOLOGY AND TRANSLATION</td>
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<tr>
<td>15:10-15:35</td>
<td>PHARMACOGENOMICS: FROM DISCOVERY TO THE CLINIC</td>
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<tr>
<td>15:45-16:15</td>
<td>W1 – INTERPRETING CLINICAL GENOMES</td>
<td>BALLROOM C</td>
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<td>16:20-16:45</td>
<td>INTEGRATING DNA AND RNA DATA FOR N OF 1 CANCER STUDIES</td>
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<td>16:45-17:10</td>
<td>TBC</td>
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<td>17:10-17:35</td>
<td>I38 - TRANSLATIONAL IMPACT OF GENOMIC SEQUENCING ON RARE CANCERS</td>
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*Chair: Stylianos Antonarakis (CH)*

*Chair: Vasilis Vasiliou (US)*

*Chair: Michael Snyder (US) Co-chair: Catherine Brownstein (US)*

*Chair: Heidi Rhem (US)*

*Chair: Elaine Mardis (US)*

*Chair: Roy Angshumoy (US)*

*Chair: Linghua Wang (US)*

*With the kind support of IBM*
W3 – FUNCTIONAL GENOMICS
Chair: Piero Carnici (JP)

16:20-16:40 ONE PLUS ONE EQUALS ZERO
Nicholas Katsanis (US)

16:40-17:00 I10 - TWO-STEP FORWARD GENETIC SCREENS IN MICE IDENTIFY NEW HEPATOCELLULAR CARCINOMA DRIVER GENES AND A NEW THERAPEUTIC DRUG TARGET
Neal Copeland (US)

17:00-17:20 I33 - FUNCTIONAL GENETIC VARIATION IN Rhesus Macaques: New Models of Human Disease
Jeff Rogers (US)

17:20-17:40 ANNOTATING HUMAN VARIANTS USING DROSOPHILA
Hugo Bellen (US)

17:45-18:30 WELCOME RECEPTION - With the kind support of The Jackson Laboratory

MONDAY 29 FEBRUARY 2016

08:00-09:00 MEET THE PROFESSORS I
Room 336 A
Edison Liu (US)
Andy Futreal (US)

MEET THE PROFESSORS II: MODELING GENETIC DISORDERS TO STUDY PATHOGENESIS
Room 337 A
Kay Davies (UK)
Huda Zogbhi (US)

MEET THE PROFESSOR III: PERSONAL GENOMICS
Room 337 B
Mike Snyder (US)

09:00-10:30 PLENARY LECTURE 2 & 3
Chair: Charles Lee (US)

09:05-09:45 GENETIC THERAPIES FOR DUCHENNE MUSCULAR DYSTROPHY
Kay Davies (UK)

09:45-10:25 A TRANSLATIONAL RESEARCH PROGRAM FOR THE HUMAN MICROBIOME
Joseph Petrosino (US)

10:30-11:00 COFFEE BREAK

11:00-13:00
<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
<th>Presenter(s)</th>
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</thead>
<tbody>
<tr>
<td>11:05-11:30</td>
<td>IMPLEMENTING RAPID, ROBUST, AFFORDABLE CANCER PREDISPOSITION GENE TESTING</td>
<td>Nazneen Rahman (UK)</td>
</tr>
<tr>
<td>11:30-11:55</td>
<td>FRONTIERS IN CANCER PRECISION MEDICINE</td>
<td>Levi Garraway (US)</td>
</tr>
<tr>
<td>11:55-12:20</td>
<td>GENOMIC CHARACTERIZATION OF BREAST CANCER IN THE MEXICAN POPULATION</td>
<td>Alfredo Hidalgo Miranda (MX)</td>
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Oral presentations:

12:20-12:30  | O15 - THE TANDEM DUPLICATOR PHENOTYPE AS A DISTINCT GENOMIC CONFIGURATION IN CANCER | Francesca Menghi (US) |
12:30-12:40  | O20 - SPATIAL ORGANIZATION OF THE GENOME AND GENOMIC ALTERATIONS IN HUMAN CANCERS | Kadir Caner Akdemir (US) |
12:40-12:50  | O16 - MODELING GENETIC INTERACTIONS ASSOCIATED WITH MOLECULAR SUBTYPES OF BREAST CANCER | Greg Carter (US) |

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<th>Time</th>
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<tbody>
<tr>
<td>11:30-11:55</td>
<td>THE CLINICAL GENOME RESOURCE</td>
<td>Heidi Rehm (US)</td>
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<tr>
<td>11:55-12:20</td>
<td>I15 - THE MATCHMAKER EXCHANGE: AN INTERNATIONAL EFFORT TO SOLVE UNSOLVED EXOMES AND DISCOVER NOVEL DISEASE GENES</td>
<td>Ada Hamosh (US)</td>
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<td>12:20-12:45</td>
<td>BRCA CHALLENGE</td>
<td>Susan Domchek (US)</td>
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<tr>
<th>Time</th>
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<th>Presenter(s)</th>
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<tr>
<td>13:00-14:00</td>
<td>EXHIBITION &amp; POSTER VISIT &amp; LUNCH</td>
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<tr>
<td>14:00-16:00</td>
<td>ORAL PRESENTATIONS 1</td>
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<tr>
<td>14:00-14:10</td>
<td>O13 - ELEVATED MUTATION AND WIDESPREAD LOSS OF CONSTRAINT AT REGULATORY AND ARCHITECTURAL BINDING SITES ACROSS 11 TUMOUR TYPES</td>
<td>Colin A. Semple (GB)</td>
</tr>
<tr>
<td>14:10-14:20</td>
<td>O14 - EXOME SEQUENCING PROVIDES EVIDENCE OF PATHOGENICITY FOR GENES IMPLICATED IN COLORECTAL CANCER</td>
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</table>
Elisabeth A. Rosenthal (US)

O12 - TRANSCRIPTOME ANALYSIS IDENTIFIES GENES, ENHANCER RNAs AND REPETITIVE ELEMENTS THAT ARE RECURRENTLY Deregulated ACROSS MULTIPLE CANCER TYPES
Bogumil Kaczkowski (JP)

O18 - PREDICTIVE BIOMARKERS TO METASTATIC PANCREATIC CANCER TREATMENT
Jennifer Brooke Goldstein (US)

O17 - RECURRENT SOMATIC MUTATION IN THE MYC ASSOCIATED FACTOR X IN BRAIN TUMORS
Hamid Nikbakht (CA)

O21 - LANDSCAPE OF TARGETED THERAPIES IN SOLID TUMORS
Sara Patterson (US)

O24 - CLINICAL VALIDITY AND ACTIONABILITY OF MULTIGENE TESTS FOR HEREDITARY CANCERS IN A LARGE MULTI-CENTER STUDY
Stephen Lincoln (US)

O22 - GENOMIC ANALYSIS REVEALS NOVEL DRIVERS AND PROGRESSION PATHWAYS IN SKIN BASAL CELL CARCINOMA
Sergey Nikolaev (CH)

O23 - IDENTIFICATION OF DIFFERENTIAL BIOMARKERS OF HEPATOCELLULAR CARCINOMA AND CHOLANGIOCARCINOMA VIA TRANSCRIPTOME MICROARRAY META-ANALYSIS
Somsak Likhitrattanapisal (TH)

O19 - DDIT4 GENE EXPRESSION AS A PROGNOSTIC MARKER IN SEVERAL MALIGNANT TUMORS
Joseph A Pinto (PE)

O11 - A MICRORNA SIGNATURE IDENTIFIES SUBTYPES OF TRIPLE-NEGATIVE BREAST CANCER AND REVEALS MIR-342-3P AS REGULATOR OF A LACTATE METABOLIC PATHWAY
Alfredo Hidalgo-Miranda (MX)

O25 - CORRELATION WITH TUMOR PLOIDY STATUS IS ESSENTIAL FOR CORRECT DETERMINATION OF GENOME-WIDE COPY NUMBER CHANGES BY SNP ARRAY
Tricia L. Peters (US)

ORAL PRESENTATIONS 2

Chair: Stefan Mundlos (DE)

O45 - MAV-SEQ: AN INTERACTIVE PLATFORM FOR THE MANAGEMENT, ANALYSIS, AND VISUALIZATION OF SEQUENCE DATA
Zeeshan Ahmed (US)

O42 - BIG DATA AND NGS DATA ANALYSIS: THE CLOUD TO THE RESCUE
Otto Dobretsberger (US)

O40 - A GENERAL STATISTIC FRAMEWORK FOR GENOME-BASED DISEASE RISK PREDICTION
Momiao Xiong (US)

O41 - INTEGRATIVE LARGE-SCALE CAUSAL NETWORK ANALYSIS OF IMAGING AND GENOMIC DATA AND ITS APPLICATION IN SCHIZOPHRENIA STUDIES
Nan Lin (US)

O44 - A BAYESIAN CLASSIFICATION OF BIOMEDICAL IMAGES USING FEATURE EXTRACTION FROM DEEP NEURAL NETWORKS IMPLEMENTED ON LUNG CANCER DATA
14:55-15:05 Victor Andrew Asuncion Antonio (JP)
O50 - BREAST AND OVARIAN CANCER PREVENTION: IS IT TIME FOR POPULATION-BASED MUTATION SCREENING OF HIGH RISK GENES?
Ian Campbell (AU)

15:05-15:15 Han Cao (US)
O47 - ALLELE SPECIFIC ENHANCER IN EPAS1 INTRONIC REGIONS MAY CONTRIBUTE TO HIGH ALTITUDE ADAPTATION OF TIBETAN
Changqing Zeng (CN)

15:25-15:35 Elissa J. Chesler (US)
O43 - CPIPE: A CONVERGENT CLINICAL EXOME PIPELINE SPECIALISED FOR TARGETED SEQUENCING
Simon Sadedin (AU)

15:45-15:55 Hoh Boon-Peng (MY)
O49 - ARCHAIC INTROGRESSION IN INDIGENOUS POPULATIONS OF MALAYSIA REVEALED BY WHOLE GENOME SEQUENCING

16:00-16:30 COFFEE BREAK

16:30-18:00 ORAL PRESENTATIONS 3
Chair: Andy Futreal (US)

16:35-16:45 Hazuki Takahashi (JP)
O33 - HIGH THROUGHPUT SCREENING PLATFORM OF COMPETENT SINEUPS: THAT CAN ENHANCE TRANSLATION ACTIVITIES OF THERAPEUTIC TARGET

16:45-16:55 Rajarshī Ghosh (US)
O36 - PERFORMANCE OF COMPUTATIONAL ALGORITHMS IN PATHOGENICITY PREDICTIONS FOR ACTIVATING VARIANTS IN ONCOGENES VERSUS LOSS OF FUNCTION MUTATIONS IN TUMOR SUPPRESSOR GENES

16:55-17:05 John J. Mulvihill (US)
O34 - THE UNDIAGNOSED DISEASES NETWORK INTERNATIONAL (UDNI): CLINICAL AND LABORATORY RESEARCH TO MEET PATIENT NEEDS

17:05-17:15 Mani Grover (AU)
O35 - NOVEL THERAPEUTICS FOR CORONARY ARTERY DISEASE FROM GENOME-WIDE ASSOCIATION STUDY DATA

17:15-17:25 Kent Small (US)
O28 - NORTH CAROLINA MACULAR DYSTROPHY (MCDR1): MUTATIONS FOUND AFFECTING PRDM13

17:25-17:35 Steve Scherer (US)
O37 - IDENTIFICATION AND ELECTRONIC HEALTH RECORD INCORPORATION OF CLINICALLY ACTIONABLE PHARMACOGENOMIC VARIANTS USING PROSPECTIVE TARGETED SEQUENCING
O38 - MELANOMA REPROGRAMMING STATE CORRELATES WITH RESPONSE TO CTLA-4 BLOCKADE IN METASTATIC MELANOMA
Tatiana Karpinets (US)

O27 - MUTATION SPECTRUM IN A PULMONARY ARTERIAL HYPERTENSION (PAH) COHORT AND IDENTIFICATION OF ASSOCIATED TRUNCATING MUTATIONS IN TBX4
Claudia Gonzaga-Jauregui (US)

ORAL PRESENTATIONS 4
Chair: David Wheeler (US)

16:35-16:45  O6 - SINGLE CELL ALLELE SPECIFIC EXPRESSION (ASE) IN T21 AND COMMON TRISOMIES: A NOVEL APPROACH TO UNDERSTAND DOWN SYNDROME AND OTHER ANEUPLOIDIES
Georgios Stamoulis (CH)

16:45-16:55  O4 - HIGH-THROUGHPUT IDENTIFICATION OF SPECIFIC QT INTERVAL MODULATING ENHANCERS AT THE SCN5A LOCUS
Ashish Kapoor (US)

16:55-17:05  O7 - ROLE OF MICRORNA IN LCL TO IPSC REPROGRAMMING
Satish Kumar (US)

17:05-17:15  O5 - IDENTIFICATION OF EXTRACELLULAR MATRIX COMPONENTS INDUCING CANCER CELL MIGRATION IN THE SUPERNATANT OF CULTIVATED MESENCHYMAL STEM CELLS
Christian Maercker (DE)

17:15-17:25  O10 - A NOVEL CAUSAL METHYLATION NETWORK APPROACH TO ALZHEIMER’S DISEASE
Zixin Hu (US)

17:25-17:35  O8 - MULTIPLE ENHANCER VARIANTS DISRUPT GENE REGULATORY NETWORK IN HIRSCHSPRUNG DISEASE
Sumantra Chatterjee (US)

17:35-17:45  O9 - METABOLOMATIC PROFILING FOR THE DIAGNOSIS OF NEUROMETABOLIC DISORDERS
Taraka R. Donti (US)

TUESDAY, 1 MARCH 2016

09:00-10:00  PLENARY LECTURE 4
Chair: Ada Hamosh (US)

