Species-independent identification of known and novel recurrent genomic entities in multiple cancer patients

Friis-Nielsen, Jens; Gonzalez-Izarzugaza, Jose Maria; Brunak, Søren

Published in: Human Genomics (Online)

Link to article, DOI: 10.1186/s40246-016-0063-5

Publication date: 2016

Document Version
Publisher's PDF, also known as Version of record

Link back to DTU Orbit

### MEETING ABSTRACTS

#### Human genome meeting 2016

Houston, TX, USA. 28 February - 2 March 2016

Published: 26 May 2016

---

**O1** The metabolomics approach to autism: identification of biomarkers for early detection of autism spectrum disorder

A. K. Srivastava1, Y. Wang1, R. Huang1, C. Skinner1, T. Thompson1, L. Pollard1, T. Wood1, F. Luo2, R. Stevenson1

1JCSRI, Greenwood Genetic Center, Greenwood, SC, USA; 2School of Computing, Clemson University, Clemson, SC, USA; 3Biochemical Genetics Laboratory, Greenwood Genetic Center, Greenwood, SC, USA

**Correspondence:** A. K. Srivastava – JCSRI, Greenwood Genetic Center, Greenwood, SC, USA

**Human Genomics** 2016, **10**(Suppl 1):O1

**Objectives**

From the first description by Leo Kanner [1], autism has been an enigmatic neuropsychiatric phenomenon. The new genetic/genomic technologies of the past decade have not been as productive as originally anticipated in unveiling the mysteries of autism. The specific etiology of the majority of cases of autism spectrum disorder (ASD) is unknown, although numerous genetic/genomic variants and alterations of diverse cellular functions have been reported. Prompted by this failure, we have investigated whether the metabolomics approach might yield results which could simultaneously lead to a blood-based screening/diagnostic test and to treatment options.

**Methods**

Plasma samples from a clinically well-defined cohort of 100 male individuals, ages 2-16+ years, with ASD and 32 age-matched typically developing (TD) controls were subjected to global metabolomic analysis.

**Results**

We have identified more than 25 plasma metabolites among the approximately 650 metabolites analyzed, representing over 70 biochemical pathways, that can discriminate children with ASD as young as 2 years from children that are developing typically. The discriminating power was greatest in the 2 year age group and weaker in older age groups. The initial findings were validated in a second cohort of 83 children, males and females, ages 2-10 years, with ASD and 76 age and gender-matched TD children. The discriminant metabolites were associated with several key biochemical pathways suggestive of potential contributions of increased oxidative stress, mitochondrial dysfunction, inflammation and immune dysregulation in ASD. Further, targeted quantitative analysis of a subset of discriminating metabolites using tandem mass spectrometry provided a reliable laboratory method to detect children with ASD.

**Conclusion**

Metabolic profiling appears to be a robust technique to identify children with ASD ages 2–10 years and provides insights into the altered metabolic pathways in ASD, which could lead to treatment strategies.

**References**


**Disclosure of interest**

None declared.

---

**O2** Phenome-wide association study for smoking- and drinking-associated genes in 26,394 American women with African, Asian, European, and Hispanic descents

R. Polimanti1, J. Geelenrter1,2,3

1Department Psychiatry, Yale Sch Med and VA CT Healthcare Center, West Haven, CT, USA; 2Department Genetics, Yale Sch Med and VA CT Healthcare Center, West Haven, CT, USA; 3Department Neurobiology, Yale Sch Med and VA CT Healthcare Center, West Haven, CT, USA

**Correspondence:** R. Polimanti – Dept Psychiatry, Yale Sch Med and VA CT Healthcare Center, West Haven, CT, USA

**Human Genomics** 2016, **10**(Suppl 1):O2

**Objectives**

To uncover novel traits associated with nicotine and alcohol use genetics, we performed a phenome-wide association study in a large multi-ethnic cohort.

**Methods**

We investigated 7,688 African-Americans (AFR), 1,133 Asian-Americans (ASN), 14,081 European-Americans (EUR), and 3,492 Hispanic-Americans (HISP) from the Women’s Health Initiative, analyzing risk alleles located in the CHRNA5–CHRNA3 locus (rs8034191, rs1051730, rs12914385, rs2036527, and rs16969968) for nicotine-related traits and ADHIB (rs1229984 and rs2066702) and ALDH2 (rs671) for alcohol-related traits with respect to anthropometric characteristics, dietary habits, social status, psychological circumstances, reproductive history, health conditions, and nicotine- and alcohol-related traits.

**Results**

The investigated loci resulted associated with novel traits: rs1229984 were associated with family income (p=4.1*10−5), having a pet (p=6.5*10−5), “felt calm and peaceful” (p=2.6*10−5), education (p=3.7*10−5), and number of term pregnancies (p=1.12*10−4) in EUR; rs1051730 and rs16969968 showed a suggestive association with “High cholesterol requiring pills ever” (p=3.8*10−4 and p=1.8*10−4) in trans-ethnic meta-analysis. We also replicated the known associations: rs80341911 was associated with cigarettes per day (CGtSDAY, p=3.4*10−5), smoking status (p=3.7*10−5), and “smoked at last 100 cigarettes” (p=7.3*10−5) in EUR; rs1051730 and rs16969968 were associated with CGtSDAY (p=9.1*10−8 and p=1.1*10−7) and lung cancer (p=7.3*10−3 and p=9.9*10−3) in EUR; rs2036527 was associated with CGtSDAY (p=3.5*10−5) in AFR; rs1229984 showed associations for alcohol servings (ALC, p=3.1*10−5), beer servings (p=3.1*10−5), wine servings (WINE, p=3.9*10−5), and “Drinks alcohol (age 50)” (p=9.3*10−4) in EUR and for ALC (p=5.2*10−4) and DIETALC (p=9.6*10−5) in HISP; rs671 resulted associated with alcohol intake (p=3.8*10−5), DIETALC (p=1.9*10−5), ALC (p=1.3*10−5), WINE (p=1.1*10−5) and “Drank 12 alcoholic beverages ever” (p=1.2*10−5) in ASN.

**Conclusion**

We provided novel genetic data regarding the consequences of smoking and drinking behaviors and confirmed ethnic differences in their genetic predisposition.

**Disclosure of interest**

None declared.
Effects of prenatal environment, genotype and DNA methylation on birth weight and subsequent postnatal outcomes: findings from GUSTO, an Asian birth cohort

X. Lin1, I. Y. Lim1, Y. Wu, A. L. Teh1, L. Chen1, J. M. Aris1, S. E. Soh1, M. T. Tint2, J. L. Macisaac3, F. Yap1, K. Kwek1, S. M. Saw1, M. S. Kobor1, M. J. Meaney1, K. M. Godfrey2, Y. S. Chong3, J. D. Holbrook1, Y. S. Lee1, P. D. Gluckman1,6, N. Karnani1, GUSTO study group

1Singapore Institute for Clinical Sciences, Singapore, Singapore; 2National University of Singapore, Singapore, Singapore; 3University of British Columbia, Vancouver, British Columbia, Canada; 4WK Women’s and Children’s Hospital, Singapore, Singapore; 5University of Southampton and University Hospital Southampton NHS Foundation Trust, Southampton, UK; 6University of Auckland, Auckland, New Zealand

Correspondence: X. Lin – Singapore Institute for Clinical Sciences, Singapore, Singapore

Human Genomics 2016, 10(Suppl 1):O3

Objectives
Prenatal environment and genetic polymorphism can have a lasting impact on offspring’s metabolic function by perturbing its epigenome. Birth weight is often used as a surrogate for the overall quality of the intrauterine environment. We present the first neonate epigenome-wide association study in an Asian mother-offspring cohort, that interrogates the effects of prenatal environment variables, umbilical cord DNA methylation and SNPs, on birth weight.

Methods
In GUSTO, a prospective mother-offspring cohort study (N=987), we examined the associations between DNA methylation, SNPs, birth weight and 11 prenatal environment variables. First, we investigated the association between perinatal methylation and birth weight to identify sites of variability in methylation. Second, we interrogated the contribution of genetic and prenatal environmental factors on this variability in the epigenome. Finally, we examined whether these methylation marks at birth were associated with offspring size and adiposity in early childhood.

Results
Methylation levels at 50 CpGs were significantly associated with birth weight, and a subset of these CpGs was located in genes and miRNA known to be involved in metabolic pathways/disorders. We further examined the influence of environmental and genetic factors on methylation at these 50 CpG sites. Sixteen CpGs were associated with both, an additional 24 CpGs were associated with only environmental factors, while only 3 CpGs were associated with genetic factors alone. Environmental factors associated with methylation were predominantly maternal-adiposity-related (pre-pregnancy body mass index, pregnancy weight gain and maternal glucose levels). Methylation levels at half of these CpGs were also associated with offspring size and adiposity in early childhood.

Conclusion
Developmental pathways to obesity begin before birth and involve genetic, epigenetic and environmental factors.

Disclosure of interest
X. Lin: None declared, I. Y. Lim: None declared, Y. Wu: None declared, A. L. Teh: None declared, L. Chen: None declared, J. M. Aris: None declared, S. E. Soh: None declared, M. T. Tint: None declared, J. L. Macisaac: None declared, F. Yap: None declared, K. Kwek: None declared, S. M. Saw: None declared, M. S. Kobor: None declared, M. J. Meaney: None declared, K. M. Godfrey: Conflict with: KVIG has received reimbursement for speaking at conferences sponsored by companies selling nutritional products. He is part of an academic consortium that has received research funding from Abbott Nutrition, Nestec and Danone, Y. S. Chong: Conflict with: YSC has received reimbursement for speaking at conferences sponsored by companies selling nutritional products. He is part of an academic consortium that has received research funding from Abbott Nutrition, Nestec and Danone, J. D. Holbrook: None declared, Y. S. Lee: None declared, P. D. Gluckman: None declared, N. Karnani: None declared.

High-throughput identification of specific QT interval modulating enhancers at the SCN5A locus

A. Kapoor1, D. Lee1, A. Chakravarti1

Messic-Knathans Institute of Genetic Medicine, Johns Hopkins University School of Medicine, Baltimore, MD, USA

Correspondence: A. Kapoor – Messic-Knathans Institute of Genetic Medicine, Johns Hopkins University School of Medicine, Baltimore, MD, USA

Human Genomics 2016, 10(Suppl 1):O4

Objectives
Genome-wide association studies (GWAS) have indicated that sequence variation in cis-regulatory elements (CRE) plays important roles in common disease risk/trait variation, but identification of these causal variants has remained a major challenge in complex trait genetics. Here, we performed reporter assays for all common variants at the QT interval associated SCN5A GWAS locus, with the goal of identifying the underlying causal variants.

Methods
A target region of ~500kb at SCN5A was defined based on recombination hotspots (rate>10cM/Mb; HapMap) flanking the 5 independent QT interval GWAS hits. Within the target region, all common variants (minor allele frequency >5%) from the 1000 Genomes European ancestry populations in moderate linkage disequilibrium (r2>0.3) with any of the 5 GWAS hits were selected. Both alleles of these variants were amplified with flanking sequences and cloned upstream of a minimal promoter driven firefly luciferase gene in pGL4.23. Human cardiomyocyte cells, AC16, were transfected with test constructs and Renilla luciferase vector (for transfection normalization) in triplicate and luciferase assays were performed 24h later. Reporter assays on a subset of variants were repeated for assessing allelic difference in regulatory activity. All cloning and reporter assays were performed in 96- and 24-well plates.

Results
Of a total 121 variants selected, 112 variants in 104 amplicons passed primer design (amplicon size 256-617bp; median 397bp), and we successfully cloned both alleles for 106 variants in 98 amplicons. In reporter assays, compared to empty vector, 24 and 40 amplicons showed enhancer (>2-fold) and suppressor (<0.5-fold) activities in AC16 cells, respectively. Of these only 4 were observed as open chromatin regions in heart tissue in NIH Epigenomics data. Overall, 12 variants showed nominally significant allelic difference (P<0.05) in reporter activity and were repeated with 18 replicates and 7 variants were identified to have repeated significant allelic difference in regulatory activity.

Conclusion
Independent of the available epigenomic data, which are of limited relevance, an unbiased in vitro reporter screen for CREs overlapping all common variants associated with QT interval at the SCN5A GWAS locus identified 7 common cis-regulatory variants. Our immediate next goals are to a) evaluate the effect of deleting these 7 CREs on SCN5A expression in AC16 cells and b) identify the trans-acting factors regulating their functions.

Disclosure of interest
None declared.

Identification of extracellular matrix components inducing cancer cell migration in the supernatant of cultivated mesenchymal stem cells

C. Maercer1, F. Graf2, M. Boutros2

1Essling University of Applied Sciences, Esslingen, Germany; 2German Cancer Research Center, Heidelberg, Germany

Correspondence: C. Maercer – Essling University of Applied Sciences, Esslingen, Germany

Human Genomics 2016, 10(Suppl 1):O5
Objectives
Some cancers show a strong tendency to metastasize to bone, a tissue of mesenchymal origin and a prominent site of mesenchymal stem cells (MSC) residing in the stem cell niche. With bone metastasis formation being one of the most detrimental steps in cancer progression, a better understanding of how bone metastases are initially formed is key to successfully targeting bone metastasis of, for example, prostate cancer. Recent reports have suggested that bone-metastasizing cancers may mimic the process of homing of hematopoietic stem cells to their bone niche.