09:00-10:00
I6 - INTERROGATING THE ARCHITECTURE OF CANCER GENOMES
Peter Campbell (UK)

10:00-10:30  COFFEE BREAK – With the kind support of Illumina

10:30-12:30  S4 - GENETICS 2: MENDELIAN GENETICS
Chair: Aravinda Chakravarti (US) Co-chair: Debbie Nickerson (US)

10:35-11:00  EXPERIENCE OF 10,000 DIAGNOSTIC EXOMES
11:00-11:25  LESSONS FROM SCALING MENDELIAN ANALYSES  
Debbie Nickerson (US)

11:25-11:50  I8 - MAPPING RARE DISEASES  
Aravinda Chakravarti (US)

11:50-12:00  O30 - BAYLOR-JOHNS HOPKINS CENTER FOR MENDELIAN GENOMICS: A FOUR YEAR REVIEW  
Shalini N Jhangiani (US)

12:00-12:10  O29 - PHENODB AND GENEMATCHER, SOLVING UNSOLVED WHOLE EXOME SEQUENCING DATA  
Nara Lygia Sobreira (US)

12:10-12:20  O31 - USING READ OVERLAP ASSEMBLY TO ACCURATELY IDENTIFY STRUCTURAL GENETIC DIFFERENCES IN AN ASHKENAZI JEWISH TRIO  
William Salerno (US)

W4 – ELSI/INTERNATIONAL DATA  

Chair: Ruth Chadwick (UK) and Co-chair: Charles Rotimi (US)

10:35-11:00  I7 - SOLIDARITY AND INTERNATIONAL DATA  
Ruth Chadwick (UK)

11:00-11:25  BUILDING THE MEDICAL INFORMATION COMMONS: DATA SHARING ETHICS AND POLICY  
Amy McGuire (US)

11:25-11:50  I34 - ETHICAL AND EQUITABLE SHARING OF INTERNATIONAL DATA: A PERSPECTIVE FROM AFRICA  
Charles Rotimi (US)

11:50-12:15  I3 - AN INTERNATIONAL PERSPECTIVE ON SHARING GENOME AND ASSOCIATED DATA  
Martin Bobrow (UK)

12:15-12:25  O32 - LEGAL INTEROPERABILITY: A SINE QUA NON FOR INTERNATIONAL DATA SHARING  
Adrian Thorogood (CA)

12:30-13:30  PwC LUNCH SYMPOSIUM  
(full programme page 20)

13:30-15:30  S5 - CANCER 2: INTERNATIONAL CONSORTIA SYMPOSIUM (ICGC)

Chair: Juergen Reichardt (EC)

13:35-14:00  I18 - INTERNATIONAL COLLABORATIONS IN CANCER GENOMICS  
Thomas Hudson (CA)

14:00-14:25  I37 - ASIAN CANCER GENOMICS AND ITS CLINICAL IMPLICATIONS  
Bin Teh (SG)

14:25-14:50  NOVEL MOLECULAR BRAIN TUMOR ENTITIES DECRYPTED BY INTEGRATIVE GENOME AND EPIGENOME ANALYSIS  
Stefan Pfister (DE)

ORAL PRESENTATIONS 5  

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<table>
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<tr>
<th>Time</th>
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| 13:35-13:45| **O26 - NANOCHANNEL BASED NEXT-GENERATION MAPPING FOR INTERROGATION OF CLINICALLY RELEVANT STRUCTURAL VARIATION**  
Alex Hastie (US) |
| 13:45-13:55| **O54 - METHODS FOR LARGE SCALE CONSTRUCTION OF ROBUST PCR-FREE LIBRARIES FOR SEQUENCING ON ILLUMINA HISEQX PLATFORM**  
Harsha Doddapaneni (US) |
| 13:55-14:05| **O55 - RAPID CAPTURE METHODS FOR CLINICAL SEQUENCING**  
Jianhong Hu (US) |
| 14:05-14:15| **O56 - A DIPLOID PERSONAL HUMAN GENOME MODEL FOR BETTER GENOMES FROM DIVERSE SEQUENCE DATA**  
Kim C. C. Worley (US) |
| 14:15-14:25| **O57 - DEVELOPMENT OF PACBIO LONG RANGE CAPTURE FOR DETECTION OF PATHOGENIC STRUCTURAL VARIANTS**  
Qingchang Meng (US) |
| 14:25-14:35| **O53 - COMPREHENSIVE COVERAGE FROM LOW DNA INPUT USING NOVEL NGS LIBRARY PREPARATION METHODS FOR WGS AND WGBS**  
Cassie Schumacher (US) |
| 14:35-14:45| **O58 - RHESUS MACAQUES EXHIBIT MORE NON-SYNONYMOUS VARIATION BUT GREATER IMPACT OF PURIFYING SELECTION THAN HUMANS**  
Ronald Alan Harris (US) |
| 14:45-14:55| **O59 - ASSESSING RNA STRUCTURE DISRUPTION INDUCED BY SINGLE-NUCLEOTIDE VARIATION**  
Zhengqing Ouyang (US) |
| 14:55-15:05| **O2 - PHENOME-WIDE ASSOCIATION STUDY FOR SMOKING- AND DRINKING-ASSOCIATED GENES IN 26,394 AMERICAN WOMEN WITH AFRICAN, ASIAN, EUROPEAN, AND HISPANIC DESCENTS**  
Renato Polimanti (US) |
| 15:05-15:15| **O3 - EFFECTS OF PRENATAL ENVIRONMENT, GENOTYPE AND DNA METHYLATION ON BIRTH WEIGHT AND SUBSEQUENT POSTNATAL OUTCOMES: FINDINGS FROM GUSTO, AN ASIAN BIRTH COHORT**  
Xinyi Lin (SG) |
| 15:15-15:25| **O1 - THE METABOLOMICS APPROACH TO AUTISM: IDENTIFICATION OF BIOMARKERS FOR EARLY DETECTION OF AUTISM SPECTRUM DISORDER**  
Anand K. Srivastava (US) |

**WEDNESDAY, 2 MARCH 2016**
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<tr>
<td>08:00-09:00</td>
<td><strong>MEET THE PROFESSORS - I</strong></td>
<td>ROOM 337 A</td>
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<tr>
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<td>Stylianos Antonarakis (CH)</td>
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<td>Eric Boerwinkle (US)</td>
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<td>08:00-09:00</td>
<td><strong>MEET THE PROFESSORS - II</strong></td>
<td>ROOM 337 B</td>
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<td>Bing Ren (US)</td>
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<td>Richard Gibbs (US)</td>
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<td>09:00-09:45</td>
<td><strong>PLENARY LECTURE 5</strong></td>
<td>BALLROOM A+B</td>
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<td><em>Chair: Andy Futreal (US)</em></td>
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<td>09:05-09:45</td>
<td><strong>TRANSFORMING HEALTHCARE</strong></td>
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<td>Lynda Chin (US)</td>
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<td>09:45-10:15</td>
<td><strong>COFFEE BREAK</strong></td>
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<td>10:15-11:15</td>
<td><strong>S6 - GENOMIC MEDICINE: MEDICAL TRANSLATION</strong></td>
<td>BALLROOM A+B</td>
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<td><em>Chair: Edison Liu (US)</em></td>
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<td>10:20-10:45</td>
<td><strong>TBC</strong></td>
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<td>Rob High (US)</td>
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<td>10:45-11:10</td>
<td><strong>ROLE OF PUBLIC HEALTH IN TRANSLATION OF GENOMIC MEDICINE</strong></td>
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<td>Muin Khoury (US)</td>
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<td>11:15-13:00</td>
<td><strong>CHEN AWARD &amp; HUGO AFRICAN AWARD LECTURES</strong></td>
<td>BALLROOM A+B</td>
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<td><em>Chair: Stylianos Antonarakis (CH)</em></td>
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<td>11:20-11:45</td>
<td><strong>I39 - GENOME EDITING USING CRISPR-CAS SYSTEMS</strong></td>
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<td>Feng Zhang (US)</td>
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<td>11:45-12:10</td>
<td><strong>THE 3D GENOME ORGANIZATION AND FUNCTION</strong></td>
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<td>Bing Ren (US)</td>
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<td>12:10-12:35</td>
<td><strong>THE SCOPE OF HUMAN GENOME RESEARCH AND TRANSLATION IN SUB-SAHARAN AFRICAN</strong></td>
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<td>Raj Ramesar (ZA)</td>
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**LUNCH SYMPOSIA PROGRAMME**
One of the greatest challenges in this remarkable era of progress in developing "precision medicine" is the capability to effectively integrate clinical and research data. As part of MD Anderson’s Moon Shot program aimed at driving goal-oriented, multidisciplinary research to reduce cancer mortality faster, PwC and MD Anderson have partnered to develop a cohesive strategy to purposefully integrate research and clinical data. The goal of this effort is to accelerate translation research by providing a dedicated infrastructure to facilitate analytics, queries, cohorting and deep dives for all patients being cared for at the institution – all in a near real-time, extensible and sustainable platform.

In this lunch symposium, attendees will learn about MD Anderson’s approach to enhancing research productivity through Big Data and Natural Language Processing. Key topics include ingestion and integration of complex and unstructured data, new tools to visualize and combine these data in a virtual workspace, and a preview of how MD Anderson intends to build on early results to make significant strides in improving patient outcomes.
# Posters Presentations

**Sunday 28 February to Wednesday 2 March**

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<td>P2</td>
<td>Missense polymorphic genetic combinations underlying Down syndrome susceptibility</td>
<td>E. S. Chen*</td>
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<tr>
<td>P5</td>
<td>Obesity and the incidence of apolipoprotein E polymorphisms in an assorted population from Saudi Arabia population</td>
<td>K. K. R. Alharbi*</td>
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<tr>
<td>P8</td>
<td>Differentiating inflammatory bowel diseases by using genomic data: dimension of the problem and network organization</td>
<td>N. Mili* - R. Molinari - Y. Ma - S. Guerrier</td>
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<tr>
<td>P9</td>
<td>Vulnerability of genetic variants to the risk of autism among Saudi children</td>
<td>N. Elhawary* - M. Tayeb - N. Bogari - N. Qotb</td>
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<tr>
<td>P10</td>
<td>Chromatin profiles from ex vivo purified dopaminergic neurons establish a promising model to support studies of neurological function and dysfunction</td>
<td>P. W. Hook - L. A. Goff - A. McCallion</td>
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<tr>
<td>P11</td>
<td>Utilization of a sensitized chemical mutagenesis screen to identify genetic modifiers of retinal dysplasia in homozygous Nr2e3rd7 mice</td>
<td>J. R. Charette - W. L. Hicks - J. K. Naggert - L. Zhao - P. M. Nishina</td>
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<tr>
<td>P14</td>
<td>The evolution of imperfection and imperfection of evolution: the functional and functionless fractions of the human genome</td>
<td>D. Graur*</td>
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<tr>
<td>P16</td>
<td>Species-independent identification of known and novel recurrent genomic entities in multiple cancer patients</td>
<td>J. Friis-Nielsen - J. M. Izarzugaza* - S. Brunak</td>
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<tr>
<td>P18</td>
<td>Discovery of active gene modules which are densely conserved across multiple cancer types reveal their prognostic power and mutually exclusive mutation patterns</td>
<td>B. S. Soibam*</td>
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<tr>
<td>P19</td>
<td>Whole exome sequencing of dysplastic leukoplakia tissue indicates sequential accumulation of somatic mutations from oral precancer to cancer</td>
<td>D. Das* - N. Biswas - S. Das - S. Sarkar - A. Maitra - C. Panda - P. Majumder</td>
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<tr>
<td>P21</td>
<td>Epigenetic mechanisms of carcinogenesis by hereditary breast cancer genes</td>
<td>J. J. Gruber* - N. Jaeger - M. Snyder</td>
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</table>
RNA SEQUENCING IDENTIFIES GENE MUTATIONS FOR NEUROBLASTOMA / K. Zhang*

PARTICIPATION OF SFRP1 IN THE MODULATION OF TMPRSS2-ERG FUSION GENE IN PROSTATE CANCER CELL LINES / M. Rodriguez-Dorantes* - C. D. Cruz-Hernandez - C. D. P. Garcia-Tobilla - S. Solorzano-Rosas

TARGETED METHYLATION SEQUENCING OF PROSTATE CANCER / N. Jäger* - J. Chen - R. Haile - M. Hitchins - J. D. Brooks - M. Snyder


NGS-SWIFT: A CLOUD-BASED VARIANT ANALYSIS FRAMEWORK USING CONTROL-ACCESSED SEQUENCING DATA FROM DBGAP/SRA / C. Xiao* - E. Yaschenko - S. Sherry

COMPUTATIONAL ASSESSMENT OF DRUG INDUCED HEPATOTOXICITY THROUGH GENE EXPRESSION PROFILING / C. Rangel-Escareño* - H. Rueda-Zarate

DATA BASE SURVEY AND INSILICO STUDIES ON SCORPION TOXIN AND THEIR INTERACTION WITH ION CHANNELS / I. A. Tayubi* - R. Mohammed - I. Ahmed - T. Ahmed


P44  POLYMORPHISM OF GLUTATHIONE S-TRANSFERASES AND SULPHOTRANSFERASES GENES IN AN ARAB POPULATION / A. H. Salem* - M. Ali - A. Ibrahim - M. Ibrahim


P47  WHOLE EXOME SEQUENCE META-ANALYSIS OF 13 WHITE BLOOD CELL, RED BLOOD CELL, AND PLATELET TRAITS. / L. Polfus* on behalf of CHARGE and NHLBI Exome Sequence Project Working Groups


P49  COMMON VARIANTS IN CASR GENE ARE ASSOCIATED WITH SERUM CALCIUM LEVELS IN KOREANS / S.-H. Jung* - N. Vinayagamoorthy - S.-H. Yim - Y.-J. Chung