Methods
In order to understand the role of MSC in metastasis formation, we investigated the interaction of primary human bone marrow MSC with established cancer cell lines able to metastasize to bone. With a trans-well migration assay we could show that MSC induced a rapid migration response of prostate and breast cancer cell lines already within two hours after start of the experiment. In order to identify factors stimulating cancer cell migration, MSC cell culture supernatant was separated by size exclusion and ion exchange chromatography. Migratory fractions then were further analyzed by mass spectrometry and antibody array analysis.

Results
With this approach we identified the extracellular matrix proteins type I and type III collagen, fibronectin and laminin 421 as potential drivers of cancer cell migration, which was confirmed by using recombinant proteins. RNAi experiments showed that the cancer cell extracellular matrix receptor beta 1 integrin obviously plays a pivotal role for cell migration.

Conclusion
From our results we conclude that the extracellular matrix as it is produced by MSC obviously plays a crucial role for cancer metastasis and therefore might be a promising anti-cancer drug target.

Disclosure of interest
None declared.

O6
Single cell allele specific expression (ASE) in T21 and common trisomies: a novel approach to understand DOWN syndrome and other aneuploidies
1Department of Genetic Medicine and Development, University of Geneva Medical School, Geneva, Switzerland; 2Geneva University Hospitals-HUG, Service of Genetic Medicine, Geneva, Switzerland; 3IGE3 Institute of Genetics and Genomics of Geneva, University of Geneva Medical School, Geneva, Switzerland
Correspondence: G. Stamoulis – Department of Genetic Medicine and Development, University of Geneva Medical School, Geneva, Switzerland
Human Genomics 2016, 10(Suppl 1):O6

Objectives
Trisomy 21 is a model disorder of altered gene expression. We have previously used a pair of monozygotic twins discordant for trisomy 21 to study the global dysregulation of gene expression, without the noise due to genetic variation among individuals (Nature:508; 345–350;2014). The majority of previous studies focused on aneuploidies were conducted on cell populations or tissues. Our study focusing on gene and allelic expression behaviour of single cells (SC), aims to reveal biological insights regarding the cellular impact of aneuploidy and uncover the mechanisms of gene dosage.

Methods
We estimated the allele specific expression (ASE) from RNAseq of ~1000 single cells in different aneuploidies. We used 352 SC fibroblasts (173 Normal and 179 T21 cells) from the pair of monozygotic twins discordant for T21, 166 SC from a mosaic T21, 176 SC from a mosaic T18, 151 SC from a mosaic T8, and 146 SC from a mosaic T13.

Results
In the monozygotic twins, a considerable number of heterozygous sites at the non-chr21 genome showed monoallelic expression (MAE); (Normal: 73.5 % monoallelic in 564,668 observations, and T21: 78.7 % monoallelic in 549,799 observations). There was also considerable MAE for chr21 sites in Normal and, surprisingly, in T21 cells as well (Normal: 63.3 % monoallelic in 5,009 observations, and T21: 72.8 % monoallelic in 6,456 observations). We classified the genes on chr21 in 3 classes according to the level of the aggregate MAE of their corresponding sites (9 monoallelic, 29 intermediate, 2 biallelic). Similar results, i.e. extensive MAE on the supernumerary chromosome genes, were also observed in the other aneuploidies.

Conclusion
We hypothesize that each class of genes contributes in a specific way to the phenotypic variability of Down Syndrome. Our analysis showed that, for genes with monoallelic expression, the abnormal gene dosage induced by the aneuploid chromosome is maybe due to the number of cells expressing the gene. This difference in the fraction of expressing cells could contribute to the development and the variability of phenotypes in aneuploidies. This study provides a new fundamental understanding of the allele specific expression in T21 and other aneuploidies.

Disclosure of interest
None declared.

O7
Role of microRNA in LCL to iPSC reprogramming
S. Kumar, J. Curran, J. Blangero
1South Texas Diabetes and Obesity Institute, School of Medicine, University of Texas Rio Grande Valley, Edinburg, TX, USA; 2South Texas Diabetes and Obesity Institute, School of Medicine, University of Texas Rio Grande Valley, Brownsville, TX, USA
Correspondence: S. Kumar – South Texas Diabetes and Obesity Institute, School of Medicine, University of Texas Rio Grande Valley, Edinburg, TX, USA
Human Genomics 2016, 10(Suppl 1):O7

Objectives
A large number of EBV immortalized lymphoblastoid cell lines (LCLs) have been generated and maintained in genetic/epidemiological studies as a perpetual source of DNA and as a surrogate in-vitro cell model. Recent successes in reprogramming LCLs into induced pluripotent stem cells (iPSCs) have paved the way to generate more relevant in-vitro disease models using this existing bio-resource. However the effects of EBV encoded oncoproteins on cellular transcription and function make LCLs a unique biomaterial to reprogramme. Accumulating evidence now provides support that miRNAs play a critical role in transcription factor-induced reprogramming of iPSCs.

Methods
To investigate the role of miRNAs in regulating gene expression and cellular functions during LCL to iPSC reprogramming, we performed a parallel genome-wide miRNA and mRNA expression analysis in six LCLs and their reprogrammed iPSCs.

Results
A total of 77 miRNAs and 5,228 mRNAs were significantly (FC-abs ≥ 2.0 and FDR ≤ 0.05) differentially expressed (DE) during LCL to iPSC reprogramming out of which 29 miRNAs and 2,317 mRNAs were significantly down-regulated and 48 miRNAs and 2,911 mRNAs were significantly up-regulated. The down-regulated miRNAs were highly enriched for LCL specific miRNAs (mir-155, let-7a-1, mir-21, mir-142, mir103, mir-320, mir-146a-b) and the up-regulated miRNAs were highly enriched for iPSC specific miRNAs (mir-302a, mir-302c, mir-371a, mir-302b, mir-302d, mir-372, mir-373mir-92a-1, mir-92a-2, mir-92b, mir-17, mir-20a, mir-18a). Further we performed target prediction analysis for all the significantly DE miRNAs using the miRNA target prediction data bases. The 3,456 genes were predicted to be the targets of the 29 miRNAs that were significantly down-regulated during LCL to iPSC reprogramming. Out of these 3,456 predicted target genes 1,023 were significantly DE during LCL to iPSC reprogramming. For the 48 miRNAs that were significantly up-regulated during LCL to iPSC reprogramming 5,063 target genes were predicted out of which 1,462 were significantly DE during LCL to iPSC reprogramming.
The significantly DE genes that were also the predicted targets of the significantly down or up regulated miRNAs were further analyzed for functional annotations and pathway analysis using Ingenuity Pathway Analysis Platform.

Conclusion

In summary, our analysis identifies DE miRNAs and their DE target genes and a global role of miRNAs in broad resetting of cellular transcriptome and function during LCL to iPSC reprogramming.

Disclosure of interest

None declared.

O8

Multiple enhancer variants disrupt gene regulatory network in Hirschsprung disease

S. Chatterjee1, A. Kapoor1, J. Akiyama2, D. Auer1, C. Berrios3, L. Pennacchio2, A. Chakravarti1

1Institute of Genetic Medicine, Johns Hopkins University, Baltimore, MD, USA; 2Genomics Division, Lawrence Berkeley National Laboratory, Berkeley, CA, USA

Correspondence: S. Chatterjee – Institute of Genetic Medicine, Johns Hopkins University, Baltimore, MD, USA

Human Genomics 2016, 10(Suppl 1):O8

Objectives

Common sequence variation in cis-regulatory elements (CREs) are the suspected etiological causes of complex disorders. We examined all common (>10% minor allele frequency) non-coding variants within a ~153kb locus surrounding the gene for receptor tyrosine kinase Ret, which is most commonly mutated in Hirschsprung disease (HSCR) or congenital aganglionicism), a form of functional intestinal obstruction in neonates (1 in 5,000 live births). We hoped to find all causal non-coding polymorphisms disrupting enhancer function leading to the disease.

Methods

We used human and mouse fetal gut at relevant developmental time points for transcriptional profiling, ChIP assays, transgenic enhancer assays and siRNA mediate knockdowns of relevant transcription factors.

Results

We demonstrate that: (i) the three polymorphisms residing in 3 distinct enhancers that increase risk of the disease by 4-, 2- and 1.7-fold. Haplotypes for these three independent variants display wide variation in risk. (ii) the three CREs are Ret enhancers with distinct temporal activities during mouse gut development; (iii) the CREs are bound by the transcription factors Rarb, Gata2/3 and Sox10, respectively, each developmentally expressed concordant with its cognate enhancer activity; (iv) variants in these CREs lead to their loss of activity and reduce Ret expression; (v) Ret is a positive feedback regulator of Sox10 and Gata2/3 transcription and; (vi) additional feedback interactions affect its ligand Gdnf, co-receptor Gfra1 and signal terminator Cbl.

Conclusion

These results explain how individually common, small effect non-coding polymorphisms can lead to large genetic effects in HSCR, since transcription attenuation of Ret from enhancer mutations are amplified through its auto-regulation. These results implicate RET as a key rate limiting step in early enteric nervous system (ENS) development and explains why >95% of HSCR cases have at least one RET loss-of-function allele. More generally, the phenotypic impact of a complex disorder can only be understood by assessing gene effects in the context of their gene regulatory networks.

Disclosure of interest

None declared.

O9

Metabolic profiling for the diagnosis of neurometabolic disorders

T. R. Donti1, G. Cappuccio2, M. Miller1, P. Atwal1, A. Kennedy3, A. Cardon4, C. Bacino1, L. Emmick5, J. Hertecant6, F. Baumer7, B. Porter7, M. Bainbridge1, P. Bonnen1, B. Graham1, R. Sutton1, Q. Sun1, S. Ese1

1Molecular and Human Genetics, Baylor College of Medicine, Houston, TX, USA; 2Department of Translational Medical Sciences, Federico II University, Naples, Italy; 3Metabolon Inc, Durham, NC, USA; 4Section of Pediatric Neurology and Neuroscience, Baylor College of Medicine, Houston, TX, USA; 5Tawam Hospital, Abu Dhabi, United Arab Emirates; 6Stanford Medical School, Stanford, CA, USA

Correspondence: T. R. Donti – Molecular and Human Genetics, Baylor College of Medicine, Houston, TX, USA

Human Genomics 2016, 10(Suppl 1):O9

Objectives

In individuals presenting with undifferentiated phenotypes such as developmental delay, hypotonia, and seizures, the list of differential diagnoses is often very long and includes metabolic/neurometabolic, genomic, and other Mendelian disorders. Here we want to demonstrate the utility of untargeted metabolic profiling to screen for a wide range of neurometabolic disorders.

Methods

Untargeted small molecule metabolic profiling was performed as described previously [1] on plasma samples from 12 patients suspected to have a neurometabolic disorder with a presentation of seizures, developmental delay and hypotonia.

Results

We identified 5 different neurometabolic disorders in these 12 patients. We observed elevations of 3-methoxytyrosine and decreased levels of dopamine and vanillylmandelate in AADC deficiency, elevations of 2-pyridylidione in ABAT deficiency, elevations of succinyladenosine in ADSL deficiency, increased citrate in citrate transporter deficiency, and elevations of imidazole propionic acid, cis and trans-urocanate in urocanase deficiency. The perturbations in the metabolomic profiles of plasma from these patients are unique, specific and not previously seen in over 300 other samples analyzed as normal controls or for other indications.

Conclusion

The standard diagnostic test for AADC, ABAT, and ADSL deficiency is CSF neurotransmitter analysis, while testing for urocanase deficiency requires an enzyme activity assay from a liver biopsy. These cases demonstrate the ability of untargeted metabolic profiling for the functional confirmation of pathogenicity of VUS found via WES; moreover, disorders for which there is no biochemical testing or where testing is only available on CSF are able to be diagnosed in a plasma sample. This also demonstrates the utility of metabolic profiling alone to screen for a wide range of neurometabolic disorders.

References


Disclosure of interest

None declared.

O10

A novel causal methylation network approach to Alzheimer’s disease

Z. Hu1, P. Wang2, Y. Zhu3, J. Zhao3, M. Xiong2 and David A Bennett4

1School of Public Health, Houston Health Science Center, Houston, TX, USA; 2University of Texas, Houston Health Science Center, Houston, TX, USA; 3Tulane University, New Orleans, LO, USA; 4Rush Alzheimer’s Disease Center, Rush University, Chicago, IL, USA

Correspondence: Z. Hu – School of Public Health, Houston Health Science Center, Houston, TX, USA

Human Genomics 2016, 10(Suppl 1):O10

Disclosure of interest

None declared.
Objectives
Alzheimer’s disease (AD) is the most common progressive neurodegenerative disease and represents a major cause of disability for elderly patients. DNA methylation—are increasingly seen as playing an important role in AD development. However its causal mechanisms remain unclear. Recent studies indicate that AD develops essentially as a result of dysfunction of molecular networks. Our purpose is to develop large-scale causal methylation networks to uncover the mechanism of AD development.

Methods
We propose to use causal graphs as a major concept and a general framework for causal methylation network analysis and develop “score and search”-based methods for exact learning causal graphs of methylation networks to find the best-scoring structures for a given methylation dataset. Specifically, we develop novel functional structural equations for modeling methylation networks and use integer programming to search the network with optimal score.

Results
The proposed methods were applied to AD data with 460045 CpG sites from 748 samples. At the first stage, the methylation data of 168 gene from the pathway Alzheimer’s disease were used to create a causal network describing the connection among the methylation sites between these genes. According to the current result, 148 gene was matched and tested in the model. We identified a largest connected causality methylation network with 47 nodes and 96 edges. Most genes were confirmed to play an important role in the AD development from the literature.