P50  INFERENCE OF MULTIPLE-WAVE POPULATION ADMIXTURE BY MODELING DECAY OF LINKAGE DISEQUILIBRIUM WITH MULTIPLE EXPONENTIAL FUNCTIONS / Y. Zhou - S. Xu*

P51  A BAYESIAN FRAMEWORK FOR GENERALIZED LINEAR MIXED MODELS IN GENOME-WIDE ASSOCIATION STUDIES / X. Wang* - V. Philip - G. Carter


P53  IDENTIFICATION OF ENHANCER SEQUENCES BY ATAC-SEQ OPEN CHROMATIN PROFILING / A. Uyar* - A. Kaygun - S. Zaman - E. Marquez - J. George - D. Ucar


P55  PATERNITY RECLAIMED: ANCESTRY TESTING UNVEILS UNIQUE CASE OF CONGENITAL CHIMERISM PROVIDING EXPLANATION FOR FALSE NEGATIVE PATERNITY TESTING / D. B. Starr* - M. Baird - B. Kirkpatrick - K. Sheets

P56  PERFORMANCE OF THE AGILENT D5000 AND HIGH SENSITIVITY D5000 SCREENTAPE ASSAYS FOR THE AGILENT 4200 TAPESTATION SYSTEM / R. Nitsche* - L. Prieto-Lafuente

P57  CLINVAR: A MULTI-SOURCE ARCHIVE FOR VARIANT INTERPRETATION / M. Landrum* - J. Lee - W. Rubinstein - D. Maglott


P64 POTENTIAL GENETIC POLYMORPHISM EFFECT AND EVALUATION OF SUBJECTIVE SATISFACTION ON MEDICATIONS IN THE POPULATION OF UKRAINE / O. Filiptsova* - M. N. Kobets - Y. Kobets - I. Burlaka - I. Timoshyna


P70 THE MOLEULARMATCH GENOTYPE-BASED THERAPEUTICS AND CLINICAL TRIALS SEARCH ENGINE / S. Neeley - J. Welsh - N. Tackes - C. Corless - S. Li - C. Davis*


WE WOULD LIKE TO Specially THANK PROfessor YUAN TSong (YT) CHEN, MRS ALICE DER-SHAN CHEN AND INQABA BIOTECHNICAL INDUSTRIES FOR SUPPORTING THE FOLLOWING AWARDS

CHEN NEW INVESTIGATOR AWARD
CHEN DISTINGUISHED ACADEMIC ACHIEVEMENT IN HUMAN GENETIC AND GENOMIC RESEARCH AWARD
HUGO-AFRICAN PRIZE AWARD
**SPEAKERS BIOGRAPHY & ABSTRACTS**

*This is a non-exhaustive list of HGM speakers’ biographies sorted by alphabetical order.*

**Zilfalil Bin Alwi - I2**

**Biography:** Professor Dr Zilfalil Bin Alwi is a senior Consultant Pediatrician & Clinical Geneticist at Hospital Universiti Sains Malaysia (USM), Kubang Kerian, Kelantan. He received his specialist training in Pediatrics from the same university and later went to study at University of Aston, United Kingdom where he obtained a PhD in Pharmacogenetics. His research interest includes genetics of childhood Spinal Muscular Atrophy, population genomics (genetic diversity of the Malay ethnic group), and genome wide studies on diseases common to the local population. Prof Zilfalil is the founder and Head of the Malaysian Node of the Human Variome Project (MyHVP). He is a member of the Board of Directors of Human Variome Project (HVP) and is the co-chair for Global Globin 2020 Challenge (GG2020) initiative-a global project by HVP which involve the systematic collection and sharing of variation data to fight haemoglobinopathies (Thalassaemias and Sickle Cell Disease). He has also served as the Director of USM Human Genome Center from 2005 to 2009. Prof Zilfalil is the Chief Editor of several journals including the Malaysian Journal of Pediatrics and Child Health and GENETIK, which is the official bulletin of the Genetics Society of Malaysia. He is a council member of the College of Pediatrics, Academy of Medicine of Malaysia and Fellow of this prestigious Academy. He is the founding and current president of the Malaysian Society of Human Genetics.

**Abstract: HUMAN VARIOME PROJECT; THE GLOBAL GLOBIN CHALLENGE 2020(GG2020)**

The haemoglobinopathies, collectively, are cause for significant morbidity and mortality, especially in parts of the world where health systems are weak. Children are the most severely affected. Despite much of the genetics and biology of haemoglobinopathies being known, and being used successfully in some countries to systematically reduce burden of disease, many low and middle income countries remain practically untouched by this knowledge and innovations. Commitment to systematic variant data collection is increasing, but this is occurring mostly in high-income countries where much of the diagnosis and testing takes place. There is a risk that countries where the burden of these diseases is highest are being left behind in a form of "genomic divide". This project seeks to apply recent developments in human genomics involving the systematic collection and sharing of variation data to fighting haemoglobinopathies (notably Thalassaemias and Sickle Cell Disease) in low- and middle-income countries. Capacity to generate quality data on variants, to store it so that it can be shared internationally is build in these countries. This genomic capacity enables 1) the building of genetic evidence base for better management of delivery of local treatment, care and eventually even cure 2) forming a foundation for genomic medicine by working with national, regional and local health care professionals to raise public awareness of the genetic basis of haemoglobinopathies. The recent developments in human genomics involving the systematic collection and sharing of variation data to fighting haemoglobinopathies especially Thalassaemias and Sickle Cell Disease will be applied in low- and middle-income countries.

**Disclosure of Interest:** None Declared
Biography: Graduated MB BCh from the University of Witwatersrand, Johannesburg. Joined the MRC Population Genetics Research Unit in Oxford, and worked on chromosome identification techniques and clinical genetics. Became Head of Dept of Medical Genetics in Amsterdam, Guys Hospital London, and finally in Cambridge. Deputy Chairman and Governor of Wellcome Trust, Deputy Chair of Nuffield Council on Bioethics, Chair and member of several Government advisory committees. Steering committee of Global Alliance for Genomics and Health. Chair of Expert SAdvisory Committee on Data Access to UK funding agencies.

Abstract: AN INTERNATIONAL PERSPECTIVE ON SHARING GENOME AND ASSOCIATED DATA
There is widespread and growing recognition of the value of early sharing of large research datasets. Neither the academic community nor legislatures have however caught up with this movement. Career incentives towards being open about data are not well developed. Data transfer laws and regulations do not align easily. Processes for accessing data are remain fragmented and awkward to navigate. But there are now many signs of real progress being made which will hopefully bear fruit over the coming decade.
Disclosure of Interest: None Declared
Catherine Brownstein – I4

Biography: Dr. Brownstein is a research associate in Genetics and Genomics and the manager of the Molecular Genetics Core Facility at Boston Children’s Hospital. An active member of the Manton Center for Orphan Disease Research and specializing in gene discovery, Dr. Brownstein has been instrumental in the elucidation of several new disease genes for conditions such as intellectual disability, nemaline myopathy, psychosis, SIDS, and hypophosphatemic rickets. Her current work focuses on advancing the fields of next generation sequencing and analysis, as evidenced in her management of the international CLARITY and CLARITY Undiagnosed competitions. Before coming to BCH and HMS, Dr. Brownstein created online patient communities for individuals with chronic or terminal diseases, and worked as a toxicologist for Massachusetts Department of Public Health.

Abstract: DIAGNOSTIC CHALLENGES AND INTERPRETIVE GENOMICS AT BOSTON CHILDREN’S HOSPITAL
As the analysis of personal genomes becomes routine, new challenges will center on interpreting the clinical relevance of genomic data. Three exciting initiatives at BCH are illustrative: 1) the Robert’s Program on Sudden Unexpected Death in Pediatrics (SUDP), 2) the Developmental Neuropsychiatry Program (DNP), and 3) the Manton Center for Orphan Disease Research.

Robert’s Program on SUDP approaches sudden unexpected death in pediatrics as the potential presentation of undiagnosed disease. Its clinical arm includes enhanced phenotyping and in-depth neuropathology, state-of-the-art genomics, and, where indicated, metabolomics. In order to gain a population-based estimate of findings, the program is offered to the family of any child under the age of three years dying suddenly and unexpectedly of natural causes in the state of Massachusetts, in collaboration with the Chief Medical Examiner.

The DNP focuses on developmental risk for very serious psychiatric disorders, especially early onset psychosis. It seeks to embrace the entire discovery cycle, from genetic and endophenotypic characterization to functional studies, including neurons differentiated from iPSC lines derived from subjects. Notably 30% of these patients are under the age of 13 years.

The Manton Center for Orphan Disease Research is one of the first centers in the world solely devoted to the study of rare diseases, focusing on patient-centered research and funding existing research efforts on rare diseases. The Center maintains a general IRB protocol suitable for enrolling subjects with any rare or undiagnosed condition, and provides consenting, enrollment and genotyping services and training, enabling discovery.

Although focused on distinct patient populations throughout BCH, each of these initiatives utilizes a common genomic toolkit, and is developing shared informatics resources and intellectual expertise. Dr. Brownstein will present the approaches of these initiatives using case demonstrations.
Biography: Han Brunner studied medicine at the University of Groningen 1975-1984. He trained as a clinical geneticist at Nijmegen University and was board certified in Clinical Genetics in 1988. In 1998 he was appointed full professor and head of the department of Human Genetics at Nijmegen University Hospital. From 2004-2008 he served as chancellor for Human Genetics, Pediatrics, and Medical Psychology at Nijmegen University Hospital. In 2014 he was also appointed chairman of the Department of Clinical Genetics at Maastricht University Medical Center, in the Netherlands. He was elected member of the board of directors of the Dutch, European (president in 2014-2015) and of the American Societies of Human Genetics. Han Brunner pursues the scientific understanding of the connections between clinical and molecular features of rare diseases, including applications to patient care. He has pioneered the discovery of a large number of disease genes, and the application of cutting-edge genomic technologies (genomic microarrays, exome sequencing, and whole genome sequencing) to discover the causes of genetic diseases. Much of this work focuses on neurodevelopmental conditions such as intellectual disability and abnormal behavior. Han Brunner was elected member of the Royal Netherlands Academy of Arts and Sciences in 2013, and of the Academia Europea in 2012. He is a Knight in the Order of the Dutch Lion since 2013. He is a co-winner of the King Faisal International Prize in Medicine 2016, with Joris Veltman.

Selected Publications:


**Abstract: EXPERIENCE OF 10000 DIAGNOSTIC EXOMES**

We are using exome sequencing in clinical diagnosis for a broad range of diseases. For the year 2016, we expect to run 8000 diagnostic exome tests. We have reviewed our experience of the first 5000 exome tests, and find that this has now become an integrated part of modern medical care for patients with rare diseases. After 5 years of experience with exomes in a clinical setting, the following conclusions are drawn:

- Exomes do better than doctors most of the time
- Exomes do not generate large numbers of incidental findings
- Incidental findings can be managed by a combination of careful informed consent, targeted analysis where possible, and informed genetic counseling
- Genomes do better than exomes, but not much at this point
- We do not understand enough of non-coding DNA to allow easy detection of variants that impact disease
- We find similar mutations for seemingly distinct neurodevelopmental disorders suggesting broad clinical heterogeneity, and fueling nosological debate
- De novo mutations are an important cause of severe genetic disease in non-consanguineous populations
Biography: Dr Peter Campbell is Head of Cancer Genetics and Genomics at the Wellcome Trust Sanger Institute, having started a Wellcome Trust Senior Clinical Fellowship in 2010. He completed specialist training in Haematology in New Zealand and Australia in 2002. Following this, he completed a PhD at the University of Cambridge in the molecular pathogenesis of myeloproliferative disorders. Since 2007, Dr Campbell has been employed at the Cancer Genome Project, Wellcome Trust Sanger Institute. His major interest is cancer genomics, and in particular genome-wide analyses of somatic mutations in tumours. The four major areas of interest have been:

- the discovery of new cancer genes;
- the identification of somatic mutation processes operative in tumours;
- the characterisation of patterns of cancer evolution;

Further details are available at: http://www.sanger.ac.uk/research/faculty/pcampbell/

Abstract: INTERROGATING THE ARCHITECTURE OF CANCER GENOMES
Cancer is driven by mutation. Using massively parallel sequencing technology, we can now sequence the entire genome of cancer samples, allowing the generation of comprehensive catalogues of somatic mutations of all classes. Bespoke algorithms have been developed to identify somatically acquired point mutations, copy number changes and genomic rearrangements, which require extensive validation by confirmatory testing. The findings from our first handful of genomes illustrate the potential for next-generation sequencing to provide unprecedented insights into mutational processes, cellular repair pathways and gene networks associated with cancer development. I will also review possible applications of these technologies in a diagnostic and clinical setting, and the potential routes for translation.

Disclosure of Interest: None Declared
Ruth Chadwick - I7

Biography: Professor Ruth Chadwick is Professor of Bioethics at the University of Manchester. From 2002-2013 she directed the ESRC Centre for Economic and Social Aspects of Genomics (Cesagen). Cesagen was a dual site research centre funded for ten years by the Economic and Social Research Council as a partnership between Lancaster and Cardiff Universities. Ruth co-edits *Bioethics and Life Sciences, Society and Policy* and has served on the Council of the Human Genome Organisation, the Panel of Eminent Ethical Experts of the Food and Agriculture Organisation of the United Nations (FAO), and the UK Advisory Committee on Novel Foods and Processes (ACNFP). She is Fellow of the Academy of Social Sciences; of the Hastings Center, New York; of the Royal Society of Arts; and of the Royal Society of Biology. In 2005 she won the World Technology Network Award for Ethics and in 2014 she was elected Fellow of the Learned Society of Wales.