Conclusion
The proposed methods provide a highly flexible general framework for causal methylation network analysis and provide more rich in information than co-methylation network. The exact learning algorithms will guarantee to find optimal solutions and hence provide accurate estimations of causal graphs of methylation networks. The causal methylation networks are able to uncover the mechanism of AD development.

Disclosure of interest
None declared.

O12
Transcriptome analysis identifies genes, enhancer RNAs and repetitive elements that are recurrently deregulated across multiple cancer types
B. Kaczkowski1, Y. Tanaka2, H. Kawaji3, A. Sandelin4, R. Andersson1, M. Itoh1, T. Lassmann4, the FANTOMS consortium1, Y. Hayashizaki3, P. Carninci5, A. R. R. Forrest6
1Division of Genomic Technologies, RIKEN Center for Life Science Technologies, Yokohama, Japan; 2Preventive Medicine and Applied Genomics unit, RIKEN Advanced Center for Computing and Communication, Yokohama, Japan; 3Department of Biology, University of Copenhagen, Copenhagen, Denmark; 4Telethon Kids Institute, the University of Western Australia, Perth, Australia; 5RIKEN Preventive Medicine & Diagnosis Innovation Program, Wako, Japan; 6Harry Perkins Institute of Medical Research, the University of Western Australia, Nedlands, Australia
Correspondence: B. Kaczkowski – Division of Genomic Technologies, RIKEN Center for Life Science Technologies, Yokohama, Japan

Results
We found low expression levels of miR-342-3p in TNBC tumors compared with other breast cancer phenotypes, and this down-regulation characterizes one of our miRNA subgroups with high risk to relapse. To characterize its functional role, miR-342-3p was transiently transfected in the cell line MDA-MB-468, showing a decrease in cell proliferation, viability and migration rates. A gene expression profile revealed 140 altered mRNAs, from which 35 are potential direct targets of miR-342-3p defined by an in-silico analysis. The monocarboxylate transporter 1(MCT1), was confirmed as one target of miR-342-3p by a luciferase assay and western blot analysis. MCT1 repression by the miRNA promotes lactate efflux changes in the tumor cells, reflected in the accumulation of exogenous lactate and the increase in levels of extracellular endogenous lactate together with a decrease level of intra and inter cellular glucose concentration.

Disclosure of interest
None declared.

O11
A microRNA signature identifies subtypes of triple-negative breast cancer and reveals MIR-342-3P as regulator of a lactate metabolic pathway
1Cancer Genomics Laboratory, National Institute Of Genomic Medicine (INMEGEN), Mexico City, Mexico; 2FUCAM, Mexico City, Mexico; 3National Tumor Institute, Milan, Italy
Correspondence: A. Hidalgo-Miranda – Cancer Genomics Laboratory, National Institute Of Genomic Medicine (INMEGEN), Mexico City, Mexico

Objectives
Triple negative breast cancer (TNBC) represents a challenging tumor type due to their poor prognosis and limited treatment options. It is well recognize that clinical and molecular heterogeneity of TNBC is driven in part by post-transcriptional regulators such as miRNAs. To stratify TNBCs, we profiled 1050 miRNAs in 132 adjuvant TNBC tumors and 40 tumors from other immunophenotypes using an Affymetrix microarray platform.

Methods
A NMF clustering analysis allowed us to identify 4 TNBC subtypes featuring unique miRNA expression patterns, disease free and overall survival rates and particular gene ontology enrichments. Our agglomerative approach was cross-validated by using two other clustering algorithms. 3 cell line models were classified according to our miRNA signature, recapitulating two different miRNA subgroups. The TNBC tumors were compared against other phenotypes identifying differentially expressed miRNAs to define interesting miRNAs for further functional analysis.
un-published, follow-up results that detail the REPS22 activation in cancer. Finally, we present 90 enhancers that are activated in cancer cell lines. With ENCODE ChiP-PET data, we linked 16 of those enhancers to promoters of known cancer genes.

**Conclusion**

Our transcriptome analysis identified candidate biomarkers with pan-cancer potential and provided new insights into enhancers and repetitive elements that are recurrently activated in cancer.

**References**


**Disclosure of interest**

None declared.

**O13**

Elevated mutation and widespread loss of constraint at regulatory and architectural binding sites across 11 tumour types

C. A. Semple

MRC Human Genetics Unit, MRC Institute of Genetics and Molecular Medicine, Edinburgh, UK

Human Genomics 2016, 10(Suppl 1):O13

**Objectives**

Disruption of gene regulation is thought to play major roles in carcinogenesis and tumour progression. Here, we characterize the mutational profiles of diverse transcription factor binding sites (TFBSs) across 1,574 completely sequenced cancer genomes encompassing 11 tumour types. We assess the relative rates and impact of mutation at the binding sites of 87 different transcription factors (TFs) by comparing the abundance and patterns of single base substitutions within putatively functional binding sites to matched control sites.

**Methods**

To detect putatively regulatory binding sites in the genome, we used a combination of computational prediction and experimental data. Position weight matrices for 118 transcription factor binding motifs were used to find TFBS motif matches in the genome. We intersected these motif matches with experimentally defined open chromatin regions to define putatively functional TFBSs. Motif matches not occurring within open chromatin were used as control, putatively non-functional sites. Comparisons between these functional and control sites underlie our methods, and we develop novel metrics to assess the relative rates and functional impact of cancer mutations at putatively functional regulatory sites.

**Results**

We observe a strong and significant excess of mutations at functional binding sites across TFs, and show that the substitutions that accumulate in cancers are often more disruptive than those that are tolerated as germline variants. Putatively functional CTCF binding sites suffer an exceptionally high mutational load in cancer relative to control sites, and those involved in the architecture of higher order chromatin structures are the most highly mutated. The mutational load at CTCF-binding sites appears to be dominantly determined by replication timing and the mutational signature of the chromosome configuration in cancer.

**Conclusion**

We show that mutations at active TFBSs are common in tumours, they appear to accumulate largely unchecked by selective processes and are independent of mutations in coding sequences, exhibiting distinct rates among tumour types. Our study thus underlines the functional importance and fragility of the regulatory genome in cancer.

**Disclosure of interest**

None declared.
detailed molecular characterization of one of these genomic configurations, the tandem duplicator phenotype (TDP).

Methods
We combined whole genome sequencing (WGS) data from 277 human genomes representing 11 cancer types and devised a robust genomic metric able to identify cancers with a chromosome called tandem duplicator phenotype (TDP) characterized by frequent and distributed tandem duplications (TDs).

Results
Enriched only in triple negative breast, ovarian, endometrial, and liver cancers, TDP tumors jointly exhibit TP53-mutations, low expression of BRCA1, and increased expression of DNA replication genes pointing at re-replication in a defective checkpoint environment as a plausible causal mechanism. The resultant TDs in TDP augment global oncogene expression and disrupt tumor suppressor genes. Importantly the TDP strongly correlates with cisplatin sensitivity in both triple negative breast cancer cell lines and primary patient-derived xenografts.

Conclusion
We conclude that the TDP is a common cancer chromotype that coordinately alters oncogene/tumor suppressor expression with potential as a marker for chemotherapeutic response.

Disclosure of interest
None declared.

O16
Modeling genetic interactions associated with molecular subtypes of breast cancer
B. Ji, A. Tyler, G. Ananda, G. Carter
The Jackson Laboratory, Bar Harbor, ME, USA
Correspondence: G. Carter – The Jackson Laboratory, Bar Harbor, ME, USA
Human Genomics 2016, 10(Suppl 1):O16

Objectives
The characterization of mRNA-expression subtypes in breast cancer facilitates genomic and genetic studies to identify biological processes that drive distinct molecular subtypes and elucidates the potential feasibility of subtype-specific drug targets. However, such therapies tend to have limited efficacy, often due to unpredicted compensation in the network of mutations. Polygenic models that account for multiple somatic mutations and their interactions can potentially improve target selection and provide a more detailed view of tumor genetic architecture.

Methods
We addressed this problem with a multi-trait genetic interaction analysis of copy-number variation and gene expression data from breast cancer samples in The Cancer Genome Atlas. Modules of co-expressed genes were derived and assessed for biological function and genetic association with mutations in oncogenes and tumor suppressors. Summary module phenotypes with pleiotropic associations, the tandem duplicator phenotype (TDP).

Results
We observed widespread evidence of genetic redundancy, in which two mutations combine to yield a less than additive effect that is similar to either mutation in isolation. In addition, we also identified interacting mutations that combinatorially associate with distinct modules and subtypes in a non-additive manner. These somatic mutant combinations were often predictive of molecular subtypes when single mutations were not.

Conclusion
Accounting for interactions among somatic mutations in tumor samples reveals high genetic redundancy and complex regulatory hypotheses for breast cancer subtypes. Our work demonstrates how integrative genetic and genomic analysis can be used to generate more precise hypotheses for tumor genetics, which may be used to prioritize therapeutic targets for robust tumor suppression.

Disclosure of interest
None declared.

O17
Recurrent somatic mutation in the MYC associated factor X in brain tumors
H. Nikbakht1, M. Montagne2, M. Zeinieh3, A. Harutyunyan1, M. Mcconechy1, N. Jabado1, P. Lavigne4, J. Majewski1
1Human Genetics, McGill University, Montreal, Quebec, Canada;
2Biochemistry, Sherbrooke University, Sherbrooke, Quebec, Canada;
3Pediatrics, McGill University, Montreal, Quebec, Canada
Correspondence: H. Nikbakht – Human Genetics, McGill University, Montreal, Quebec, Canada
Human Genomics 2016, 10(Suppl 1):O17

Objectives
Activation of MYC pathway has been shown in diverse cancers. MYC Associated Factor X (MAX) plays a key role in the MYC-MAX-MAD gene regulatory network; however, its direct involvement in cancer has not yet been reported. Here we report discovery of a novel recurrent somatic mutation in MAX in brain tumors and study its effects on the development and progression of tumors.

Methods
We found a mutation on Arg 51 residue to Glu in MAX gene in a patient with bilateral thalamic pediatric astrocytoma in which the primary tumors (left and right thalamus) had nearly identical mutation profiles except for the presence of the MAX R51Q only in one.

We used this unique opportunity to study the effects of this mutation on the progression and development of brain tumors. We performed differential expression on these samples to find the pathways affected by this mutation. Using ChipSeq we studied changes in the chromatin conformation in genes regulated by this network. We used CD experiments, to study how this mutation affects the affinity between Max and other proteins in this family and with DNA.

Results
We screened our dataset and found 7 cases in 180 HGAs exome sequenced by our group (3.8%) with this mutation. We also identified 14 cases in published datasets.

We found that this mutation always appears later in tumor development in subclonal fashion and is accompanied by at least one driver such as H3 K27M.

Our differential expression and ChipSeq experiments revealed lack of a global effect of this mutation but specific effects on groups of genes involved in some pathways such as apoptosis. We also demonstrate that this mutation has no effect on the binding efficacy between proteins in its regulatory network, but a Max R51Q homodimer binds less efficiently to nonspecific DNA than its wild type. It however, only affects the binding between Myc/MAX heterodimer to DNA in E-boxes.

Conclusion
We identify MAX as a new cancer gene, particularly relevant to brain cancer.

Our results show the possible effects of MAX mutation in promoting tumor progression and development. It also suggests the effect of this mutation on the spread of the tumor.

These findings shed new light on the mechanisms underlying cancer progression and the involvement of MYC signalling in development of brain tumors which, in turn, can point us towards new targets for therapeutic approaches.
Disclosure of interest
None declared.

O18
Predictive biomarkers to metastatic pancreatic cancer treatment
J. B. Goldstein1, M. Overman2, G. Varadhachary3, R. Shroff4, R. Wolff4, M. Javle5, A. Futreal6, D. Fogelman7
1Genomic Medicine, MD Anderson Cancer Center, Houston, TX, USA; 2Gastrointestinal Medical Oncology, MD Anderson Cancer Center, Houston, TX, USA
Correspondence: J. B. Goldstein – Genomic Medicine, MD Anderson Cancer Center, Houston, TX, USA
Human Genomics 2016, 10(Suppl 1):O18

Objectives
In 2015, we demonstrated that a strong family history of BRCA related tumors portends a better prognosis in metastatic pancreatic cancer patients. We now investigate if this holds true for more recent patients treated with standard-of-care FOLFIRINOX (FNX) or Gemcitabine/nab-paclitaxel (GA). We hypothesize that targeted sequencing of these tumors for DNA repair pathway aberrations will better predict outcomes than the surrogate marker of family history, which may be subject to patient bias.

Methods
We identified patients with de novo stage 4 pancreatic cancer initially treated at MD Anderson Cancer Center with first-line FNX or GA. We excluded patients with prior surgical resection (bypass was allowed) or radiation as initial therapy, and patients with unknown family history. Survival analysis was performed using the Kaplan-Meier method.

Results
We identified 153 patients initially treated with FNX and 80 patients treated with GA. Median age of the entire cohort was 62 years (36–84), 58% were male. Median OS was 286 and 295 days, respectively. Approximately 5% of patients had a family history of 3 or more BRCA tumors (breast, ovarian, prostate, pancreas). Median OS for these patients was 469 days, as compared to 285, 268, and 296 days for patients with 0, 1, and 2 affected family members. Median survival in patients with 3+ family members affected was 463 days and 511 days for patients on FNX and GA respectively (95% CI 240-636d, 0–1092 d). For patients with 0–2 such family members, median OS was 283 and 268 days, respectively. As expected, ECOG 0–1 and the absence of liver metastases were associated with longer survival. We identified 126 of 153 FNX patients and 51 of 80 GA patients with pathology specimens available for targeted sequencing.

Conclusion
As in our earlier report, we see a trend towards increased survival in patients with 3 or more family members with BRCA related tumors. However, the small number of these patients precludes a definitive assessment. We believe that targeted sequencing of DNA repair pathway and associated genes will better elucidate the mechanism of survival benefit over biased family history.

References

Disclosure of interest
None declared.

O19
DDIT4 gene expression as a prognostic marker in several malignant tumors
L. Bravo1, W. Fajardo1, H. Gomez2, C. Castaneda2, C. Rolfo3, J. A. Pinto2
1Escuela de Medicina Humana, Universidad Privada San Juan Bautista, Lima, Peru; 2Unidad de Investigación Básica y Traslacional, Oncosalud-AUNA, Lima, Peru; 3Oncology Department, University Hospital Antwerp, Antwerp, Belgium
Correspondence: J. A. Pinto – Unidad de Investigación Básica y Traslacional, Oncosalud-AUNA, Lima, Peru
Human Genomics 2016, 10(Suppl 1):O19

Objectives
The DDIT4 gene (DNA-damage-inducible transcript 4) encodes a protein related to adverse environmental conditions, whose action is the inhibition of mTOR. In a recent work we found DDIT4 levels was associated with the outcome in triple negative breast cancer (J Clin Oncol 33, 2015 (suppl; abstr 1097)). There are not previous reports relating DDIT4 with prognosis of cancer patients. Our aim in this study was to explore the influence of this gene in several types of malignant tumors.

Methods
We evaluated the influence of DDIT4 expression in the outcome (either, disease-free survival or progression-free survival or overall survival). Univariate Cox regression analysis of DDIT4 in the online platforms KM Plotter (http://kmplot.com/) and SurvExpress (http://bioinformatica.mty.itesm.mx/) was done. Datasets were split based in the median of expression. Cancer types evaluated include: Acute Myeloid Leukemia, Brain Cancer, Breast Cancer, Bone Cancer, Cervical Cancer, Head and Neck Cancer, Hematological Cancer, Liver Cancer, Lung Cancer, Pancreatic Cancer, Ovarian Cancer and Prostate Cancer.

Results
A high level of DDIT4 was significantly associated with a worse outcome in breast cancer (n=4142), P=3x10−14 (HR=1.64, CI95%: 1.44-1.87); acute myeloid leukemia (n=168), P=3.47x10−3 (HR=2.31, CI95%: 1.55-3.43); glioblastoma multiforme (n=538), P=0.005809 (HR=1.31, CI95%:1.08-1.59); ovarian cancer (n=1648), P=0.0096 (HR=1.2, CI95%: 1.04-1.37); head and neck squamous cell carcinoma (n=283), P=0.03347
Those related with mTOR inhibition.

In addition elucidation of DDIT4 participation in cancer aggressiveness could lead to improve the therapeutic strategies, mainly those related with mTOR inhibition.

Conclusion

DDIT4 is a promising molecular marker for outcome in several types of cancer. In addition elucidation of DDIT4 participation in cancer aggressiveness could lead to improve the therapeutic strategies, mainly those related with mTOR inhibition.

Disclosure of interest

None declared.

Fig. 2 (abstract O19).

O20

Spatial organization of the genome and genomic alterations in human cancers

K. C. Akdemir1, L. Chin2, A. Futreal1, ICGC PCWG Structural Alterations Group

1Genomic Medicine, MD Anderson Cancer Center, Houston, TX, USA;
2University of Texas System, Houston, TX, USA

Correspondence: K. C. Akdemir – Genomic Medicine, MD Anderson Cancer Center, Houston, TX, USA

Human Genomics 2016, 10(Suppl 1):O20

Objectives

The hierarchical folding of genomic DNA within the nucleus is closely related with transcriptional regulation. Recent chromosome conformation studies have suggested that mammalian chromosomes are structured into tissue-invariant topologically associating domains (TADs) where the DNA within a domain is interacting more frequently than with regions in other domains. Genes within the same TADs represent similar gene-expression, histone-modification profiles. Therefore regions separating different TADs (boundaries) have important roles in reinforcing the stability of this domain-wide organizations. TAD boundary disruptions in human limb malformations and cancer lead to dysregulation of certain genes, due to de novo promiscuous enhancer exposure to promoters. Here we sought to identify relationship between genomic architecture and genomic alterations in human cancers.

Methods

We utilized approximately 200 thousand somatic genomic alterations (deletions, inversions, duplications) and more than 34 million somatic mutations from 2575 high-coverage whole genome sequencing data across 45 different cancer studies with paired normal samples. We integrated mutations, gene expression and structural alterations with TAD boundaries that we have identified from 5 different human cell lines, representing three different germ layers.

Results

Our analysis revealed a strong correlation between the mutational landscape and the TAD organization of the genome. In addition, we found that TAD boundaries inflicted structural alterations that not only affected nearby gene regulation but also the distribution of mutations in human cancers.

Conclusion

Structural alterations affecting the spatial organization of the human genome, could lead to dysregulation of genes as well as aberrant mutation distributions in human cancers.

Disclosure of interest

None declared.

O21

Landscape of targeted therapies in solid tumors

S. Patterson, C. Statz, S. Mockus
The Jackson Laboratory for Genomic Medicine, Farmington, CT, USA

Correspondence: S. Patterson – The Jackson Laboratory for Genomic Medicine, Farmington, CT, USA

Human Genomics 2016, 10(Suppl 1):O21

Objectives

Precision medicine initiatives in oncology focus on specific genetic aberrations as predictive biomarkers for targeted therapies. Next-generation sequencing technologies have driven a projectile shift in patient management through somatic tumor profiling. Due to the rapid pace of this ensuing momentum, it is difficult to grasp such a dynamic landscape. Therefore, an analysis of the targeted therapy landscape was conducted and methods employed are disseminated to foster interoperability among datasets.

Methods

A Clinical Knowledgebase (CKB) was created to capture and rapidly retrieve therapeutic information related to patient molecular aberrations. One requirement was the development of a drug class controlled vocabulary to categorize drugs relative to their target specificity, including both pan-level and more gene specific targeted drugs. Additionally, to support capture of combination therapies, one or more single drug entries can be concatenated to a therapy. Drug classes are annotated to molecular variants and therapies are annotated to complex molecular profiles. Using the JAX-CKB, an analysis was conducted on the number and types of targeted therapies for solid tumors associated with 358 genes and in actively recruiting clinical trials.

Results

The CKB drug class ontology currently contains 198 terms, consisting of 113 parent and 83 child terms. There are 1006 targeted therapies in CKB and of these, 59 are FDA approved. Pan drug classes include PI3K inhibitors and mTOR inhibitors, which contain 34 and 41 individual drugs within each class, respectively. The drug class VEGFR inhibitors (Pan) has the highest number of hits in actively recruiting clinical trials, and 19 drug classes, including EZH2 inhibitor and p53 activator, are represented in a single solid tumor clinical trial. Furthermore, the most common drug in solid tumor clinical trials is Bevacizumab.

Conclusion

Consistency and interoperability of knowledgebases to support clinical next-generation sequencing is pivotal. The JAX-CKB, described here, is built upon controlled vocabularies and ontologies to achieve this mission. Methods on the design and build are shared to foster collaborative processes in this rapidly evolving NGS domain. Furthermore, analysis of content regarding targeted therapies provides an objective view of clinical trial research investigating targeted therapies in solid tumors.
GENOMIC ANALYSIS REVEALS NOVEL DRIVERS AND PROGRESSION PATHWAYS IN SKIN BASAL CELL CARCINOMA


1Department of Genetic Medicine and Development, University of Geneva, Geneva, Switzerland; 2Department of Dermatology, Hospital of Valais, Sion, Switzerland; 3Department of Pathology, NYU School of Medicine, New York, NY, USA; 4Department of Physics, University of Connecticut, CT, USA; 5Department of Dermatology, University Hospitals of Geneva, Geneva, Switzerland; 6Swiss Institute of Bioinformatics, Swiss Institute of Bioinformatics, Lausanne, Switzerland; 7Institute of Information Transmission Problems, Russian Academy of Sciences, Moscow, Russian Federation; 8Department of Molecular Oncology, Genentech Inc, San Francisco, CA, USA; 9Service of Clinical Pathology, University Hospitals of Geneva, Geneva, Switzerland; 10Department of Genetic Medicine and Development, University of Geneva Medical School, Geneva, Switzerland; 11University of Paris 7, Hospital of Saint-Louis, Paris, France; 12Service of Genetic Medicine, University Hospitals of Geneva, Geneva, Switzerland; 13Department of Biochemistry and Molecular Biology, University of Würzburg, Würzburg, Germany

Correspondence: S. N. Nikolaev – Department of Genetic Medicine and Development, University of Geneva, Geneva, Switzerland

Human Genomics 2016, 10(Suppl 1):O22

Objectives
Basal cell carcinoma of the skin (BCC) is the most common malignant neoplasm in humans. BCC is primarily driven by aberrant activation of the Sonic Hedgehog (Hh) pathway. However, its extensive phenotypic variation remains to be explained.

Methods
The genetic profiling of 293 BCCs revealed the highest mutation rate observed in cancer (65 Mutations/Mb), with strong prevalence of UV-light signature mutations.

Results
85% of BCCs harbored mutations in Hh pathway genes: mutually exclusive PTCH1 (73%) and SMO (20%) (P=6.6x10−16), SUFU (8%), and in TPS3 (61%). 85% of BCCs also harbored additional driver mutations in other genes implicated in BCC tumorigenesis. Recurrent driver mutations were observed in MYCN (30%), PPP6C (15%), STK19 (10%), LATS1 (8%), ERBB2 (4%), PIK3CA (2%), RAC1 (1%) and N/K/H-RAS (2%). Loss of function (LoF) and deleterious missense mutations were observed in PTP1N4 (23%), RB1 (8%) and FBXW7 (5%). In line with the mutational profiles detected by DNA sequencing, we observed activation of the Hh pathway as well as upregulation of target genes of the Hippo-YAP pathway and activation of MYCN target genes in RNAseq experiments.

Conclusion
The functional analysis of the novel tumorigenic driver mutations in MYCN, PTP1N4 and LATS1 demonstrates their relevance in BCC tumorigenesis and provides an expanded molecular understanding of BCC.

Disclosure of interest
None declared.

O23
Identification of differential biomarkers of hepatocellular carcinoma and cholangiocarcinoma via transcriptome microarray meta-analysis

S. Likhitrattanapisal
Department of Biology, Faculty of Science, Mahidol University, Bangkok, Thailand

Human Genomics 2016, 10(Suppl 1):O23

Objectives
Hepatocellular carcinoma (HCC) and cholangiocarcinoma (CCA) are the members of hepato-biliary diseases. As both HCC and CCA arise from similar cell types, they often exert high levels of similarity in terms of phenotypic characteristics, thus leading to difficulties in HCC and CCA differential diagnoses. In this study, a meta-analysis was performed on HCC and CCA transcriptome microarray data for the purpose of investigating differential transcriptome networks and potential biomarkers of CCA and HCC.

Methods
Raw data from 9 HCC and CCA gene expression microarray datasets, consisting 1,185 samples in total, were methodologically compiled and analyzed. For determining differentially-expressed genes in the cancers, gene expression were compared between cancer and its respective normal samples (HCC vs Normal Liver and CCA vs Normal Bile Duct) using t-test and k-fold validation (P < 0.05).

Results
Comparing to normal samples, 226 differentially-expressed genes were specifically observed in HCC, 249 genes in CCA, and 41 genes in both. Gene Ontology and KEGG pathway enrichment analyses showed different patterns between functional transcriptome networks of HCC and CCA. Cell cycle and glycolysis/gluconeogenesis pathways were specifically affected in HCC whereas complement and coagulation cascades as well as glycine, serine and threonine metabolism were predominantly presented in CCA.

Conclusion
Our meta-analysis revealed different dysregulation in transcriptome networks between HCC and CCA. Some genes in these networks were selectively discussed in the context of HCC-CCA transition, unique characteristics of HCC and CCA, and their potentiality as HCC/CCA differential biomarkers.

Disclosure of interest
None declared.

References
Clinical validity and actionability of multigene tests for hereditary cancers in a large multi-center study

S. Lincoln, A. Kurian, A. Desmond, S. Yang, Y. Kobayashi, J. Ford, L. Ellisen

1Invitae, San Francisco, CA, USA; 2Stanford Medical Center, Palo Alto, CA, USA; 3Massachusetts General Hospital, Boston, MA, USA; 4Stanford Medical Center, San Francisco, CA, USA

Correspondence: S. Lincoln – Invitae, San Francisco, CA, USA

O24

Clinical genetic testing is rapidly evolving with the introduction of next-generation sequencing (NGS) however questions remain about these new tests. First, can NGS methods be deployed that deliver equal or improved performance vs. traditional methods on the full spectrum of (often complex) disease causing variants? Second, do expanded NGS tests provide medical benefits which outweigh the increased uncertainty that naturally follows from testing more genes in more patients? In recently published work [1,2] we tested a large panel of cancer risk genes by NGS in a clinically representative population to evaluate these questions. Here we expand upon that work.

Methods

We tested a large panel of 25–32 cancer risk genes by NGS in a representative cohort of over 1000 patients meeting current medical guidelines for BRCA1/2 testing. Traditional genetic test results were available for the patients for comparison. Using an interpretation system (Sherloc) based on ACMG 2015 guidelines and employing only publicly available data, variants uncovered by NGS were classified.

We established a uniform algorithm based on current practice guidelines to recommend management actions for the non-BRCA1/2 positive individuals, and we evaluated which of these recommendations would represent changes in management above and beyond any recommendations based on personal and family history alone.