Abstract: SOLIDARITY AND INTERNATIONAL DATA
It is today widely if not universally recognised that it is important to maximise the value of collections of genomic samples and data. For example, the ICH guideline issued for public consultation early this year states that as a general principle there is a need and an opportunity to ‘maximise the value of the collected samples and the data generated from them’ and from this principle a number of implications for action follow, regarding standards for collection and storage. There is a question for ethics, however, regarding the principles at stake. The maximisation principle is sometimes held to be at odds with principles that make the interests of the individual ‘paramount’. While informed consent, underpinned by autonomy considerations, is a constraint, there is also increasingly a turn towards other principles that emphasise the common good, such as solidarity, and indeed the HUGO Committee on Ethics, Law and Society has recognised the importance of this principle in the genomics context. There are challenges in interpreting and applying solidarity, however, and this presentation will ask who should show solidarity to whom in relation to data sharing and what actions that implies.

Disclosure of Interest: None Declared
**Aravinda Chakravarti - I8**

**Biography:** Aravinda Chakravarti came to the United States in 1974 to study human genetics at the University of Texas at Houston and obtained his Ph.D. in 1979 for developing a theoretical basis for disease prediction in families using genetic linkage. After a brief fellowship at University of Washington in Seattle he accepted a teaching position at the University of Pittsburgh in 1980. He has served on the faculty of University of Pittsburgh, Case Western Reserve University and is currently at Johns Hopkins University where he was the Inaugural Director of the McKusick-Nathans Institute of Genetic Medicine, and is now Director, Center for Complex Disease Genomics and Professor of Medicine, Pediatrics, Molecular Biology & Genetics, and, Biostatistics at the Johns Hopkins University School of Medicine and the Bloomberg School of Public Health. His research is on experimental and computational methods for discovering and interpreting patterns of human genetic variation and its use in dissecting the molecular basis of human disease.

He has played an integral role in the Human Genome Project as participant, organizer, Chair of the NIH Third Plan of the U.S. Human Genome Project (1998), the HapMap and 1000Genomes projects, and is one of the founding editors of Genome Research and the Annual Reviews of Genomics & Human Genetics. He was the 2008 President of the American Society of Human Genetics, has been elected to the US National Academy of Science in 2015 and the US National Academy of Medicine in 2007, Fellow of the American Association for the Advancement of Science in 2014, Pravasi Fellow of the Indian National Academy of Sciences in 2014 and Honorary Fellow of the Indian Academy of Sciences in 2008. He was selected as one of The World’s Most Influential Scientific Minds (by Thomson Reuters) in 2014.

**Abstract: MAPPING GENES FOR RARE DISEASES**

Genome and exome sequencing are powerful tools for identification of the molecular basis of Mendelian disorders. However, for many rare disorders the genetic inheritance is unproven and therefore searches of rare disease-causing mutations can be ambiguous if other forms of inheritance, such as digenic etc., are plausible. I will discuss ways in which alternative hypotheses of inheritance for rare disorders can be accommodated and tested within such searches.

**Disclosure of Interest:** None Declared
Biography: Dr. Lynda Chin graduated with an M.D. degree from Albert Einstein College of Medicine in 1993 and is a board-certified dermatologist. She conducted her clinical and scientific training at Columbia Presbyterian Medical Center and the Albert Einstein College of Medicine, where she completed in parallel her residency training in the hospital and postdoctoral fellowship in the laboratory. She began her independent career as a private practice dermatologist in New York City, until she joined the Dana-Farber Cancer Institute and Harvard Medical School as an assistant professor in 1998, and rose to the rank of professor in 2009. Dr. Chin was also a senior associate member of the Broad Institute of MIT and Harvard. In 2011, Dr. Chin was recruited to The University of Texas MD Anderson Cancer Center to become the founding Chair of the Department of Genomic Medicine, with a mission to integrate genomics in the practice of medicine, and to bring to bear the power of big data on the cancer problem. She also serves as the Scientific Director of the Institute of Applied Cancer Science, an organization designed to bring together the best attributes of academia and industry in a new construct to rapidly translate cancer genomics knowledge into effective therapeutic endpoints.

During her 15 plus years of research career, Dr. Chin ran an impactful program spanning the fields of transcription, telomere biology, mouse models of human cancer, cancer genomics, and personalized cancer medicine. Dr. Chin has held leadership roles in The Cancer Genome Atlas (TCGA) since its pilot phase, including serving on its executive subcommittee. She conceived and led the establishment of the Disease Working Group, a structure through which disease experts outside of TCGA can interact with genomic and computational scientists in TCGA. She co-led the first marker publication from TCGA (on glioblastoma) and chaired the disease working groups for both GBM and melanoma. Internationally, Dr. Chin has been active in the formation of the International Cancer Genome Consortium, serving as leader of the working group that drafted the policy on “Clinical and Pathological Issues” and is a member of the Scientific Steering Committee. Dr. Chin’s productivity and impact as an academic researcher are reflected by her election as a member of the National Academy of Medicine (NAM – IOM) in 2012, and to the Association of American Physicians (AAP) in 2015.

Throughout her career, Dr. Chin has championed a model of integration, collaboration and cooperation between the research and clinical care enterprises, and between academia and industry. At MD Anderson, Dr. Chin has been the driver of its visionary Network Democratization Project, a cancer care transformation effort to bring MD Anderson expertise to patients everywhere. To enable this patient-centric cancer care delivery model, Dr. Chin has built a Technology Core with strategic partnership with major industry giants, including IBM-Watson to build MD Anderson Oncology Expert Advisor™ cognitive decision support system, PwC to build a Healthcare Information Interchange to facilitate data fluidity and continuity so collaboration and coordination along the entire care delivery continuum is possible, and AT&T to develop a healthcare communication service that provides secure and compliant data and communication in motion and at rest as a foundation for a personal connected health platform that afford patients anywhere-access to the healthcare system.

Building on her work at MD Anderson, in 2015, Dr. Chin took on the Chief Innovation Officer and Associate Vice Chancellor role at the University of Texas System to build an Institute for Health Transformation, with a mission to not only leverage and develop innovative, technology-enabled solutions, but to implement them at scale to demonstrate societal impact of improving access and affordability of quality healthcare in Texas and beyond. As
a flagship initiative, Dr. Chin is creating a public-private ecosystem of technology, service, retail and healthcare industries to tackle the challenge of diabetes care and management in South Texas for an underserved population with major unmet medical needs and significant socioeconomic barriers.
Neal Copeland - I10

Biography: Dr. Neal Copeland received his Ph.D. in Biochemistry from the University of Utah. Following postdoctoral studies at Harvard Medical School, he joined the staff of The Jackson Laboratory, and then the National Cancer Institute-Frederick, where he was Director of the Mouse Cancer Genetics Program. He moved to the Institute of Molecular and Cell Biology in Singapore in 2006, where he served as Executive Director of the Institute. In 2011, he returned to the US to serve as Director of the Cancer Biology Program at Houston Methodist Research Institute. For more than 35 years he has co-headed a laboratory with Dr. Nancy Jenkins. The focus of their current research is cancer genetics and they have co-authored more than 800 papers together. Both have served on numerous scientific advisory and editorial boards and consulted for several biotechnology and pharmaceutical companies. Both are members of the US National Academy of Sciences.

Abstract: TWO-STEP FORWARD GENETIC SCREENS IN MICE IDENTIFY NEW HEPATOCELLULAR CARCINOMA DRIVER GENES AND A NEW THERAPEUTIC DRUG TARGET

High throughput sequencing technologies have identified thousands of infrequently mutated genes in hepatocellular carcinoma (HCC). However, high intra- and inter-tumor heterogeneity, combined with large numbers of infrequently mutated genes, has made it difficult to discriminate between drivers and passengers of HCC. In my presentation, I will show how we have used Sleeping Beauty transposon mutagenesis in mice combined with high throughput shRNA library screening to identify new drivers of HCC and a new potential drug target. Whole-genome transposon mutagenesis produced an unbiased catalogue of 1917 high confidence HCC candidate cancer genes (CCGs) and highlighted the importance of Ras signaling in HCC. Pooled shRNA libraries targeting 250 selected CCGs were then introduced into immortalized mouse liver cells and the cells monitored for their tumor-forming ability following injection into nude mice, leading to the identification of 27 new HCC tumor suppressor genes (TSGs). shRNA knockdown of four TSGs, including Acaa2, Hbs1l, Ralgapa2, and Ubr2 in multiple human HCC cell lines confirmed their role in human HCC. Subsequent studies showed that the tumor suppressive function of Ralgapa2 is mediated through Rala and Ralb inhibition, revealing an oncogenic role for the Ral pathway in HCC. Lastly, we found that dual inhibition of the Ras downstream pathways, Ral and Raf, by RBC8 and Sorafenib, synergistically suppressed in vitro HCC tumor cell proliferation and in vivo tumor cell growth, providing a potential new therapeutic approach for treating HCC patients. Two-step forward genetic screens in mice therefore appear to provide a rich resource for identifying new drivers of HCC and potential new therapeutic targets.

Disclosure of Interest: None Declared
Biography: Kay Davies is the Dr Lee's Professor of Anatomy in the Department of Physiology, Anatomy and Genetics and Director of the MRC Functional Genomics Unit at the University of Oxford. Her research interests lie in the molecular analysis and development of treatment for human genetic disease, particularly, Duchenne muscular dystrophy (DMD) and the application of genomics for the analysis of neurological disorders and gene-environment interactions. She is co-founder of a company, Summit Therapeutics, which aims to deliver utrophin modulation to the clinic for the therapy of DMD which currently has a drug in Phase 1 trials. She has published more than 400 papers and won numerous awards for her work. She is a founding fellow of the UK Academy of Medical Sciences and was elected a Fellow of the Royal Society in 2003. She has been a Governor of the Wellcome Trust since 2008 and became Deputy Chairman in October, 2013. She was made Dame Commander of the British Empire for services to science in 2008.

Abstract: THERAPY FOR DUCHENNE MUSCULAR DYSTROPHY IN THE GENOMIC ERA
Genomics is beginning to have a major impact in guiding diagnoses and treatment of many diseases. Genetic approaches, thought to be pipedreams five years ago for diseases such as Duchenne muscular dystrophy, are now showing promise in clinical trials. Approaches include precision medicine strategies such as exon skipping, stop codon read through and correction using CRISPR technology. Broader approaches using gene therapy and modulation of related gene expression are also moving to the clinic.
Susan Domcheck – I12

**Biography:** Susan M. Domchek, MD is the Basser Professor in Oncology at the Perelman School of Medicine of the University of Pennsylvania. She serves as Executive Director of the Basser Center for BRCA1/2 at the Abramson Cancer Center and Director of the Marianne and Robert MacDonald Women's Cancer Risk Evaluation Program, which focuses on genetic evaluation and medical management of individuals with inherited risk factors for cancer. She is a Senior Fellow at the Leonard Davis Institute of Health Economics. An elected member of the American Society of Clinical Investigation, Dr. Domchek is also a member of the American Society of Clinical Oncology for which she had served on a number of committees. A significant contributor to the oncology literature, she has authored/co-authored more than 200 articles appearing in scholarly journals including the New England Journal of Medicine, the Journal of the American Medical Association and the Journal of Clinical Oncology. Dr. Domchek also serves on a number of editorial review boards, including the Journal of Clinical Oncology.
Ada Hamosh - I15

Biography: Ada Hamosh MD, MPH, the Dr. Frank V. Sutland Professor of Pediatric Genetics, is the Clinical Director of the McKusick-Nathans Institute of Genetic Medicine at Johns Hopkins University School of Medicine, the Scientific Director of Online Mendelian Genetics in Man (OMIM®), and the Co-Chair of the Phenotype Review Committee of the combined and Baylor-Hopkins Centers for Mendelian Genomics (CMG), a National Human Genome Research Institute-funded project to identify the genes responsible for known and novel Mendelian disorders. Dr. Hamosh received her BA in Biology from Wesleyan University, MD from Georgetown University, and MPH from Johns Hopkins School of Hygiene and Public Health. She completed a pediatrics residency and clinical and clinical biochemical fellowship at Johns Hopkins Hospital. Dr. Hamosh has authored over 80 papers and serves on several international committees representing genome-phenome relationships as well as phenotype ontologies, including IRDiRC (the International Rare Disease Research Consortium), the Human Variome Project, the ClinGen Project, GA4GH (Global Alliance for Genomic Health), and the Human Genome Organization (HUGO).

Over the past 3 years, she and colleagues have developed PhenoDB (http://phenodb.org), a web-based tool for the collection, storage, and analysis of standardized phenotype and genotype data for use in the CMG project that is freely available to all for clinical and research use. She has also worked with colleagues to develop GeneMatcher (http://genematcher.org), a website to enable matches of clinicians and researchers with an interest in the same gene. GeneMatcher is part of the Matchmaker Exchange. Dr. Hamosh serves on the steering committee of that group.

Abstract: THE MATCHMAKER EXCHANGE: AN INTERNATIONAL EFFORT TO SOLVE UNSOLVED EXOMES AND DISCOVER NOVEL DISEASE GENES

Objectives: The goal of the Matchmaker Exchange is to connect clinicians, researchers and patients with unsolved exome data or candidate genes or undiagnosed disease deposited in distinct databases to find each other without having to reenter data.

Methods: The Matchmaker Exchange (MME) was launched conceptually in October 2013.

Results: Two years later a robust API is in place that allows exchange of data regarding phenotypes, features, genes, and variants between matchmakers. Live for bidirectional exchanges among GeneMatcher (http://genematcher.org), PhenomeCentral (http://phenomecentral.org) and DECIPHER (http://decipher.sanger.ac.uk), the MME is open for other databases to implement the API and each of the member groups welcomes deposition of data. Use agreements, consent policies, and background information are available at http://matchmakerexchange.org.

Conclusion: Current efforts are focused at allowing single hypothesis based matching and improving phenotype matching. The MME is supported by the Global Alliance for Genomics and Health and the International Rare Disease Research Consortium. A complete description of the MME is available in an open access issue of Human Mutation published in September 2015. This includes several new disease genes described as the result of successful matches. Copies of this issue will be available at the HGM meeting.

Disclosure of Interest: A. Hamosh Grant/Research support from: NIH
Robert H. High - I17

Biography: Rob High is an IBM Fellow, Vice President and Chief Technology Officer, Watson Group. He has overall responsibility for the Watson technical agenda and thought leadership in cognitive computing. He has published multiple white papers and video blogs on the role of Watson in the emerging era of cognitive computing.

Abstract:
The world of big data and information processing is rapidly changing the way that we exploit the tremendous volume and velocity of data in decision support. In this talk we will describe the motivation and benefits that cognitive computing offers in transforming the delivery of personalized, democratized, and evidence-based health care. We will draw from principles and examples developed in support of the Oncology Expert Advisor in collaboration with the MD Anderson Cancer Center.
Thomas Hudson - I18

Biography: Dr. Thomas J. Hudson is President and Scientific Director of the Ontario Institute for Cancer Research (OICR), which focuses on translational research in prevention, detection, diagnosis and treatment of cancer.

Dr. Hudson is internationally renowned for his work in genomics and human genome variation. At the Whitehead/MIT Center for Genome Research, he led a team that generated physical and gene maps of the human and mouse genomes. Dr. Hudson has been a founding member of the International Haplotype Map Consortium, the Public Population Project in Genomics (P3G) and the International Cancer Genome Consortium. Dr. Hudson is a member of the Steering Committee of the Global Alliance for Genomics and Health which is developing an international framework to allow genetic and clinical data to be collected, managed and shared in an effective, responsible, interpretable manner.

Dr. Hudson's laboratory at OICR is involved in the study of genome variation that affects cancer predisposition, progression, and response to therapy. His main project focuses on the genetic architecture of loci associated with risk of colorectal cancer. Dr. Hudson has co-authored more than 300 peer-reviewed scientific publications.

Dr. Hudson is Professor in the Departments of Molecular Genetics and Medical Biophysics at the University of Toronto. He is a fellow of the Royal Society of Canada and an Officer of the Order of Canada.

Abstract: INTERNATIONAL CANCER GENOME CONSORTIUM

The International Cancer Genome Consortium (ICGC) was established to bring together researchers from around the globe to comprehensively analyze the genomic, transcriptomic, and epigenomic changes in 50 different tumour types or subtypes that are of clinical and societal importance across the globe (International network of cancer genome projects. Nature 464, 993-998 (15 April 2010)). ICGC developed policies and quality control criteria to help harmonize the work of member projects located in different jurisdictions. Data produced by ICGC projects are made rapidly and freely available to qualified researchers around the world via through the ICGC Data Coordination Center (http://dcc.icgc.org), based at the Ontario Institute for Cancer Research.

As of November 2015, the ICGC has received commitments from researchers and funding organizations in Asia, Australia, Europe, North America and South America for 89 project teams in 17 jurisdictions to study more than 25,000 tumour genomes. The November 2015 release (Version 20) includes datasets from 66 ICGC projects. In total, ICGC data release 20 comprises data from 14,767 cancer genomes.

The Pan-Cancer Analysis of Whole Genomes (PCAWG) project of the ICGC and The Cancer Genome Atlas (TCGA) is coordinating analysis of more than 2,800 cancer genomes, with the extensive use of cloud computing. Because of the very large size of the pan-cancer dataset, with 5,000 whole genome sequences, PCAWG is using a distributed compute cloud environment comprised of academic and commercial compute cloud partners in the USA, Europe and Asia that meets the project’s technical requirements and the bioethical framework of ICGC and its member projects (see ICGC in the clouds; https://dcc.icgc.org/icgc-in-the-cloud). Each genome is being characterized through a suite of standardized algorithms, including alignment to the reference genome, uniform quality assessment, and the calling of multiple classes of somatic mutations. Scientists participating in the research projects of PCAWG are addressing a series of fundamental questions about cancer biology and evolution based on these data.

The first phase of ICGC, which is slated for completion in 2018, has focused on developing extensive catalogs of tumour genomic information. The proposed second phase, ICGCmed, will link genomics to clinical information.
and health, including lifestyle, patient history, response to therapies, and underlying causes of disease, for a broad spectrum of cancers, including preneoplastic lesions, early cancers and metastases. The goal will be to accelerate the movement of genomic information into the clinic to guide prevention, early detection, diagnosis, and prognosis, and provide the information needed to match a patient’s disease to the most effective combinations of therapy.

More information can be found on www.icgc.org.

Disclosure of Interest: T. Hudson Grant / Research support from: OICR, Genome Canada, CIHR, NIH, Employee of: OICR
**Nicholas Katsanis - I19**

**Biography:** Dr. Katsanis obtained his first degree in Genetics from UCL in London in 1993 and his doctorate from Imperial College, University of London in 1997. He then joined the laboratory of Dr. Lupski at Baylor College of Medicine, where he initiated his studies on Bardet-Biedl syndrome. In 2002, he relocated to the Institute of Genetic Medicine, Johns Hopkins University where he led studies that unified several allied conditions under the ciliopathy umbrella. In 2009, he moved to Duke University to establish the Center for Human Disease Modeling, where he is the Director; this new structure aims to facilitate collaboration across disciplines and to develop physiologically relevant tools to study variation found in human patient genomes. As part of that effort, Dr. Katsanis leads the Taskforce for Neonatal Genomics. This multidisciplinary group of physicians and basic scientists strives to synthesize genomic and biological data for the faster diagnosis, improved/focused clinical care, and potential therapeutic paradigms, for infants and neonates with genetic conditions. In parallel, the Katsanis lab pursues questions centered on the signaling roles of vertebrate cilia, the translation of signaling pathway defects on the causality and possible treatment of ciliary disorders, and the dissection of second-site modification phenomena as a consequence of genetic load in a functional system. In recognition of his work, Dr. Katsanis was awarded the Young Investigator Award from the American Society of Nephrology in 2009, the E. Mead Johnson Award from the Society for Pediatric Research in 2012 and has delivered several Distinguished lectures. Dr Katsanis is a Professor in the Departments of Cell Biology and Pediatrics and holds the Brumley Distinguished Professorship. He has published over 250 research papers, reviews, and book chapters, serves on several advisory, editorial, and organizational boards and has delivered over 150 lectures in 20 countries.

**Abstract: ONE PLUS ONE EQUALS ZERO**

Disruptive technologies in human genomics have led to the definition, with unprecedented accuracy and depth, of a torrent of rare and common variation, some of which has been shown to be causally associated with human genetic disease. At the same time, and despite our now full appreciation of the diversity of each individual genome, the interpretation of genetic variation has remained oversimplified and heavily reliant of coarse outlines derived from population frequencies and evolutionary conservation. Here, I will discuss how apparently deleterious alleles in human genes can be benign or beneficial depending on the rest of the genomic context and I will elaborate on how such observations can both improve our interpretative ability of patient exomes and facilitate the development of rational drug discovery.

**Disclosure of Interest:** N. Katsanis Shareholder of: co-Founder and CSO of Rescindo Therapeutics Inc
Muin J. Khoury - 120

Biography: Muin J. Khoury, MD, PhD Director, Office of Public Health Genomics, CDC. Dr. Khoury is the founding director of the CDC's Office of Public Health Genomics. The Office was formed in 1997 to assess the impact of advances in human genetics and the Human Genome Project on public health and disease prevention. CDC's Office of Public Health Genomics serves as the national focus for integrating genomics into public health research and programs for disease prevention and health promotion. Dr. Khoury has developed a number of successful ongoing national and international initiatives to translate advances in genomics and related technologies to recommendations and actions that improve health and prevent disease throughout the life stages. Since 2007, he has also served the National Cancer Institute as senior advisor in public health genomics in the Division of Cancer Control and Population Sciences. Between 2011 and 2015 he led the Epidemiology and Genomics Research Program in the same Division.

Dr. Khoury received his B.S. degree in Biology/Chemistry from the American University of Beirut, Lebanon and his medical degree and Pediatrics training from the same institution. He received a Ph.D. in Human Genetics/Genetic Epidemiology and training in Medical Genetics from Johns Hopkins University. Dr. Khoury is board certified in Medical Genetics.

Dr. Khoury received the Public Health Service Special Recognition Award in 1990 for his outstanding contribution to the scientific literature in the areas of birth defects and genetic epidemiology. In 1994, he received the Arthur Fleming Award for outstanding government service. In 1998, Dr. Khoury was credentialed for the Senior Biomedical Research Service for outstanding contributions to public health. In 2000, he received the CDC Research Honor Award for outstanding national leadership in genetics and public health. In 2005, he received the National Cancer Institute visiting scholar award for leadership and vision in genetic epidemiology and public health.

Dr. Khoury has published extensively in the fields of genetic epidemiology and public health genetics. He has over 500 scientific publications including articles, books and book chapters. In 1993, he published a textbook entitled: "Fundamentals of Genetic Epidemiology". In 2000, he was the lead editor for the book entitled: "Genetics and Public Health in the 21st Century: Using Genetic Information to Improve Health and Prevent Disease". His 2004 book entitled "Human Genome Epidemiology" illustrates the applications of epidemiologic methods and approaches to the continuum of genomic information from research to practice. In 2010, he published a completely updated second edition of "Human Genome Epidemiology".

Dr. Khoury is a member of many professional societies and serves on the editorial boards of several journals. He is a frequent keynote speaker at many academic institutions, professional organization meetings, as well as state, regional, national and international conferences. He also serves on several scientific, public health, and health policy national and international committees. He is an adjunct professor in the Departments of Epidemiology and Environmental and Occupational Health at Emory University Rollins School of Public Health and an associate in the Department of Epidemiology at Johns Hopkins University Bloomberg School of Public Health.

Abstract: TRANSLATIONAL GENOMICS: AN EXPANDED RESEARCH AGENDA FOR IMPROVING INDIVIDUAL AND POPULATION HEALTH
In this talk, I describe and give examples of 4 phases of translational genomic research: T1 research, which bridges discovery to candidate health applications, or “bench to beside”. T1 research encompasses the development of new diagnostic tests or interventions in the clinical setting but in a limited fashion. An example of T1 research would be evaluating gene–environment interactions or evaluating the function of genomic variants. T2 research evaluates the clinical utility of candidate genomic applications in clinical practice. For example, this type of research would include whether a genomic application performs better than the standard of care in improving health outcomes or developing evidence from the clinical setting to informed evidence-based guidelines. T3 research includes studies that assess implementation and integration of genomics into routine clinical practice. T3 research would include, for example, the evaluation of implementing genomic applications in community-based centers. T4 research evaluates population health impact of genomic medicine. An example of T4 research would be performing nationwide surveillance to evaluate how the implementation of a particular genomic test has affected population health.

Fulfilling the promise of genomics to improve health requires all 4 phases of translational research. This expanded translation model provides a public health approach that can assess the contribution of genomics to health in the context of social and environmental determinants of disease; evaluate genomic applications that may improve health care; design strategies for integrating genomics into practice; address ethical, legal, and social issues; and measure the population health impact of new technologies.

**Disclosure of interest**: None declared
Elaine Mardis graduated Phi Beta Kappa from the University of Oklahoma with a B.S. degree in zoology. She then completed her Ph.D. in Chemistry and Biochemistry in 1989, also at Oklahoma. Following graduation, Dr. Mardis was a senior research scientist for four years at BioRad Laboratories in Hercules, CA. In 1993, Dr. Mardis joined the faculty at Washington University School of Medicine. Recruited for her expertise in DNA sequencing and automation technology, she served as Director of Technology Development at the (then) Washington University Genome Sequencing Center, helping create methods and automation pipelines for sequencing the Human Genome. She has served as Co-director of the McDonnell Genome Institute since 2002. In 2014, Dr. Mardis was named the Robert E. and Louise F. Dunn Distinguished Professor of Medicine.

Dr. Mardis has research interests in the application of next-generation sequencing to characterize cancer genomes and transcriptomes, and using these data to support therapeutic decision-making. She co-led the teams that first used next-generation sequencing to characterize the whole genome of an AML patient (Nature 2008), first sequenced and compared a primary tumor to its metastasis and xenograft, and first reported whole genome sequencing of samples from a breast cancer clinical trial. Beyond cancer genomics discoveries, Dr. Mardis is leading efforts to facilitate the translation of basic science discoveries about human genetic diseases into the clinical setting, especially focused on the use of next-generation sequencing. Her translational research efforts aim to devise NGS-based diagnostics, decision-support tools and databases, and the use of genomics to design personalized cancer vaccines.

Dr. Mardis was elected to the AACR Board of Directors in 2015. She serves as an associate editor of *Molecular Cancer Research*, *Disease Models and Mechanisms* and *Annals of Oncology*, and acts as a reviewer for *Nature, the New England Journal, Cell* and *Science*. She is the Editor-in-Chief of *Molecular Case Studies*. She serves on the scientific advisory boards of Qiagen Ingenuity, DNA Nexus, and ZS Genetics, and is a member of the Supervisory Board of Qiagen N.V. Dr. Mardis received the 2010 Scripps Translational Research award for her work on cancer genomics, and was named a Distinguished Alumni of the University of Oklahoma College of Arts and Sciences in 2011. Discover Magazine featured her work in cancer genomics as one of their top 100 science stories of 2013. In 2014 and 2015, she was one of the most highly cited researchers in the world, according to Thompson-Reuters.