Results

We find 100% concordance with traditional methods on both sequence and copy-number alterations using a battery of 5 calling algorithms and associated biochemistries, we find 99.8% concordance with BRCA1/2 classifications produced by a different laboratory that uses a large proprietary database. Finally, we find that 52% of genetic test results positive for genes other than BRCA1/2 would warrant consideration of a change in care for mutation-positive patients under current medical practice guidelines.

Conclusion

In appropriately referred patients, multi-gene panel testing yields clinically relevant findings with potential management impact, for substantially more patients than does BRCA1/2 testing alone.

References

1. Lincoln, JMD 2015
2. Desmond, JAMA Oncol 2015

Disclosure of interest


O25

Correlation with tumor ploidy status is essential for correct determination of genome-wide copy number changes by SNP array


1Pathology & Immunology, Baylor College of Medicine, Houston, TX, USA; 2Pathology, Texas Children’s Hospital, Houston, TX, USA

Correspondence: T. L. Peters – Pathology & Immunology, Baylor College of Medicine, Houston, TX, USA

Human Genomics 2016, 10(Suppl 1):O25

Objectives

Neuroblastoma, the most common extra-cranial solid tumor in the pediatric population, is a histologically and clinically heterogeneous neoplasm. Tumors characterized only by whole chromosome changes tend to act favorably, whereas tumors with MYCN gene amplification and/or segmental chromosomal aberrations have poor outcomes. Given the clinical relevance, our aim was to verify the accuracy of OncoScan FFPE SNP Array (Affymetrix) in assessing genome-wide copy number changes in tumor samples by comparison to other tumor ploidy testing methods.

Methods

39 neuroblastic tumors from 38 patients were analyzed using the OncoScan FFPE SNP Array at a pediatric hospital. Tumor slides were macrodissected to increase tumor purity, genomic DNA was isolated and arrays hybridized according to manufacturer’s protocol. Data was analyzed using the OncoScan Console and results viewed using Chromosome Analysis Suite (ChAS) and OncoScan Nexus Express. Copy number results determined by SNP array were compared to ploidy results obtained by karyotype analysis and/or flow cytometry. Additionally, chromosome 1 and 2 aneuploidy data were used as a surrogate ploidy marker in cases where cytogenetics and flow cytometry were unavailable.

Results

Data were obtained for 33 of the 39 samples. Review showed that 3 of the 33 samples required centering of the tumor ploidy baseline. Two samples from 2 lesions in one patient showed widely discordant copy number calls by the software, with one assigned a near tetraploid status and the other a near diploid status. Karyotype analysis confirmed a near tetraploid state. Correlation by karyotype, flow cytometry or chromosome 1 and 2 aneuploidy revealed an additional 4 discordant cases (total of 5/33 cases or 15%).
Conclusion
Despite complex algorithms used by the OncoScan software to assign copy number calls, in 15% of the analyzed cases a 2nd method was necessary to correctly assign tumor ploidy baseline. The complex chromosomal copy number changes present in tumors, in addition to tumor impurity, heterogeneity, and poor sample quality, can challenge the software's ability to correctly assign ploidy state. Our results demonstrate that a second independent method may be necessary in complex tumor cases to correctly assign ploidy that truly reflects tumor biology and may be necessary for correct patient management.

Disclosure of interest
None declared.

O26
Nanochannel based next-generation mapping for interrogation of clinically relevant structural variation
BioNano Genomics, Inc., San Diego, CA, USA
Correspondence: A. Hastie – BioNano Genomics, Inc., San Diego, CA, USA
Human Genomics 2016, 10(Suppl 1):O26

Objectives
Structurally complex loci underlie many diseases. These loci can be very challenging to resolve by currently available methods such as karyotyping, clinical array, PCR-based tests, and NGS. Next-generation mapping by BioNano Genomics Irys® System offers a high-throughput, genome-wide method able to interrogate genome structural differences hundreds of kilobase pairs and span interspersed and even long tandem repeats making it ideally suitable for elucidating the structure and copy number of complex regions of the genome, such as complex pseudogene and paralogous gene families. Clinically relevant regions often contain genes with paralogs and other complex repetitive structures complicating the interpretation of data and diagnosis of disease. We present several examples of genetic loci that can be easily interrogated with genome map data including tandem repeats, paralogous gene families, and loci flanked by segmental duplications.

Methods
Some open reading frames or entire genes are randomly amplified with variable copy number such as tRNAs, kringle IV, and D4Z4. The LPA gene contains variable copies of a repeat, kringle IV, that results in different lengths of the resultant Lp(a) protein; related to coronary heart disease, cerebrovascular disease, atherosclerosis, thrombosis, and stroke. Tandem repeat is D4Z4, associated with facioscapulohumeral muscular dystrophy (FSHD), with a low copy number (<10 units), occurring in 95% of FSHD cases.

Results
We show that the Irys System can accurately measure the copy number of the kringle IV domain and D4Z4. A second class of complex structural variation are those that involve genes with paralogs such as amylase and UGT2B17, two genes whose copy number have been shown to be involved in human health. We show deletions of UGT2B17 in a family trio and > 10 different structures at the Amylase region. The third class of genomic variation are those flanked by segmental duplications, especially important because spontaneous rearrangements are common between paralogous segmental duplications causing copy number aberrations and translocation, thus resulting in developmental disorders, such as the 22q11.2 deletion syndrome mediated by segmental duplication rearrangements.

Conclusion
We show the assembly of the region, including the normal and pathogenic alleles, using molecules that span and disambiguate the structure of the segmental duplications.

Disclosure of interest
None declared.

O27
Mutation spectrum in a pulmonary arterial hypertension (PAH) cohort and identification of associated truncating mutations in TBX4
C. Gonzaga-Jauregui1, L. Ma2, A. King1, E. Berman Rosenzweig3, U. Krishnan1, J. G. Reid1, J. D. Overton1, F. Dewey1, W. K. Chung1
1Regeneron Genetics Center, Regeneron Pharmaceuticals, Tarrytown, New York, NY, USA; 2Department of Pediatrics, New York, NY, USA; 3Department of Medicine, Columbia University Medical Center, New York, NY, USA
Correspondence: C. Gonzaga-Jauregui – Regeneron Genetics Center, Regeneron Pharmaceuticals, Tarrytown, New York, NY, USA
Human Genomics 2016, 10(Suppl 1):O27

Objectives
To identify the genetic determinants of Pulmonary Arterial Hypertension (PAH) in a cohort of pediatric PAH patients.

Methods
We performed whole-exome sequencing (WES) in a cohort of 60 probands with PAH and family members when available (180 total individuals) without a molecular diagnosis after most of the series was screened for mutations in BMPR2. In addition, we performed WES in additional 118 singleton cases. We screened all samples for variants in known PAH associated genes and performed trio-based analysis to identify novel candidate PAH genes.

Results
We identified known and novel mutations in the known PAH genes. In addition we identified novel truncating variants in TBX4 occurring de novo or inherited from an asymptomatic parent in 5 patients and a de novo predicted deleterious nonsynonymous variant in one additional patient.

Conclusion
TBX4 is a transcription factor of the T-box gene family. It is expressed in a variety of tissues during early mouse development including the atrium of the heart, the limbs, and the mesenchyme of the lung and trachea. TBX4, jointly with TBX5, has been shown to interact with FGF10 during lung growth and branching. Mutations in TBX4 have been previously reported to cause small patella syndrome, an autosomal-dominant skeletal dysplasia characterized by patellar aplasia or hypoplasia. A study in 2012 [1] identified an association of TBX4 mutations with PAH in 6 patients.

References

Disclosure of interest
**O28**

NORTH CAROLINA macular dystrophy (MCDR1): mutations found affecting PRDM13

K. Small1, A. DeLuca2, F. Cremers3, R. A. Lewis3, V. Puech5, B. Bakall6, R. Silva-Garcia1, K. Rohnschneider1, M. Leys8, F. S. Shaya1, E. Stone1

1Molecular Insight Research Foundation, Glendale; 2PhenoDB and genematcher, solving unsolved whole exome sequencing (WES) data.

Objectives

To identify mutations causing North Carolina macular dystrophy (NCMD, MCDR1).

Methods

We performed targeted Nex Gen sequencing of the MCDR1 region (870kb) in 8 affected individuals from 3 families representing 3 different haplotypes affected with chromosome 6 linked NCMD (MCDR1). In addition to our original 11 MCDR1 families recently published (141 total subjects), we now have an additional cohort of 23 families with the NCMD phenotype available for study (total of 367 subjects, 32 families).

Results

We initially found 14 rare variants spanning 870kb of the disease-causing allele. One of these variants (V1, ch6:1000400906) was absent from all published databases and all 261 controls, but was found in a total of 13 NCMD kindreds. This variant lies in a DHS upstream of both the PRDM13 and CCNC genes.

Sanger sequencing of 1 kb centered on V1 was performed in the 118 affected and 33 unaffected members of the 21 NCMD families. A complete duplication of the PRDM13 gene was also discovered in a single family (V4). The 4 mutations V1 to V4 segregated perfectly in the 242 imprinted genes identified 4,337 rare functional variants. These variants are being further evaluated to define causality.

Conclusion

We identified 4 rare mutations in a non-coding region, each capable of arresting human macular development by causing over expression of PRDM13. Additional families with the NCMD phenotype continue to support that these mutations are causative of MCDR1 / NCMD.

References


Disclosure of interest

None declared.

**O29**

PhenoDB and genematcher, solving unsolved whole exome sequencing data


1Johns Hopkins University School of Medicine, Baltimore, MD, USA; 2FS Consulting, Salem, MA, USA; 3Center for Inherited Disease Research, JHU SOM, Baltimore, MD, USA

Correspondence: N. L. Sobreira – Johns Hopkins University School of Medicine, Baltimore, MD, USA

Human Genomics 2016, 10(Suppl 1):O29

Objectives

To identify the causative variant(s) and gene(s) of rare Mendelian phenotypes by the re-analysis of unsolved whole exome sequencing (WES) data.

Methods

To address some of these cases, we have incorporated maternal and paternal imprinting analysis and polygenic analysis to the PhenoDB Variant Analysis tool. We also analyzed WES data from 1063 samples for rare, functional variants in known imprinted genes, in the genes on pseudoautosomal regions, genes that escape X-inactivation, and genes on chromosome Y. To facilitate data sharing as well as improve the search for patients or model organisms with variants in specific candidate genes we have also been adding capabilities to GeneMatcher (www.genematcher.org). In GeneMatcher there is an option to match based upon OMIM number, genomic location and, as of October 2015, on phenotypic features. As part of the Matchmaker Exchange (MME) (http://matchmakerexchange.org/), we have also developed an API that was implemented in August 2015 and allows the GeneMatcher users to submit their data to query PhenomeCentral and/or DECIPHER. Also, as part of the MME we have been working with other matchmaker databases on the API implementation to connect them to GeneMatcher and have been working on the version 2.0 of the API that will allow for more detailed queries.

Results

We found that the genes in the pseudoautosomal regions are not captured by the Agilent SureSelect v4 baits that we used to sequence these samples. The analysis of variants in the genes on chromosome Y identified 52 rare functional variants and the analysis of variants in the 242 imprinted genes identified 4,337 rare functional variants. These variants are being further evaluated to define causality.

As of December 2015, 3,568 genes were submitted to GeneMatcher by 984 individuals from 48 countries and 1252 matches (60 matches with PhenomeCentral and 34 matches with DECIPHER).

Conclusion

The GeneMatcher approach has enabled collaborations and the description of novel Mendelian phenotypes and novel Mendelian genes like SPATA5, HNRNPK and TELO2. We expect that further use of GeneMatcher and other MME matchmaker databases will enable many new gene/phenotype connections and that the full impact this approach will be revealed in the published literature over the next years.

Disclosure of interest

None declared.

**O30**

Baylor-Johns Hopkins Center for Mendelian genomics: a four year review


1Human Genome Sequencing Center, Baylor College of Medicine, Houston, TX, USA; 2Department of Molecular and Human Genetics, Baylor College of Medicine, Houston, TX, USA; 3Mckusick-Nathans Institute of Genetic Medicine, Johns Hopkins School of Medicine, Baltimore, MD, USA

Correspondence: S. N. Jhangiani – Human Genome Sequencing Center, Baylor College of Medicine, Houston, TX, USA

Human Genomics 2016, 10(Suppl 1):O30

Objectives

At its inception in 2011 the Baylor-Johns Hopkins Center for Mendelian Genomics (BHCMM), as one of three NIH funded Centers for Mendelian Genomics (CMGs), began its efforts towards: i) novel gene/mutation discovery, ii) elucidating the molecular bases of disease, iii) understanding the genetic susceptibility to disease traits, and iv) determining the genetic/genomic architecture of disease. Collectively
the CMGs have sequenced ~19,000 patient samples in collaboration with more than 500 investigators from 36 countries in the past four years. The BHCMG has learned many lessons from its contribution of 5,200 exomes ranging in 475 phenotypes and presented in 82 publications.

Methods
The Human Genome Sequencing Center (HGSC) at the Baylor College of Medicine has generated 46 TB of whole exome sequencing (WES) data using the HGSC-VCrome capture reagent and now includes ‘Spike-in PKv2’ to capture more difficult regions and additional gene targets. The HGSC-VCrome capture reagent, along with a multiplex strategy and use of full-length blocking oligos employed for hybridization, has yielded 7.7Gb of data per exome providing a coverage of 96% at 20X or greater. The Spike-in PKv2 reagent is comprised of 3,643 additional unique gene targets derived from GeneTests, OMIM, selected cancer genes and Baylor Miraca Genetics Laboratory positive cases. The addition of this reagent converts >700-800 genes from partially covered to fully covered at ≥20X coverage.