**Abstract: INTEGRATING DNA AND RNA DATA FOR N OF 1 CANCER STUDIES**

Massively parallel sequencing and analysis of cancer cases has enabled a revolution in precision cancer medicine. Sequencing DNA alone is an incomplete picture, however, and some patients have few obvious cancer drivers that emerge, even from whole genome analyses. While RNA poses significant challenges, it can provide additional information that is complementary to DNA analyses and in some cases can reveal the downstream manifestations of epigenomic/regulatory alterations that are not attainable from a DNA-only approach. My talk

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**Elaine Mardis - I21**

**Biography:** Elaine R. Mardis, Ph.D.
Robert E. and Louise F. Dunn Distinguished Professor of Medicine
Professor of Genetics and Molecular Microbiology
Co-director, McDonnell Genome Institute at Washington University School of Medicine
will outline specific N of 1 cases where combined RNA- and DNA-based analysis was critical to understanding the patient’s disease and to assigning treatment options.
Mark McCarthy - I22

Biography: Mark McCarthy is the Robert Turner Professor of Diabetes Medicine at the University of Oxford, based at both Oxford Centre for Diabetes, Endocrinology and Metabolism and the Wellcome Trust Centre for Human Genetics. His research group is focused on the identification and characterisation of genetic variants influencing risk of type 2 diabetes and related traits, and on using those discoveries to drive biological inference and translational opportunities.

Abstract: DISSECTING DIABETES: FROM GENETICS AND GENOMICS TO BIOLOGY AND TRANSLATION
The growing prevalence of type 2 diabetes highlights the limitations of available preventative options, and high rates of diabetes complications attest to the inadequacies of current treatments. Novel therapeutic strategies need to be informed by a more complete understanding of the molecular and physiological basis of disease, delivering validated interventional targets and biomarkers to define disease risk, progression, and subtype. My group, working within large global consortia, uses human genetics to deliver this understanding. Growing availability of exome sequence and array data now delivers coding variant associations that can plug directly into functional studies. However, the main repository of variant association for T2D remains ~100 common variant signals uncovered by GWAS, most of which map outside coding sequence. We are implementing a multifaceted approach that combines genome-scale and focused functional studies to unlock the biology within these loci. We use fine-mapping to improve localisation of causal variants, and map these onto regulatory annotations from key tissues, most notably the human islet. This provides a platform for identifying downstream transcripts through tissue-specific cis-eQTL analyses and conformational capture. We combine these “regulatory variant” data with transcript level information to define the best-supported transcripts in each GWAS region. Finally, we connect loci through analyses of protein-protein interaction, co-expression and pathway data. These efforts are starting to bear fruit, with around one-third of GWAS signals now featuring a well-supported priority transcript. We follow up these priority candidates through cellular, molecular, rodent and human studies to consolidate mechanistic evidence. To build engagement, we are co-developing, via the Accelerating Medicines Partnership, a dedicated T2D knowledge portal that facilitates access to these data for the wider research community.
Biography: Amy McGuire, J.D., Ph.D., is the Leon Jaworski Professor of Biomedical Ethics and Director of the Center for Medical Ethics and Health Policy at Baylor College of Medicine. She researches ethical and policy issues in human genetics, with a particular focus on genomic research and the clinical integration of emerging technologies. Currently, she is studying issues related to genomic data sharing, the policy implications of emerging business models for next generation sequencing, and ethical and policy issues arising in the clinical integration of genomic technologies. Her research is funded by the NIH-NHGRI, NCI, and NICHD, and she is a member of the Advisory Committee for the Greenwall Faculty Scholars Program in Bioethics.

Abstract: BUILDING THE MEDICAL INFORMATION COMMONS: DATA SHARING ETHICS AND POLICY

National and international public-private partnerships, consortia and other initiatives are being formed to collect and share data on a large scale. Many predict that this will contribute to the creation of a medical information commons; a networked environment in which diverse sources of health, medical, and genomic data on large populations become broadly available for research use and clinical application. There is a presumption that access to large amounts of data, especially genomic data, will advance research and improve public health. However, the success of these initiatives depends on policies and practices that promote data sharing, are consistent with international standards, address barriers to participation, and attend to the ethical, legal and social issues that arise when data on individuals become widely shared resources. In this presentation, I will discuss barriers to the creation of a medical information commons, from the perspective of data contributors and data holders, and describe efforts to address these barriers from a policy and research perspective.
Biography: Debbie Nickerson, Ph.D., is a Professor in the Department of Genome Sciences and Director of the Northwest Genomics Center at the University of Washington in Seattle. Her research is focused on uncovering the genetic basis of rare Mendelian and common complex human phenotypes. She has pioneered the development of new methods and tools that have been widely adopted for the identification and genotyping of human sequence variation, including exome sequencing, and has explored new approaches for data sharing.

Abstract: LESSONS FROM SCALING MENDELIAN ANALYSES
Next generation sequencing is becoming an essential tool in human genetic analysis. Over the past several years, a rapidly evolving framework of new experimental approaches and analytical tools have led to the discovery of the genes underlying hundreds of rare Mendelian disorders. Of the more than 7,000 Mendelian disorders that have been described, thousands remain unsolved, but are now being explored. Many successful paradigms have emerged from these analyses, and examples of the hits and challenges arising from on-going work in the Centers for Mendelian Genomics will be highlighted. New insights into human biology and gene function are also developing and will be highlighted as well.

Disclosure of Interest: None Declared
Biography: Maynard Olson is Professor Emeritus of Medicine and Genome Sciences at the University of Washington. During his research career, Olson developed a number of experimental and computational methods, such as high-resolution, clone-based physical mapping, sequence-tagged-site-content mapping, and yeast-artificial-chromosome cloning that have been widely used in genome analysis. He also carried out extensive studies of natural genetic variation in the human and bacterial genomes. In addition to his research activities, Olson participated in the formulation of policy for the Human Genome Project, serving on the original National Research Council Committee on Mapping and Sequencing of the Human Genome, the National Advisory Council of the National Human Genome Research Institute, and numerous other advisory groups, as well as testifying several times about the Human Genome Project in front of Congressional Committees. More recently, Olson served on the National Research Council Committee that issued the report “Toward Precision Medicine” in 2011. Olson has received several awards for his contributions to genome research, including the Genetics Society of America Medal in 1992, the City of Medicine Award in 2000, the Gairdner International Award in 2002, and the Gruber Genetics Prize in 2007; he was elected to the National Academy of Sciences in 1994. Olson’s undergraduate education was at the California Institute of Technology, and he received his Ph.D. in chemistry from Stanford University in 1970. After earlier faculty appointments at Dartmouth College and Washington University, he came to the University of Washington in 1992.

Abstract: AT 30, GENOMICS COMES OF AGE
HGM 2016 marks a historic moment in the short history of genomics. One can fairly say that genomics has, during the past few years, come of age. We now actually have the capabilities we set out to develop in the mid-1980’s and have considerable experience putting them to use. The early news is mostly good. Fears that genome sequences would reveal more than most people want to know about themselves have proven exaggerated, as have fears the sequences would be uninterpretable. Genome sequencing has become an astonishingly powerful research tool and has established a modest, but real, foothold in medicine. Now comes the hard part: as our community comes of age, we are acquiring adult responsibilities for which we are ill prepared. Technical, scientific, and economic challenges abound, and, more ominously, we need to re-fashion our contract with society. Technically, we need better quality control and more standardized protocols, especially at the analysis step. This need for standardization conflicts with an even more compelling need for continued innovation—a balance that is not easily struck. Scientifically, we need new goals: for 30 years, genomics could thrive just by picking the successive tiers of low-hanging fruit that came within reach as technology improved. The ways we train students, fund research, collaborate, publish, and reward success are all adapted to that environment. Mature sciences need a more sophisticated game plan and attendant changes in the way they do business. Finally, and most importantly, we need a new social contract. We will only make headway on our central scientific challenge, developing an improved understanding of genotype-phenotype correlations, by studying large

Disclosure of Interest: None Declared
Biography: Joseph F. Petrosino, Ph.D. is an associate professor of molecular virology and microbiology at Baylor College of Medicine, where he also holds joint appointments in the Human Genome Sequencing Center, and the Department of Ophthalmology. Dr. Petrosino was a principal investigator for the NIH Common Fund Human Microbiome Project and in 2011 established the Alkek Center for Metagenomics and Microbiome Research (CMMR). With over 150 collaborations, the CMMR is pursuing over 300 metagenomics projects internationally with the goal to improve human health through detection and modulation of the microbiome and to translate new discoveries into new diagnostics and therapeutics. Among the latest CMMR projects initiated is a comprehensive microbiome analysis of 20,000+ type 1 diabetes samples from the NIH/NIDDK TEDDY (The Environmental Determinants of Diabetes in the Young) prospective cohort with the goal to identify microbial taxonomic and functional associations, and potentially triggers, for this disease. From 2012-2014, Dr. Petrosino was an American Society for Microbiology Distinguished lecturer and has contributed to more than 70 peer-reviewed microbiome studies.

Abstract: A TRANSLATIONAL RESEARCH PROGRAM FOR THE HUMAN MICROBIOME
The Alkek Center for Metagenomics and Microbiome Research (CMMR) at Baylor College of Medicine is coordinating and leading research and development efforts in these areas across the Texas Medical Center, and with collaborators from around the US and abroad. CMMR researchers are developing molecular and informatics tools and resources to advance over 300 diverse clinical and basic research projects pertaining to the organisms that comprise the microbiome, the genetic makeup of these bacteria, viruses and fungi, and how these commensal microorganisms interact with human cells and tissues during the course of life in health and disease. Recent projects include those focused on type 1 Diabetes (examining >20,000 samples with the NIDDK TEDDY and JDRF nPOD cohorts), inflammatory bowel disease, cancer and chemotherapy, and unknown agents of sepsis in immunocompromised subjects. The intent is for these projects to lead to the development of new treatments and diagnostics for a variety of heritable and infectious diseases as well as the development of additional reagents having other biotech applications.

Disclosure of interest: None declared
Stefan Pfister - I27

Biography: Pfister, Stefan Prof. Dr. med.
German Cancer Research Center
Division of Pediatric Neurooncology (B062) University Hospital Heidelberg Department of Pediatric Hematology and Oncology Im Neuenheimer Feld 280
D-69121 Heidelberg
Germany
Email: s.pfister@dkfz.de

*June 7, 1974

Education & Academic Career
2015 Master in Management
Since 2014 Full Professor in Pediatrics
Since 2012 Head of the Division of Pediatric Neurooncology at the German Cancer Research Center Heidelberg
2010 Postdoctoral Lecture Qualification (Habilitation) at the University of Heidelberg
Since 2010 Consultant in Pediatrics
Since 2006 Group Leader: Molecular Genetics of Childhood Brain Tumors (German Cancer Research Center and University Hospital Heidelberg)
2006 - 2009 Resident at Heidelberg University Hospital, Department of Pediatric Hematology and Oncology
2004 - 2006 Postdoctoral Fellow at the German Cancer Research Center, Division Molecular Genetics.
2002 - 2004 Resident at Mannheim University Hospital, Department of Pediatrics
1999 - 2000 Postdoctoral Fellow at the Dana-Farber Cancer-Institute, Harvard Medical School, Department of Tumor Immunology, Boston, USA.
1997 - 1999 Dissertation at the University of Tübingen, Department of Pediatric Oncology
1994 - 2002 Medical studies at the Universities of Hamburg and Tübingen

Honors and Awards
2014 Richtzenhain Award
2013 German Cancer Award (Translational part)
2013 Cancer Award of Württemberg
2011 Alfred-Müller Award for Neurooncology
2011 Fritz-Lampert Award for Pediatric Hematology and Oncology
2009 Kind-Philipp Award for Pediatric Oncology
2009 Sibylle Assmus Award for Neurooncology
2008 Dr. Maresch-KlingelhöffER Award for Pediatric Oncology
2008 Dr.-Hella-Bühler Research Award

Activities in the Scientific Community
Coordination of the national clinical sequencing program in pediatric oncology (INFORM) Coordination of the national reference center for molecular diagnostics in pediatric brain tumors (Molecular Neuropathology 2.0) Biology Chair of the Innovative Therapies for Children with Cancer (ITCC) consortium Biology Chair of the European pediatric low-grade glioma trial (SIOP-LGG) Biology Chair of the European medulloblastoma trial (SIOP-PNET)

Key publications (from >120 original publications) h-Index = 45, total citations >7000
Raj Ramesar - I29

**Biography:** Raj Ramesar is Professor and Head of the Division of Human Genetics at the University of Cape Town and its Affiliated Hospitals in South Africa. This facility has wide-ranging clinical responsibilities from the quaternary and tertiary care levels, to extensive rural outreach programmes, in addition to diagnostic and research capabilities. His interest is in using the exciting developments in the field of genomic sciences to investigate human biodiversity. Africa offers the opportunity to use population lineages in all of their richness towards identifying aspects of human biology, that have to do with both health and disease.

As the Director of the MRC Human Genetics Research Unit, the emphasis of his research has been on disease susceptibility in South African populations, progressing from the commonly recognised inherited diseases, to those that are more complex yet more common and relevant to a large burden of disease. In this regard, he has been involved in researching Retinal Degenerative diseases for the past 25 years – and has been working very closely with the lay support group: Retina South Africa, in terms of developing and maintaining an active and translational research agenda. Furthermore, his most recent research enterprise is embodied in a large scale project entitled: ‘Human Diversity and Health’. As Director of the national Colorectal Cancer Research Consortium his focus has been on the genetics of familial colorectal cancers, and the most effective translation of laboratory findings to the field for optimum benefit of patients and their kin. His most recent research involves whole exomic and whole genome sequencing for disorders seen in South Africa, as well as investigating responses to drugs in local populations.

Raj recently received the (Vice Chancellor’s) Alan Pifer Award for ‘outstanding research in cancer genetics which shows relevance to the advancement of South Africa’s disadvantaged populations’. He was also recently (December 2015) elected to the College of Fellows of the University of Cape Town. Apart from being on the editorial board of several international journals, Raj serves as co–chair of the Scientific and Medical Advisory Board of Retina South Africa, he is on the Executive of the African Society for Human Genetics, and is the latter organisation’s Liaison Officer to the International Federation of Human Genetics Societies. As Chair of the Local Organising Committee, he organised the Joint Conference of the African and Southern African Societies in Cape Town ([www.humangenetics2011.org](http://www.humangenetics2011.org)). Raj also led a successful bid to host the International Congress of Human Genetics in Cape Town in 2021. He serves on several international advisory panels pertaining to genomic research, including that for: Human Heredity and Health: Africa (or H3Africa).