Results
Success rates in this program have varied by phenotype and cohort collections ranging from 37% to 85%. The BHCMG has established valuable sample acquisition approaches and resources, enhanced sequencing methodology, curated a well-characterized phenotype-rich genetic database enabling genotype/phenotype relationships and encouraged collaborative efforts (i.e. GeneMatcher) to implicate 491 genetic database enabling genotype/phenotype relationships and valuable sample acquisition approaches and resources, enhanced sequence is particularly applicable to SV typing.

Methods
The REWG has developed a Framework for Responsible Sharing of Genomic and Health-Related Data (REWG) specifically promotes the legal interoperability of every citizen to benefit from the progress of science. This human rights basis gives the Framework political and legal dimensions that reach beyond the moral appeals of bioethics. Specific policies build on the Framework. The Consent policy provides guidance for balancing individual autonomy with the public good, and addresses sharing of legacy data where consent is silent on data sharing. The Regulatory and Ethics Working Group (REWG) establishes Task Teams with diverse, international membership across sectors to develop tools and solutions to facilitate data sharing. Existing Task Teams address Consent, Privacy & Security, Accountability, Paediatrics, Ageing and Dementia, Registered Access, Participant Values, and Machine Readable Consent.

Results
Using BAA on a trio sequenced by the Personal Genome Project (PGP), the BAA variant caller detected a 3.4kb insertion inherited in the offspring that matched an alternate allele assembly now in GRCh38. The breakpoint and sequence of the insert were reported. The resolution of this inserted sequence allowed for five SNPs and an indel that were inherited from the father and a single SNP inherited from the mother to be distinguished in the offspring.

Conclusion
This level of resolution and accuracy in calling allows for structural variants, and even differences between structural variants, to be compared across individuals. This is important both for understanding the etiology of disease in larger studies as well as identifying de novo variants in an offspring in a clinical setting. Here, we further present results from 100 HiSeq X samples sequenced at 30x, including multiple classes of structural variants and multi-sample classification of shared breakpoints.

References

Disclosure of interest
None declared.

O31
Using read overlap assembly to accurately identify structural genetic differences in an Ashkenazi Jewish Trio
S. Shekar1, W. Salerno2, A. English3, A. Mangubat4, J. Brustle1
1Spiral Genetics, Seattle, WA, USA; 2Human Genome Sequencing Center, Baylor College of Medicine, Houston, TX, USA
Correspondence: S. Shekar – Spiral Genetics, Seattle, WA, USA
Human Genomics 2016, 10(Suppl 1):O31

Objectives
Accurately identifying genetic differences between individuals or within samples taken from the same individual (tumor with normal control) is important to understanding the etiology of diseases, particularly for disease areas where large structural changes in the genome have been associated with the disease, such as neurological conditions,cardiological conditions and cancer. In clinical practice, identifying a previously uncharacterized de novo SV in an offspring that could be causing a condition is challenging with current methods that often have high false discovery rates.

Methods
Here, we present Biograph Anchored Assembly (BAA), an SV caller using whole read overlap assembly of reads that do match the reference exactly. In a previous study with next-generation sequencing of the reference individual HS1011 (English et al. (2015)), the method has been shown to have high sensitivity compared to other SV callers and a false discovery rate of less than 5%. The method is based upon the BioGraph data storage format (BAF). The BAF is a specialized index of the read overlap graph of a genome that can be queried up to one million times a second. Querying by both coordinate and sequence is particularly applicable to SV typing.

Results
Using BAA on a trio sequenced by the Personal Genome Project (PGP), the BAA variant caller detected a 3.4kb insertion inherited in the offspring that matched an alternate allele assembly now in GRCh38. The breakpoint and sequence of the insert were reported. The resolution of this inserted sequence allowed for five SNPs and an indel that were inherited from the father and a single SNP inherited from the mother to be distinguished in the offspring.

Conclusion
This level of resolution and accuracy in calling allows for structural variants, and even differences between structural variants, to be compared across individuals. This is important both for understanding the etiology of disease in larger studies as well as identifying de novo variants in an offspring in a clinical setting. Here, we further present results from 100 HiSeq X samples sequenced at 30x, including multiple classes of structural variants and multi-sample classification of shared breakpoints.

References

Disclosure of interest
None declared.

O32
Legal interoperability: a sine qua non for international data sharing
A. Thoragood, B. M. Knoppers, Global Alliance for Genomics and Health - Regulatory and Ethics Working Group Centre of Genomics and Policy, McGill University, Montreal, Quebec, Canada
Correspondence: A. Thoragood – Centre of Genomics and Policy, McGill University, Montreal, Quebec, Canada
Human Genomics 2016, 10(Suppl 1):O32

Objectives
The successful translation of genomic discovery into improvements in human health hinges on the effective and responsible sharing of genomic and health related data. The Global Alliance for Genomics and Health (GA4GH) brings together over 375 leading healthcare, research, disease advocacy, life science, and information technology organizations committed to establishing harmonized approaches to data sharing. The Regulatory and Ethics Working Group (REWG) of the GA4GH specifically promotes the legal interoperability of data.

Methods
The REWG establishes Task Teams with diverse, international membership across sectors to develop tools and solutions to facilitate data sharing. Existing Task Teams address Consent, Privacy & Security, Accountability, Paediatrics, Ageing and Dementia, Registered Access, Participant Values, and Machine Readable Consent.

Results
The REWG has developed a Framework for Responsible Sharing of Genomic and Health-Related Data, which aims to activate the human right of every citizen to benefit from the progress of science. This human rights basis gives the Framework political and legal dimensions that reach beyond the moral appeals of bioethics. Specific policies build on the Framework. The Consent policy provides guidance for balancing individual autonomy with the public good, and addresses sharing of legacy data where consent is silent on data sharing. The Privacy and Security policy emphasizes that safeguards should be proportionate to the risk of harm to patients. The new Accountability Policy provides best practices for transparency of data handling, as well as processes for monitoring and responding to non-compliance with data sharing standards.
Conclusion
In addition to these policies, ongoing initiatives within the REWG are tackling a host of related questions. What language is appropriate for consent to broad data sharing? Is there a middle ground between open and controlled access? Can conditions of data access be rendered machine readable, so as to enable automated data discovery? Can researchers be held accountable for not sharing data where patients have consented to broad sharing? And how do patients and the public feel about sharing their data for broad research purposes?

References

Disclosure of interest
None declared.

O33
High throughput screening platform of competent sineups: that can enhance translation activities of therapeutic target
H. Takahashi1, K. R. Nitta1, A. Kozuhara1, A. M. Suzuki1, H. Sharma1, D. Cotella2, C. Santoro3, S. Zucchelli3, S. Gustincich3, P. Carninci1
1Center for Life Science Technologies, Division of Genomic Technologies, RIKEN, Yokohama, Japan; 2Dipartimento di Scienze della Salute, Universita’ del Piemonte Orientale, Novara, Italy; 3Area of Neuroscience, SISSA, International School for Advanced Studies, Trieste, Italy
Correspondence: H. Takahashi – Center for Life Science Technologies, Division of Genomic Technologies, RIKEN, Yokohama, Japan
Human Genomics 2016, 10(Suppl 1):O33

Objectives
Short interspersed elements B2 (SINE B2) are broadly distributed transposable elements in whole mouse genome. Evolutionally, SINE B2s share common ancestors with tRNAs. Among the various remarkable functions of recently discovered non-coding RNA functions, we discovered a new class of antisense non-coding RNAs (SINEUPs) that promote translation of partially overlapping sense coding mRNAs with no effects on RNA levels. In order to develop synthetic SINEUPs to up-regulate therapeutically interesting genes, we have determined that SINEUPs function requires two essential domains; one is SINE B2 element, also called the Effector Domain (ED), and the other is overlapping antisense RNA sequence, which provide specificity and is called the Binding Domain (BD). We have produced functional SINEUPs for a PD associate gene, PARK7 (DJ-1), as well as other genes. This synthetic SINEUP specifically enhances translation level of PARK7 mRNAs in human neuronal cell lines. Through a novel high-throughput screening (HTS) system, we aim at further optimization of the ED and BD of SINEUPs to produce very effective SINEUPs against any possible mammalian protein.

Methods
We report here our HTS, which is based on high-resolution automated fluorescent imaging of CeligoS instrument. We screened with the HTS several BDs for a hepatic transcription factor alpha (Hnf4-alpha), which is associated to maturity-onset diabetes of the young type 1.

Results
In addition, we validated that several SINEUPs targeting Hnf4-alpha are able to upregulate translation in mouse hepatoma cells and hepatocyte cells. We also validated that other EDs derived from natural SINE B2 sequences revealed target mRNA specific translation enhancement.

Conclusion
To conclude, synthetic SINEUPs are promising tools for gene/RNA therapy of haploinsufficiencies, and the HTS system is a powerful SINEUPs screening platform.

Disclosure of interest
None declared.

O34
The undiagnosed diseases network international (UDNI): clinical and laboratory research to meet patient needs
J. J. Mulvihill1, G. Baynham1, W. Gahl2, S. C. Groft3, K. Kosaki4, P. Lasko5, B. Melegh1, D. Tarsusco6
1Division of Genomic Medicine, National Human Genome Research Institute, Bethesda, MD, USA; 2Office of Population Health, Department of Health, Perth, Australia; 3Undiagnosed Diseases Program, National Human Genome Research Institute, Bethesda, MD, USA; 4National Center for Advancing Translational Sciences, National Institutes of Health, Bethesda, MD, USA; 5Center for Medical Genetics, Keio University School of Medicine, Tokyo, Japan; 6Department of Biology, McGill University, Montreal, Quebec, Canada; 7Department of Medical Genetics, University of Pecs, Pecs, Hungary; 8National Center for Rare Diseases, Istituto Superiore di Sanita, Rome, Italy
Correspondence: J. J. Mulvihill – Division of Genomic Medicine, National Human Genome Research Institute, Bethesda, MD, USA
Human Genomics 2016, 10(Suppl 1):O34

Objectives
Rare and undiagnosed disorders challenge patients, families, and clinicians. In 2008, NIH started an Undiagnosed Diseases Program (UDP), with the goals of providing answers to patients with mysterious conditions that eluded diagnosis and advancing medical knowledge about diseases. The UDP has expanded in the US, as the Undiagnosed Diseases Network, with 6 additional clinical sites, a coordinating center, 2 DNA sequencing cores, a model organisms screening center, a metabolomics core, and a biorepository. For further expansion, meetings were held in Rome and Budapest with clinical scientists from 7 nations.

Methods
The plan includes launching the UDNI (Australia, Canada, Hungary, Italy, Japan, Sweden, and the United States). The goals are to improve the level of diagnos and care for such patients by common protocols, to facilitate research in disease etiology, and to create a collaborative research community. A comprehensive “–omics” approach would include exomic and genomic sequencing as well as metabolomics. The interim website is http://test.areasl.t.com/udni/home.

Results
To date, several principles are being implemented: Engaging centers of excellence, fostering a collaborative research environment, establishing a cooperative governance structure, designing a common research protocol, providing a uniform patient experience, collecting data by recognized standards, protecting patient data, observing ethical, legal, and social guidelines, devising broad data sharing, stimulating dissemination of results, and ensuring a well-functioning network. A Board of Directors integrates working committees, including Patient Advocacy, Clinical Management, Sequencing, Databases, and Repositories.

Conclusion

Disclosure of interest
None declared.

O36
Performance of computational algorithms in pathogenicity predictions for activating variants in oncogenes versus loss of function mutations in tumor suppressor genes
R. Ghosh, S. Plon
Pediatrics-Oncology, Baylor College of Medicine, Houston, TX, USA
Correspondence: R. Ghosh – Pediatrics-Oncology, Baylor College of Medicine, Houston, TX, USA
Human Genomics 2016, 10(Suppl 1):O36

Objectives
Several computational methods have been developed to predict whether amino acid substitutions result in disease. This type of analysis
is included in the ACMG/AMP guidelines for pathogenicity classification of variants and is being used by the Clinical Genomics (ClinGen) resource. These methods are generally blind to the underlying disease mechanism. Little is known about how mechanism of disease affects the predictive ability of these algorithms for variants implicated in inherited diseases. We address this by focusing on two classes of genes that differ in their molecular mechanism of action. Activating/gain-of-function mutations in oncogenes and loss-of-function mutations in tumor-suppressor genes (TSG) are pathogenic in cancer development. Moreover, unlike TSG, oncogenes are recurrently mutated at several amino acid positions.

**Methods**

We obtained 5078 missense variants in 29 oncogenes and 50 TSG, classified based on their pattern of mutations in COSMIC(11), from the ClinVar database and annotated them with 20 computational algorithms. These variants had clinical assertions provided by the submitting laboratory. We analyzed variants classified as either pathogenic or benign in oncogenes (n=321) and TSG (n=832).

**Results**

We found less concordance among the algorithms assessed for pathogenic variant prediction in either class of genes. Also the set of algorithms that were concordant in predicting benign and pathogenic variants differed on whether the variant was an oncogene or TSG. The concordant (e.g. GERP++) algorithms are primarily based on evolutionary conservation. A combination of GERP++ and the functional prediction algorithm FATHMM is more likely to produce discordant results for oncogenes. This implies that curators choosing different sets of computational algorithm are likely to result in different inferences for the same variants. We are developing statistical approaches to identify algorithms that produces maximal separation of benign and pathogenic variants for oncogenes and TSGs and applying them in a larger set of variants in the list of 56 genes recommended for reporting for incidental findings differing in their disease mechanism.

**Conclusion**

We find evidence that disease mechanism needs to be taken into consideration when deciding on algorithms for predicting pathogenicity. Our findings may aid in further classification of variants of uncertain significance.

**References**


**Disclosure of interest**

None declared.

---

**O38**

**Melanoma reprogramming state correlates with response to CTLA-4 blockade in metastatic melanoma**


MD Anderson Cancer Center, Houston, USA

**Correspondence:** T. Karpinets – MD Anderson Cancer Center, Houston, USA

**Human Genomics 2016, 10(Suppl 1):O38**

**Objectives**

Targeting immune checkpoints has proven to be an effective strategy for the treatment of metastatic melanomas. However, less than half of patients respond to the immune checkpoint blockade. A complete understanding of molecular mechanisms underlying tumor response is lacking. In this study, we propose that the degree of melanoma cell “re-programming” may contribute to melanoma tumor resistance to immune therapy.

**Methods**

We employ RNA-sequencing (RNA-seq) and Reverse Phase Protein Array (RPPA) data from 68 early passage melanoma cell lines derived from tumor infiltrating lymphocyte harvests of 63 patients to identify biological processes and marker genes underlying the melanocyte “re-programming”. We propose a scoring system of the process based and employ it to study effects of the re-programming on outcomes of the immune therapy using a transcriptomics dataset (Van Allen et al, 2015) from pretreatment metastatic melanoma tumor samples from patients treated with ipilimumab (anti-CTLA-4).

**Results**

Melanoma cells grouped into 3 major concordant clusters by both RNA-seq and RPPA analysis (Fig. 5). Examination of the genes underlying the clustering revealed profound differences in the expression of genes associated with melanocyte differentiation (including MITF) and with the Epithelial to Mesenchymal Transition (EMT) process. We determined the mean Z value for genes within each process, and designated the difference between the mean expressions as the “re-programming score” (RPS). Using the same set of marker genes for melanoma tumor samples we significantly separated responders from non-responders of the immune therapy and revealed 2 groups of non-responding tumors. Each group had a different subset of highly expressed EMT-associated genes, and opposite expression of the differentiation-associated genes. Combining a subset of genes that
are differentially expressed between responders and non-responders we markedly enhanced the prognostic value of the cytolytic score, a known prognostic feature.

Conclusion
The proposed scoring system of the melanocyte re-programming based on the RPS may hold prognostic value for immunotherapy treatments outcomes.

Disclosure of interest
None declared.

O39
Data-driven refinement of complex disease classification from integration of heterogeneous functional genomics data in GeneWeaver
E. J. Chesler 1, T. Reynolds 2, J. A. Bubier 1, C. Phillips 3, M. A. Langston 3, E. J. Baker 4
1The Jackson Laboratory, Bar Harbor, ME, USA; 2Baylor University, Waco, TX, USA; 3University of Tennessee, Knoxville, TN, USA.

Correspondence: E. J. Chesler – The Jackson Laboratory, Bar Harbor, ME, USA
Human Genomics 2016, 10(Suppl 1):O39

Objectives
Challenges in research, diagnosis and treatment of complex disease emerge from the poor alignment of the underlying biology of disease with a nosology defined by externally manifest signs and symptoms. Aggregate functional genomics data can enable the development of a data driven nosology in which disease characteristics, research models, diagnostic categories and drugs are more precisely aligned to specific, biologically based facets of disease.

Methods
GeneWeaver consists of a database and analysis tools for aggregation of heterogeneous functional genomics data across species, including curated pathways, ontology annotations, publication data, genetic mapping, transcriptome and proteome experiments, and other functional genomics data including user-submitted experimental results. Each is described with meta-content, enabling retrieval by disease related terms. Gene identifiers are harmonized to enable aggregation of data through homologous genes and gene products. To evaluate specificity of disease descriptors, we analyzed intersections among gene sets associated with disease-related terms. These gene sets were derived from studies of nine different organisms and consisted of genome-wide experiments, curated annotations to ontology terms and genes associated to disease-related terms through transitive association of genes, publications and MeSH terms.

Results
Analyses of term-to-term associations reveals that genes associated to co-occurring or difficult to discern diseases exhibit weak overlap across many different terms, especially those associated with psychiatric disorders which display extensive cross-disorder overlap. In contrast, more well-bounded disorders, such as degenerative ocular disorders, reveal strong and specific overlap and good matching of empirically derived data sets and annotations. By enumerating all intersecting associations of genes to disorders, we are simultaneously able to identify genes that differentiate among overlapping disorders, potentially defining the specific and unique aspects of these conditions for precise differentiation of disease.

Conclusion
The integration of heterogeneous functional genomics data provides insight into the latent biological basis underlying the organization of heterogeneous disease.

Supported by NIH AA18776, jointly funded by NIAAA and NIDA.

Disclosure of interest
None declared.

O40
A general statistic framework for genome-based disease risk prediction
M. Xiong 1, L. Ma 1, N. Lin 1, C. Amos 2
1University of Texas School of Public Health, Houston, TX, USA; 2Geisel School of Medicine at Dartmouth, Hanover, NH, USA

Correspondence: M. Xiong – University of Texas School of Public Health, Houston, TX, USA
Human Genomics 2016, 10(Suppl 1):O40

Objectives
How to efficiently extract biomarkers for risk prediction and treatment selection from millions or dozens of millions of genomic variants raises a great challenge. Traditional paradigms for identifying variants of clinical validity are to test association of the variants. However, significantly associated genetic variants may or may not be efficient for diagnosis and prognosis of diseases. Alternative to association studies for finding genetic variants of predictive utility is to systematically search variants that contain sufficient information for phenotype prediction.

Methods
To achieve the goal, we introduce concepts of sufficient dimension reduction (SDR) which project the original high dimensional data to very low dimensional space while preserving all information on response phenotypes. We then formulate a clinically significant genetic variant discovery problem into the sparse SDR and optimal scoring problem and develop algorithms that can select significant genetic variants from high dimensional data. To speed up computation, we apply the alternating direction method of multipliers to solving the sparse optimal scoring problem which can easily be implemented in parallel.

Results
To illustrate its application, the proposed method is applied to a coronary artery disease (CAD) dataset from the Wellcome Trust Case Control Consortium (WTCCC) study, Rheumatoid Arthritis (RA) dataset from the GWAS of North American Rheumatoid Arthritis Consortium (NARAC) and the early-onset myocardial infarction (EOMI) exome sequencing datasets which have European origin from the NHLBI’s Exome Sequencing Project. To evaluate the performance of the SDR for disease risk prediction, we present Table 1 that lists AUC of our SDR and other 10 existing methods. Table 1 clearly demonstrated that our proposed SDR method has much larger AUC than other 10 existing methods.

Conclusion
We shift the paradigm of feature selection from P-value and risk score ranking to optimal genome-wide searching. The SDR-based optimal genome-wide searching methods substantially outperform other existing methods for disease risk prediction. Our results strongly demonstrate that the rich genetic variation information provides powerful resources for disease risk prediction.

Disclosure of interest
None declared.
Big data and NGS data analysis: the cloud to the rescue

Objectives
In the wake of the development of new Next Generation Sequencing (NGS) instruments and methodologies, genetic research has become more prominent during the past several years. However, many laboratories and institutions still face significant issues in their modus operandi: Storage, processing, and sharing of NGS data and results. We propose a novel approach to overcome mentioned issues: Wikinome, a cloud based platform specifically designed and developed to deal with the issues typical bioinformatics laboratories are confronted with, allowing faster and more efficient ways to conduct NGS data analysis.

Methods
Wikinome allows its users to store, manipulate, analyze and share their data and results from anywhere, using desktop computers, laptops, or even mobile devices, without the need of maintaining a high powered computer in the lab. Once the NGS data are uploaded, it can be analyzed using various pipelines that can be planned and executed using any of Wikinome’s clients. Utilizing a Service oriented Architecture (WCF), all steps of an analysis workflow are called individually to perform the underlying analysis process, such as reads-mapping, reads-clustering, or performing a BLAST search. Access-controlled files in a Big Data Storage environment allow users to share data with collaborators at the ease of a button click, instead of physically or digitally moving data.

Results
We have successfully implemented a platform allowing all people and institutions that conduct genetic sequence analysis, to completely move their analysis procedures into the cloud, independent from the sequencing instruments that were used to produce the NGS data. Utilizing standard modules such as quality control, reference-mapping, gene-detection, de-novo assembly, alignment, and BLAST, Wikinome not only allows users to define custom analysis workflows, users can even add services hosted inside their own labs, without the need of exposing them in the cloud. Instead of working with command-line based algorithms and tools, users are automatically notified upon finishing certain procedures of the currently running workflow, and have access to live updates. Users can also add their own custom analysis modules and share them with collaborators within the Wikinome network.

Conclusion
With Wikinome, we have successfully developed a solution to perform analysis on NGS data on a previously unthinkable scale with the potential to overcome many of the typical Big Data issues in the field of genetic research and analysis.

Disclosure of interest
None declared.

O42
Big data and NGS data analysis: the cloud to the rescue

Disclosure of interest
None declared.
features for parallelization, so that pipelines can easily run on different distributed clusters or on dedicated computing resources. To ensure that the solution can be freely shared, it is released under the GPLv3 open source license.

Results

We have developed Cpipe, a shared, open source sequencing pipeline designed for clinical users. Cpipe includes support for the full range of features required in real world clinical sequencing applications. It allows for customized sets of targeted regions, prioritized genes, screening of incidental findings, automatic exclusion of sequencing artefacts and population variants, PDF provenance and quality reports. Cpipe produces a clinically interpretable report available in Excel format. Results can be optionally imported into an LOVD (Leiden Open Variant Database) instance for curation. Cpipe is available at http://cpipeline.org.

Conclusion

Cpipe offers an open source solution that any clinical laboratory can employ, either as their main analysis pipeline or as a benchmark for comparison to improve their results.

References


Disclosure of interest

None declared.

O44

A Bayesian classification of biomedical images using feature extraction from deep neural networks implemented on lung cancer data.

V. A. A. Antonio, N. Ono, Clark Kendrick C. Go

Correspondence: V. A. A. Antonio – Computational Systems Biology Laboratory, Nara Institute of Science and Technology, Ikoma-cho, Japan

Objectives

This project aims the formulated algorithm will be implemented explicitly on lung cancer pathological images. Specifically, this project has two goals. First, it aims to apply the concept of deep neural networks to supervised learning in the classification of images, with the understanding that modifying existing machine learning methods to target specific image sets can optimize the precision and accuracy of the analysis. The algorithm that will be formulated will be able to sort a given set of data (in this case, images) into desired sets with given qualifications. Second, it aims to apply the concept of deep neural networks, supplemented by Bayesian networks to pattern analysis of lung cancer data sets. Performing Bayesian network procedures on given lung cancer data can help us determine parameter values that will characterize those data. In turn, those parameters can be used to infer whether or not new data can be classified with the given training data or otherwise.

Methods

First, we take tiles of size 512x512 from images published on the cancer genome atlas database (http://cancergenome.nih.gov). Several samples from those 512x512 will be segmented further into 32x32 subregions, which served as training data for the algorithm. The main output will be an algorithm embedded in a web application wherein the user can just input newly acquired images, and the program can provide classify which 32x32 subregions depict cancer cells. A demonstration of the application can be shown during the presentation.

Conclusion

An executable program, whose input is a lung cancer image, will be segmented into 32x32 subregions, each of whose features will be extracted using deep neural networks and will undergo a Bayes’ classification scheme, and determine whether the subregion is normal or abnormal, either because of a broken cell, a stained cell, or an actual cancer cell.

Disclosure of interest

V. A. Antonio Grant/Research Support from: CICP Research Project (https://cicp.naist.jp/ja/node/85), N. Ono: None declared.

O45

MAV-seq: an interactive platform for the Management, Analysis, and Visualization of sequence data.

Z. Ahmed, M. Boli setey, Z. Zeeshan, E. Anguiano, D. Ucar

The Jackson Laboratory for Genomic Medicine, Farmington, CT, USA

Correspondence: Z. Ahmed – The Jackson Laboratory For Genomic Medicine, Farmington, CT, USA

Objectives

The increasing amount of heterogeneous genomic datasets generated today necessitates a robust platform for efficient data management and analysis. To address this need, we developed a software for the Management, Analysis, and Visualization of sequence data (MAV-seq), capable of addressing the issues related to the exponential growth of genomic applications and their datasets of enormous size and diversity. Our software also integrates various genomic pre-processing pipelines with user-friendly graphical interface to enable biologist with no programming experience conduct complex data analyses.

Methods

MAV-seq (Figure) is a desktop application developed to integrate bioinformatics methods, software engineering principles, human computer interaction guidelines and big data analytics. The graphical user interface (GUI) and back end development of MAV-seq is performed in Java and Python, and schemas for backend data storage are implemented in MySQL and MariaDB relational database management systems. MAV-seq allows direct data manipulation using GUI as well as data import and export in ‘csv’ file formats.

Results: We developed MAV-seq as an interactive, user friendly, cross platform, encrypted and multi-roles based system for the management of sample repertoires and automation of the data pre-processing of epigenomic and transcriptomic data. It supports users in performing downstream data analysis by integrating several analysis pipelines for diverse data sets including ATAC-seq, mRNA-seq, tRNA-seq, Chip-seq, WES, WGS. MAV-seq can be customized for increasingly large scaled and complex datasets of different types. Moreover, it can directly interact with multiple data clusters to locate, input and process genomics data by automatically generating and running multiple-sequential and parallel pipelines.