**Abstract: THE SCOPE OF HUMAN GENOME RESEARCH AND TRANSLATION IN SUB-SAHARIAN AFRICAN**

The practise of Human and Medical Genetics was started in South Africa in the 1970’s – and has evolved from being a subspecialty, to having its own ‘colleges’ and achieving specialist status. This reflects the practitioner’s motivation as well as government’s understanding of genetics as an important aspect of health care. Clinical Genetic services in South Africa are provided through several academic (tertiary and quaternary hospitals) – and this is supported by a network of diagnostic laboratories within the National Health Services Laboratories, which in turn is fed by research done on locally relevant diseases and implementable technologies. Research, especially in the largely indigenous population (>80% of a total of approximately 53 million people), has proven absolutely essential, in terms of addressing genetic diversity and genetic heterogeneity and developing locally-relevant genetic testing, together with the practise of Genetic Counselling . Work on chronic disorders such as cancers, retinal dystrophies as well as psychiatric diseases (amongst others) has provided the means for working
on both Mendelian diseases, as well as large-scale population-based projects involving genome-wide association studies and next generation sequencing technologies. What has been essential in the local setting is the emphasis on translation of research findings for predictive testing and disease prevention as applicable to familial cancers, while harnessing the potential for therapeutics for retinal disease, and working with credible lay organisations such as Retina South Africa, CANSA, and the Genetic Alliance of South Africa.

As head of one of the larger academic Human Genetics facilities in Africa – at the University of Cape Town – has provided both opportunities as well as challenges in terms of ensuring that research and education/training programmes are kept at the forefront of discovery science, while also attempting to contribute to the larger African research and practise landscape, with a view to being relevant at a public health level. This presentation will provide an overview of the work being done in our African setting.

**Disclosure of interest:** None declared
**Heidi Rehm - I30**

**Biography:** Heidi L. Rehm, PhD, FACMG is the Director of the Partners Healthcare Laboratory for Molecular Medicine (LMM), the Clinical Director of the Broad Institute's Clinical Research Sequencing Platform and Associate Professor of Pathology at Brigham & Women's Hospital and Harvard Medical School. Both clinical labs focus on the rapid translation of new genetic discoveries into clinical tests and bringing novel technologies and software systems into molecular diagnostics to support the integration of genomics into clinical use. Dr. Rehm has also been a leader in genomic medicine research, supporting several programs from discovery (Center for Mendelian Genomics), to translation (MedSeq, BabySeq, eMERGE) to building standards to support clinical genomics (ClinGen, GA4GH, ACMG).

**Abstract: THE CLINICAL GENOME RESOURCE**

Laboratory for Molecular Medicine, Partners Personalized Medicine; The Broad Institute of Harvard and MIT; Brigham & Women's Hospital; Harvard Medical School, Boston, MA USA

With the plummeting cost of sequencing, genetic data is becoming increasingly available for use in the diagnosis, treatment and prediction of disease. However, robust and accurate use of genomics in the practice of medicine will require high quality knowledgebases. To address this need, the NIH funded Clinical Genome Resource Program (ClinGen) is building authoritative resources to define the clinical relevance of genes and variants for use in precision medicine and research. This includes working closely with NCBI's ClinVar database to support the deposition and public sharing of variant-level data. As of Jan. 2016, over 450 laboratories had submitted over 120,000 unique interpreted variants. Prior analyses in May 2015 showed that ~11% of variants had interpretations submitted by more than one lab, and of those ~17% were interpreted differently (Rehm et al. 2015). ClinGen has adopted the new ACMG/AMP-developed guidelines to assist labs in resolving differences in variant interpretation. Through pilot efforts the majority of differences in variant interpretation appear to be resolvable and efforts are underway to resolve these differences. In addition, ClinGen approves expert panels and practice guidelines (marked as 3 and 4 star submissions in ClinVar) to allow the submission of high quality, expert reviewed variant interpretations for reliable use in clinical care. Additional expert panels have been and continue to be formed by ClinGen to expand the expert review process.

Although improvements in variant interpretation are critical to the accurate use of genetic information in clinical care, assessment of gene-disease relationships and supporting novel gene discovery are also critical. ClinGen has developed guidelines for assessing the strength of evidence for gene-disease relationships and is supporting numerous projects to curate genes with reported associations to specific diseases. ClinGen rules were applied to the curation of 1400 gene-disease pairs for the BabySeq project allowing improved interpretation of newborn sequencing results.

In summary, the open sharing and curation of gene and variant information will be critical to ensure a safe and successful implementation of genomic medicine into clinical care.
Disclosure of interest:
- Supported by NIH grants U41HG006834 and U19HD077671.
- Employee of Partners/BWH/MGH offering fee-for-service molecular diagnostics (LMM) and software (GeneInsight partnered with Sunquest)
- Employee of Broad Institute offering fee-for-service exome and NGS panel testing (Broad CRSP)
- NIH funding (ClinGen, MedSeq (CSER Consortium), BabySeq (NSIGHT Consortium), eMERGE, Center for Mendelian Genomics)
Mary Relling - I31

Biography: Mary V. Relling, Pharm.D.
Member and Chair, Department of Pharmaceutical Sciences, St. Jude Children’s Research Hospital, Memphis, TN
Dr. Relling earned her undergraduate B.S. degree from the University of Arizona College of Pharmacy and her doctoral degree from the University of Utah College of Pharmacy. She completed post-doctoral fellowships with Dr. William Evans at St. Jude and with Dr. Urs Meyer at University of Basel. She joined St. Jude as a faculty member in 1988, and in 2003 was named chair of the Department of Pharmaceutical Sciences. She is also a professor at the University of Tennessee in the Colleges of Medicine and Pharmacy.
Her primary interests are in treatment and pharmacogenetics of childhood leukemia and clinical implementation of pharmacogenetic testing. Dr. Relling is Chair of NIH’s Pharmacogenomics Research Network and co-founder of CPIC, the Clinical Pharmacogenetics Implementation Consortium. She has published over 300 original scientific manuscripts. She was elected to the Institute of Medicine in 2009.

Abstract: PHARMACOGENOMICS: FROM DISCOVERY TO THE CLINIC
There is substantial research ongoing to discover the genomic basis of interindividual differences in drug response. After more than 60 years of discovery research, there are some genetic tests that are ready for clinical use now. Although there is substantial hype that the widespread introduction of genomic information will revolutionize health care, the use of these well-established genetic tests to inform clinical decision making remains uncommon. At St. Jude, we continue to study the genomic basis of interpatient variability in response to antileukemic medications. We have also implemented a protocol, PG4KDS (www.stjude.org/pg4kds) to perform preemptive array-based pharmacogenetic testing on all patients, and to create clinical decision support to facilitate evidence-based prescribing advice for individual patients for those tests that are ready for clinical use. We have also co-created the Clinical Pharmacogenetics Implementation Consortium (CPIC) (www.cpicpgx.org) as a shared project between PharmGKB (https://www.pharmgkb.org) and NIH’s Pharmacogenomics Research Network (www.pgrn.org). CPIC’s goal is to accelerate proper use of pharmacogenomics in the clinic via its freely available, peer-reviewed, standardized, and detailed gene/drug pharmacogenetic clinical practice guidelines.[PMID: 21270786] An underlying assumption of CPIC guidelines is that genotypes will become preemptively available: guidelines focus on HOW available genetic test results should be used to optimize drug therapy, rather than WHETHER tests should be obtained.

Disclosure of Interest: None Declared
Biography: Dr. Ren is currently Member of the Ludwig Cancer Research (LCR) and Professor of Cellular and Molecular Medicine at the University of California, San Diego (UCSD) School of Medicine. He is also a co-director of the UCSD Bioinformatics and Systems Biology Graduate Program. Dr. Ren obtained his Ph.D. from Harvard University in 1998, and subsequently conducted postdoc research at the Whitehead Institute. He joined the faculty at LCR and UCSD in 2001, and was promoted to Associate Professor in 2007 and to Full Professor in 2009. Dr. Ren has made important contributions to the understanding of gene regulatory mechanisms and chromatin organization in mammalian cells. As a postdoctoral fellow, he invented ChIP-chip, a transformative approach for genome-wide determination of transcription factor binding and covalent chromatin modifications. As an independent investigator, Dr. Ren exploited this approach for annotation of cis regulatory sequences in the human genome. He discovered signature chromatin modification patterns at transcriptional enhancers, and proposed a chromatin-modification-signature based enhancer mapping strategy for annotation of these regulatory sequences in genomes. Dr. Ren and colleagues further demonstrated that cell type specific activities of enhancers correlate with their chromatin modification states, a finding that set the stage for global analysis of gene regulatory mechanisms during mammalian development. In recent years, Dr. Ren also investigated the molecular architecture of chromatin in mammalian cells and made several key discoveries: 1) He found that the genome is partitioned into thousands of megabase-sized “topological domains”, a structural feature that is highly conserved during development and through evolution; 2) He showed that topological domains are units of genome organization that physically constrain the long-range regulatory interactions between enhancers and their target genes; and, 3) he and colleagues demonstrated that the cis regulatory elements and transcription factors regulate the formation of topological domains. As a principal investigator, Dr. Ren has actively participated in the NIH ENCODE project, the Roadmap Epigenome project, and the Common Fund 4D Nucleome project over the years. He is a recipient of the Kimmel Scholar award, the Young Investigator Award of the Chinese Biological Investigator Society, and an elected fellow of the American Association for the Advancement of Science.

Abstract: THE 3D GENOME ORGANIZATION AND FUNCTION
The 3-dimensional chromatin organization plays a critical role in gene regulation. Great strides have been made recently to characterize and identify cis regulatory elements from epigenome profiles in different cell types and tissues, but efforts have just begun to functionally characterize these long-range control elements. Mapping interactions between enhancers and promoters, and understanding how the 3D landscape of the genome constrains such interactions is fundamental to our understanding of genome function. I will present recent findings related to 3D genome organization in mammalian cells, with a particular focus on how chromatin organization contributes to transcriptional regulation. I will describe higher-order organizational features that are observed at the level of both the whole chromosome and individual loci. I will highlight changes in genome organization that occur during the course of differentiation, and discuss the functional relationship between chromatin architecture and gene regulation. Taken together, mounting evidence now shows that the genome organization plays an essential role in orchestrating the lineage-specific gene expression programs through modulating long-range interactions between enhancers and target genes.
Jeffrey Rogers – I33

Biography: Jeffrey Rogers, Ph.D. is Associate Professor in the Human Genome Sequencing Center and Dept. of Molecular and Human Genetics, Baylor College of Medicine. After receiving his Ph.D. in Anthropology from Yale University, and postdoctoral training in the Yale School of Medicine, Dr. Rogers has pursued a career in the genetic and genomic analysis of nonhuman primates. His studies include the development and application of various genetic resources for the analysis of primates, and long-standing work on nonhuman primate models of human psychiatric illnesses and other common complex diseases. Dr. Rogers has collaborated on the de novo sequencing and assembly of several nonhuman primate genomes, as well as conducting field studies of the population genetics of wild baboons.

Abstract: FUNCTIONAL GENETIC VARIATION IN RHESUS MACAQUES: NON-SYNONYMOUS VARIATION, NEW DISEASE MODELS AND STRONGER PURIFYING SELECTION THAN AMONG HUMANS

R.A. Harris1, M. Raveenedran1, C. Xue1, L. Cox2, G. Fan3, B. Ferguson4, J. Horvath5, S. Kanthaswamy6, M. Kubisch7, M. Platt8, D.G. Smith6, E. Vallender9, R. Wiseman10, X. Liu11, J. Below11, R. Chen11, D.M. Muzny1, R.A. Gibbs1, F. Yu1, J. Rogers1

1Human Genome Sequencing Center, Baylor College of Medicine
2Southwest National Primate Research Center
3Univ. of California, Los Angeles
4Oregon National Primate Research Center
5North Carolina Museum of Natural Sciences
6California National Primate Research Center
7Tulane National Primate Research Center
8Duke University
9New England National Primate Research Center
10Wisconsin National Primate Research Center
11Univ. of Texas Health Sciences Center, Houston

Objectives: The goal of this project is to discover and characterize novel functional genetic variation in rhesus macaques (Macaca mulatta), the premier nonhuman primate widely used in biomedical research related to human disease.

Methods: We used the Illumina HiSeq platform to generate whole genome sequence coverage (mean = 26x) for 133 unrelated rhesus macaques from nine research populations. We mapped the reads to the rhemac2 rhesus reference genome and identified SNVs using both SNPTools and GATK. Only SNVs scored as high quality by both software tools were used in subsequent analyses.

Results: We identified >43 million SNVs across 133 rhesus macaques, with the average number of variant sites per animal >9 million. This is 2.5-fold greater SNV density than is observed in the human 1000Genomes Project. This population of macaques contained >126,000 non-synonymous variants, >2600 stop codon gains and >42,000 splice region variants. A targeted search of 166 genes previously known to cause human retinal degeneration or other eye diseases identified >157,000 total variants, including 157 alleles predicted to
adversely affect gene function. Specific human disease genes affected in macaques include ABCA4 (causes macular degeneration), MYO7A (causes progressive blindness, Usher syndrome 1B) and GUCY2D (Leber’s congenital amaurosis). More broadly across human diseases, we found 165 variants that are exact matches to human disease-causing mutations cataloged in HGMD and/or ClinVar. The ratio of non-synonymous to synonymous sites is lower in rhesus macaques than in humans, an indication that purifying selection has had a stronger influence on variation among macaques than among humans. Despite this, the macaques exhibit putative damaging variants in thousands of genes that will be valuable in modeling human genotype-phenotype relationships.

**Conclusions:** Rhesus macaques exhibit 2.5x higher total density of SNVs than do humans, with about 20% higher counts of non-synonymous variation per individual. Many rhesus orthologs of human disease genes present low frequency damaging mutations. Due to their close physiological, neurobiological and immunological similarities to humans, this array of putative functional variants in macaques provides an extensive resource for development of new genetic models of human disease, employing a model species that mimics several aspects of human biology more closely than other laboratory animals.
Charles Rotimi - 134

Biography: Dr. Charles Rotimi, a genetic epidemiologist, is the Chief of the Metabolic, Cardiovascular and Inflammatory Disease Genomics Branch and the Director of the Center for Research on Genomics and Global Health, in the National Human Genome Research Institute, at NIH. His lab conducts genomic and epidemiologic studies that explore the patterns and determinants of metabolic disorders with particular emphasis on disease etiology and health disparities in African ancestry populations. His lab gives particular attention to ways in which scientists document and describe the non-random pattern of human genetic variation with respect to human history, notions of identity and disease risks in different populations. He is a member of board of the American Society of Human Genetics, a member of the Executive and Scientific Committee for the International Federation of Human Genetics Societies, member of HUGO council and the founding president of the African Society of Human Genetics. Recently, he successfully led the establishment of the Human Heredity and Health in Africa (H3Africa) initiative with over $76 million commitment from the NIH and Wellcome Trust. H3Africa is revolutionizing genomic research across the African continent.

Abstract: ETHICAL AND EQUITABLE SHARING OF INTERNATIONAL DATA: A PERSPECTIVE FROM AFRICA
Inequity and lack of diversity are, arguably, the most pressing ethical issues in genomic science. International collaborations and data sharing in genomic science are now the norm. The benefits and impacts of these partnerships are obvious and expanding. However, not all scientists and communities are benefiting from these global collaborations. African scientists and their communities have been excluded for several reasons including limited local and international funding opportunities, lack of adequate infrastructure and shortage of African scientists with genomic skills. Moreover, in the limited instances when African scientists have been invited to take part in international collaborations they have done so as “second class” partners. Although some of these issues are beginning to be addressed by funding agencies and scientists, it is clear that if not adequately resolved they have the potential to threaten and invariably compromise international partnerships, including data sharing. In this presentation, I will discuss how the Human Heredity and Health in Africa (H3Africa) initiative is addressing these issues including how local ethics review committees are challenged by the complex issues surrounding “broad” data sharing given cultural beliefs and practices. I will also discuss how H3Africa has negotiated fairness in genomics in resource-challenged settings.
Disclosure of Interest: None Declared
Biography: Michael Snyder is the Stanford Ascherman Professor and Chair of Genetics and the Director of the Center of Genomics and Personalized Medicine. Dr. Snyder received his Ph.D. training at the California Institute of Technology and carried out postdoctoral training at Stanford University. He is a leader in the field of functional genomics and proteomics, and one of the major participants of the ENCODE project. His laboratory study was the first to perform a large-scale functional genomics project in any organism, and has developed many technologies in genomics and proteomics. These including the development of proteome chips, high resolution tiling arrays for the entire human genome, methods for global mapping of transcription factor binding sites (ChIP-chip now replaced by ChIP-seq), paired end sequencing for mapping of structural variation in eukaryotes, de novo genome sequencing of genomes using high throughput technologies and RNA-Seq. These technologies have been used for characterizing genomes, proteomes and regulatory networks. Seminal findings from the Snyder laboratory include the discovery that much more of the human genome is transcribed and contains regulatory information than was previously appreciated, and a high diversity of transcription factor binding occurs both between and within species. He has also combined different state-of-the-art “omics” technologies to perform the first longitudinal detailed integrative personal omics profile (iPOP) of person and used this to assess disease risk and monitor disease states for personalized medicine. He is a cofounder of several biotechnology companies, including Protometrix (now part of Life Technologies), Affomix (now part of Illumina), Excelix, and Personalis, and he presently serves on the board of a number of companies.
Biography: Dr Teh obtained his MD (1992) from the University of Queensland, Australia and his PhD (1997) from the Karolinska Institute, Sweden. Following postdoctoral works at Karolinska Institute, he joined the Van Andel Research Institute (VARI), USA in 2000 as a Senior Scientific Investigator heading the Laboratory of Cancer Genetics. From 2003, he served as the Deputy Director (Research Operations) of VARI and from 2008, Director of VARI International. He established the National Cancer Centre Singapore (NCCS)-VARI laboratory, which serves as a bridge between translational research and clinical medicine. In 2010 he received the Singapore Translational Research Investigator Award and relocated to Singapore. He served as the SingHealth Group Director for Translational Research from 2010-2012. His laboratory, together with those of Professors Patrick Tan and Steve Rozen, focus on Asian Cancer Genomics and in the last 5 years have made seminal discoveries in the field including biliary tract cancer, urological cancer and breast tumors. He holds Adjunct Professorships at several universities worldwide including Baylor College of Medicine, USA, Nanjing University and Sun Yat-Sen University, China and the Karolinska Institute, Sweden. Dr. Teh has published extensively, with over 300 publications in high impact scientific journals. He has been member of various editorial boards for journals including Lancet Oncology, Cancer Research, Molecular Cancer Therapeutics, International Journal of Oncology, Journal of Clinical Endocrinology and Metabolism, Clinical Genitourinary Cancer, and the American Journal of Translational Research. Dr Teh is a recipient of the 2015 Singhealth Distinguished Researcher Award and co-recipient of the 2015 Singapore President Science Award.

Abstract: ASIAN CANCER GENOMICS AND ITS CLINICAL IMPLICATIONS
Our works focus on the genomic profiling of Asian-centric cancers using high-throughput technologies and the data is correlated with clinicopathological information. The goals are to 1) understand the molecular mechanism underlying these cancers; and 2) to identify potential therapeutic targets and novel biomarkers related to the behavior of the disease. In this talk, I will first describe our works on cholangiocarcinoma (biliary tract cancer) including cases related to liver fluke infection. There is significant difference in the spectrum and frequency of the alterations between fluke-related and non-fluke related cases, explaining the difference in their underlying pathogenesis. Second, I will describe our recent discovery of the molecular fingerprint of a herbal carcinogen called Aristolochic Acid, which is associated with upper urinary tract urothelial cancer. This discovery not only enhances our understanding of the molecular mechanism of this carcinogen, but allows screening for the involvement of this carcinogen in other cancer types such as liver cancer. Third, I will present our recent genomic studies of the fibroepithelial tumors of the breast, from the very common benign fibroadenoma to the rare but malignant Phyllodes tumors. Several frequently mutated genes such as MED12 and RARA will be highlighted and discussed.

Disclosure of Interest: None Declared
Biography: Dr. Wang’s primary interests are to advance the scientific understanding of human cancers through genomic sequencing approaches and to explore novel diagnostic, prognostic, and therapeutic possibilities for cancer patients. Dr. Wang received her undergraduate degree in Clinical Medicine from Taishan Medical University in China. She received her PhD in Genome Sciences from The University of Tokyo in September 2011. Her PhD dissertation focused on genomic analysis of pancreatic cancers. She joined Human Genome Sequencing Center at Baylor College of Medicine (BCM) as a Postdoctoral Associate and became a faculty Instructor in 2014 and an Assistant Professor in 2015. Dr. Wang has extensive experience in integrated genomic analysis of next-generation sequencing data and currently leads multiple national and international large-scale cancer genomics projects in the Center, including the Exceptional Responder Initiative launched by NCI and several TCGA cancers. In addition, Dr. Wang leads the analysis in the somatic and germline mutation discovery of the highly successful “rare cancer” project at BCM.

Abstract: TRANSLATIONAL IMPACT OF GENOMIC SEQUENCING ON RARE CANCERS

Over the past decade, we have witnessed remarkable advancements in our understanding of the molecular genetics of cancers by second-generation sequencing. The genomes of the common cancer types have been systematically characterized through national and international projects. These advances have led to a wide range of new molecular targets, many of which are in clinical trials now, and beginning to influence therapies. However, rare cancers have received relatively little attention from the genomics community, mainly due to the scarcity of available samples. The molecular pathogenesis for most of the rare cancer types is still largely unknown and there has been little or no improvement in clinical management strategies. The International Rare Cancer Initiative classifies cancer types with an incidence of ≤3 newly diagnosed cases out of a population of 100,000 persons per year as rare, the cumulative burden of all rare cancers worldwide accounts for a significant proportion of diagnosed malignancies, more than 20%, which is higher than any of the most often studied common cancer type.

Since early in 2012, we have begun the shine the spotlight of genomics on rare cancers, which is the first large-scale rare cancer genomic project in United States. So far, we have performed integrated genomic analysis of more than 10 rare but devastating adult and childhood cancer types. Our studies of these rare cancers have led to many novel discoveries potentially translatable to the clinic for diagnostic and therapeutic applications, identified new treatment options that can be applied to other tumor types and expanded our knowledge of cancer pathways. Thus the impact of genomics on the outlook for patients is substantial in rare cancers. Here I will examine our success stories of rare cancer studies and explore the potential translational impact of genomic sequencing on rare cancers, to provide some context as to the experiment design and research conduct guide for rare cancer studies.

Disclosure of Interest: None Declared
Feng Zhang - 139

Biography: Feng Zhang is a Core Member at the Broad Institute of MIT and Harvard, an Investigator at the McGovern Institute for Brain Research at MIT, and an Assistant Professor in the Department of Brain and Cognitive Sciences. He was born in Shijiazhuang (Hebei Province, China) in 1981 and moved to Des Moines, Iowa in 1993. His introduction to engineering biological tools for mammalian systems began as a sophomore in high school with an opportunity to intern in the gene therapy lab of John Levy in Des Moines, Iowa. He obtained an A.B. in Chemistry and Physics from Harvard University in 2004 working with Xiaowei Zhuang. As a PhD student in the Chemistry Department at Stanford University, Zhang worked with Karl Deisseroth to develop optogenetics technologies for dissecting brain circuits, using light-sensitive proteins from microbes to enable control of neuronal activity in living organisms with light. After finishing his Ph.D. in 2009, Feng joined the Harvard Society of Fellows as a Junior Fellow (2009-2010), focusing on developing gene editing tools based on transcription activator-like effectors (TALEs). In 2011, Zhang began his own laboratory at the Broad and McGovern Institutes, where he harnessed CRISPR-Cas systems for gene editing in eukaryotic cells. His lab continues to play a critical role in the development of gene editing technologies and applications that are accelerating research around the world.

Abstract: GENOME ENGINEERING USING CRISPR-CAS SYSTEMS
Advances in genome sequencing technology have accelerated the rate at which we can identify genetic variants associated with phenotypes related to human health and disease, but functionally interrogating these variants remains time intensive. Being able to quickly find the causative variants in a sea of natural variation is essential to the goal of personalized medicine. To this end, new genome editing tools adapted from the microbial CRISPR-Cas system can be employed to rapidly screen through variants for functional effects as well as to model diseases based on patient-specific mutations. In this presentation I will discuss how the CRISPR-Cas system can be deployed as a powerful discovery platform, highlighting recent findings from CRISPR screens, and describe therapeutic applications for this powerful tool. Finally, I will present recent work exploring the next generation of genome editing technologies beyond Cas9, and how these new tools will further expand our ability to connect genotype to phenotype and, ultimately, treat human disease.

Disclosure of Interest: Feng Zhang is a founder of Editas Medicine and a scientific advisor for Editas Medicine and Horizon Discovery.
Biography: Dr. Huda Zoghbi is an Investigator with the Howard Hughes Medical Institute and is a Professor of Pediatrics, Neurology, Neuroscience, and Molecular and Human Genetics at Baylor College of Medicine. She is also the founding Director of the Jan and Dan Duncan Neurological Research Institute at Texas Children’s Hospital.

Dr. Zoghbi is interested in understanding healthy brain development and aging as well as what goes awry in specific neurological conditions. She uses genetics to unravel the root causes of various disorders. She has published seminal work on the genetic basis of the autism spectrum disorder Rett syndrome and on late-onset neurodegenerative diseases. Dr. Zoghbi serves as a board member for several professional organizations and educational institutions, including serving as the current year President of the Board for the McKnight Endowment Fund for Neuroscience, a trustee for Rice University, and a senior editor for the scientific journal eLife. She was elected to the Institute of Medicine in 2000 and to the National Academy of Sciences in 2004. Among Dr. Zoghbi’s honors are the IPSEN Prize in Neuronal Plasticity, the Vilcek Prize, the Gruber Prize in Neuroscience, the Dickson Prize in Medicine, the Pearl Meister Greengard prize, the Skolnick Prize, the March of Dimes Prize in Developmental Biology, a Doctor of Medical Sciences Honorary Degree from Yale University, and the Mortimer D. Sackler, M.D. Prize for Distinguished Achievement in Developmental Psychobiology.

Abstract: GENETIC APPROACHES TO TACKLE NEURODEGENERATIVE DISORDERS

The discovery of genes causing neurological diseases ranging from childhood postnatal neurological disorders such as Rett syndrome and autism to neurodegenerative diseases such as the spinocerebellar ataxias (SCAs) has transformed the ability to diagnose these diseases accurately and provided the promise of better understanding and treatment of these devastating disorders. The path from gene discovery to therapy, however, is not a straightforward one and requires deep understanding of pathogenic mechanisms and key molecular and anatomical determinants of various symptoms and pathologies. We have used genetic, behavioral, physiological and molecular approaches to interrogate the pathogenesis of several of these diseases, with surprising results. These studies are providing insights into these respective disorders and are beginning to identify potential therapeutic entry points.