Conclusion

MAV-seq is a comprehensive data management and analyses platform that is newly designed, developed, tested, validated and deployed at The Jackson Laboratory for Genomic Medicine. With this platform, we aim to advance genome-wide big data management, standardization and automation, which will expedite the pace and improve the levels of efficiency in loading, handling, tracking, securing, sharing, processing, analyzing and visualizing data.

Acknowledgements

Funding for research and development is acknowledged for Project: “Research Oriented Data Management and Analysis” at the Ucar Lab by The Jackson Laboratory, USA.
Objective

Tibetans have shown their physiological phenotypes adaptive to hypoxia environment, including relative low hemoglobin concentration and higher oxygen saturation. Among tens of candidate genes revealed by various studies that relate to living in high altitude, EPAS1 and EGLN1 showed strongest selection signals as well as solid correlation to lower hemoglobin concentration in Tibetans. However, several tens of Tibetan specific SNPs in EPAS1 were all found in introns and the mechanism of this important gene contributing to genetic adaptation in Qinghai-Tibet Plateau is still elusive. This study aims at the function of Tibetan specific SNPs in EPAS1.

Methods

1) 82 candidate genes were designed for capture and sequencing in 45 Tibetans samples to discover more SNPs for further association and functional studies. 2) Statistical tests including Chi-square tests, haplotype association, and integrative haplotype score, and Refseq and NONCODE were used for annotation. 3) Cell culture of HepG2 and HEK293 under normoxia and hypoxia (1%) for all functional assays. 4) Enhancer validation in a dual-luciferase reporter system. 5) Circular chromosome conformation in situ fluorescence hybridization (C-FISH) (both are very low resolution). Circular chromosome conformation capture (4C) in HepG2 followed by sequencing in Hi-Seq 2000.

Results

By re-sequencing 82 genes selected from previous studies and our recent discoveries, totally 9947 SNPs were revealed in 45 Tibetans individuals (15 from Bomi; 20 from Anduo; 10 from Dingri). Six genes were consistently identified by three statistical tests. In addition to EPAS1 and EGLN1, studies on quantitative traits identified DISC1 and EDAR in association with diameter of Main Pulmonary Artery and SaO2, respectively. By integrating enhancer annotation data from FANTOM5 and ENCODE, 12 EPAS1 intronic regions were resulted. Further validation for the enhancer function demonstrated that three of them are true enhancers. Moreover, enhancer 1 showed an allele specific activity in both HepG2 and HEK293 cell lines. Especially, two Tibetan-Han divergent SNPs showed the additive effect in enhancer activity. Further 4C-sequencing results of Enhancer 1 demonstrated the similar chromosomal conformation structures in most enhanced regions under hypoxia and normoxia treatments but a few interactions were shown to be hypoxia sensitive. Annotation with Refseq and NONCODE database revealed that targets potentially regulated by Enhancer 1 were mostly non-coding RNAs.

Conclusion

An allele-specific enhancer in EPAS1 intronic region may contribute to high altitude adaptation in Tibetans.

Disclosure of interest

None declared.

O47

Allele specific enhancer in EPAS1 intronic regions may contribute to high altitude adaptation of Tibetans

C. Zeng, J. Shao

Beijing Institute of Genomics, Chinese Academy of Sciences, Beijing, China

Correspondence: C. Zeng – Beijing Institute of Genomics, Chinese Academy of Sciences, Beijing, China

Human Genomics 2016, 10(Suppl 1):O47

Objective

With the discovery of human-specific genetic changes, the role of structural variation in human adaptation is beginning to emerge. However, the role of structural variation is still not well understood. Here, we present a genome-wide approach to identify structural variation associated with the traits linked to high altitude adaptation.

Methods

Using high-throughput sequencing, we sequenced three linked families from the NIST GIAB Project, where we have found hundreds of inversions, insertions, deletions, and inversions greater than 5 kbp, tens of large SV events detected by NGS, we uncovered hundreds of insertions, deletions, and inversions greater than 5 kbp, a large portion of which was novel, and some are located in the regions likely leading to disruption of gene function or regulation. Based on the pedigree structure, we estimated that the Mendelian concordance rate was 96%. We have also begun analysis of a trio of Ashkenazi Jewish descent from the NIST GIAB project, where we have found hundreds of inversions, insertions, and deletions, including large deletions in the UGT2B17 gene (involving in graft versus host disease, osteopathic health, and testosterone and estradiol levels) in the mother and son.

Conclusion

We show that NGM is a robust and effective method for structural variation detection in the human genome. Systematic whole genome structural variation within disease population cohorts is needed, in addition to the conventional SNP analysis, to study the effects of a full spectrum of genomic variations in human disease and complex traits.

Disclosure of interest

None declared.
O49
Archaic introgression in indigenous populations of Malaysia revealed by whole genome sequencing
Y. Chee-Wei1, L. Dongsheng2, W. Lai-Ping2, D. Lian2, R. O. Yue See Hoon2,3, Y. Yunus4, F. Aghakhanian4, S. S. Mokhtar4, C. V. Lok-Yung3, J. Bhak3, M. Phipps2, X. Shuhua5, T. Yik-Ying6, V. Kumar7, H. Boon-Peng3,8
1Biotechnology Research Institute, Universiti Malaysia Sabah, Kota Kinabalu, Malaysia; 2Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences Shanghai, Shanghai, China; 3Saw Swee Hock School of Public Health, National University of Singapore, Singapore, Singapore; 4Institute of Medical Molecular Biotechnology, Universiti Teknologi Mara, Sungai Buloh; 5Jeffrey Cheah School of Medicine and Health Sciences, Monash University Sunway Campus, Petaling Jaya, Malaysia; 6Personal Genomics Institute, Genome Research Foundation, Suwon, Republic Of Korea; 7Jeffrey Cheah School of Medicine and Health Sciences, Monash University Sunway Campus, Petaling Jaya, Malaysia; 8Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences Shanghai, Shanghai, China; 3UCSI University, Kuala Lumpur, Kuala Lumpur, Malaysia
Correspondence: H. Boon-Peng – UCSI University, Kuala Lumpur, Kuala Lumpur, Malaysia
Human Genomics 2016, 10(Suppl 1):O49

Objectives
The investigations of the indigenous populations from Malaysia and their migration history have been scarce. In this study, we performed the whole genome sequence for Malaysian indigenous (MI) genomes from Peninsular Malaysia (PM) and Northern Borneo (NB). The genomic structures of these samples were assessed, followed by identification of the archaics genomes introgression between these samples with Denisovan and Neandertal.

Methods
Seventeen genomes from indigenous populations from PM and NB were sequenced using Illumina Hi-Seq, thus unveiled the full spectrum of genetic architecture of the MI. Population genetic structure of these samples were assessed with PCA and ADMIXTURE. Inference of coalescent time and effective population size were performed using PSMC, and gene flow was estimated using TreeMix. Archaic introgression was estimated using the D-stat and f-test. S* analysis was applied to identify the introgressed genome segments.

Results
The divergence between Negrito and Austronesian occurred ~20K years ago, and were gradually replaced by the Austronesian expansion. Events of multiple gene flow into PM and NB was observed, in line with previous investigations. However no evidence of significantly higher gene flow from archaic genomes to Mls was observed, and that the archaic DNA segments found in Mls were different from those carried by the East Asia and Europeans.

Conclusion
Our analyses further strengthens the findings of the population structure of the indigenous people revealed by various earlier studies using SNP array, yet suggests that the history of these populations are far more complex than expected. The archaic genome introgression provided evidence of no significantly higher archaic genome component in our samples. This preliminary study complements the gaps of various speculations about archaic genomes introgression in the regions of SEA and Oceanic.

Disclosure of interest
None declared.

O50
Breast and ovarian cancer prevention: is it time for population-based mutation screening of high risk genes?
I. Campbell1, M.-A. Young2, P. James3, Lifepool4,5
1Research Division, Peter MacCallum Cancer Centre, East Melbourne, Australia; 2Familial Cancer Centre, Peter MacCallum Cancer Centre, East Melbourne, Australia
Correspondence: I. Campbell – Research Division, Peter MacCallum Cancer Centre, East Melbourne, Australia
Human Genomics 2016, 10(Suppl 1):O50

Objectives
Germline mutations in BRCA1 and BRCA2 confer high lifetime risk of breast and ovarian cancer but importantly these risks are not irreversible. Identification of asymptomatic carriers could significantly reduce the incidence of these diseases. As a first step toward population based BRCA gene screening, we are sequencing the entire coding region of 20 known and proposed HBOC genes in 4,000 cancer-free Australian women.

Methods
Cancer-free women were selected from the LifePool study (www.life pool.org) which is a cohort of women attending the Australian population, based mammographic screening program. All exons of the target genes were enriched using the Haloplex system (Agilent) and sequenced on a HiSeq2500 instrument (Illumina). The data were filtered for known pathogenic or novel loss of function mutations.

Results
To date, data from 1,997 women has identified 17 with actionable mutations in BRCA1 (4 mutations), BRCA2 (9 mutations) or PALB2 (4 mutations). All 17 women subsequently accepted an invitation to attend a Familial Cancer Centre and then proceeded to formal clinical genetic testing. In addition 4 women had pathogenic mutations in BRIP1.

Conclusion
Our unique pilot data directly demonstrates a population carrier frequency of ~1% for pathogenic mutations in these recognized high risk breast and/or ovarian cancer genes and that such testing is well accepted by the screened population.

Disclosure of interest
None declared.

O53
Comprehensive coverage from low DNA input using novel NGS library preparation methods for WGS and WGBS
C. Schumacher, S. Sandhu, T. Harkins, V. Makarov
Swift Biosciences Inc, Ann Arbor, MI, USA
Correspondence: C. Schumacher – Swift Biosciences Inc, Ann Arbor, MI, USA
Human Genomics 2016, 10(Suppl 1):O53

Objectives
In order to conduct comprehensive analysis of whole genome sequencing (WGS) or whole genome bisulfite sequencing (WGBS), unbiased, even coverage of the genome is required. To maximize time and cost efficiency, it is imperative to attain coverage from the lowest possible sequence read depth. Highly efficient conversion of DNA fragments into library molecules is especially imperative when DNA input quantity or quality is limited. To address these concerns, we have developed two novel library preparations which enable highly efficient DNA library preparation from low input while maintaining even genomic coverage.

Methods
The WGS method uniquely repairs damage on both the 3′ and 5′ termini to enhance ligation efficiency to DNA fragments. Combined with sequential ligation steps, this single tube method supports PCR-free sequencing from inputs as low as 10 ng circulating, cell-free DNA (cfDNA) or 50 ng physically sheared DNA. For WGBS, our library preparation is performed on denatured, bisulfite-converted fragments. This improves library recovery significantly compared to traditional library prep methods that ligate methylated adapters to double-stranded DNA prior to bisulfite conversion. Our adapter attachment to single-stranded DNA supports inputs from 100 pg to 10 ng Input quantities down to 10 pg can be used with PCR amplification.

Results
Using the WGS method, library conversion efficiency was ~50% for physically sheared DNA and up to 90% for cfDNA. Human WGS using this method demonstrates high complexity with exceptional coverage of GC-rich promoter regions. At inputs as low as 1 ng human DNA, at 6X coverage, the genome was fully represented with consistent, uniform coverage. Libraries made with the WGBS method required less PCR amplification than other available kits and this improvement was further seen in the sequencing data, particularly at 1 ng input. Human WGBS demonstrated comprehensive coverage of CpG islands when 10 ng input was used at low depth of sequencing. This library preparation
method enables single base resolution of methylation status throughout the genome, even from limiting DNA input quantities.

**Conclusion**
We have demonstrated the utility of increasing the efficiency of library preparation as a means of improving sequencing results obtained through both WGS and WGBS. This innovative technology enables sequencing of sample types that have been previously unavailable due to input or quality limitations.

**Disclosure of interest**

**OS4**
Methods for large scale construction of robust PCR-free libraries for sequencing on Illumina HiSeqX platform


Human Genome Sequencing Center, Baylor College of Medicine, Houston, TX, USA

**Correspondence:** H. Doddapaneni – Human Genome Sequencing Center, Baylor College of Medicine, Houston, TX, USA

**Human Genomics 2016, 10(Suppl 1):OS4**

**Objectives**
With drastic drop in the cost of whole genome sequencing (WGS) on Illumina’s HiSeqX systems, it’s now economically feasible to plan large scale sequencing projects in research as well as clinical settings. However, successful execution of such projects will require design of robust sample preparation (library) workflows that can work with a spectrum of DNA quality and quantities. This is especially true for the highly desirable PCR-Free libraries that are known to provide improved gene and genome representation compared to PCR amplified libraries. Here we discuss the use of multiple PCR-Free protocols for use on HiSeqX.

**Methods**
Previously we automated Illumina TruSeq PCR-Free protocol, which is recommended to use with 1 ug of good quality DNA to prepared size selected libraries. However, to broaden the scope of samples that can be used for preparing PCR-Free libraries, we evaluated two additional library construction methods 1. Swift Biosciences 25 library kit and 2. Kapa Biosystems, hyper prep kit. PCR-Free libraries were prepared using 200 ng - 1 ug DNA of HGSC internal human control sample (HS1011) with these kits and sequenced on HiSeqX to generate 34-38X genome coverage data.

**Results**
Exome representation as measured by complete coverage of Online Mendelian Inheritance in Man (OMIM) genes at 20X read depth was lowest for the TruSeq PCR-Free libraries (2687 genes) when compared to the 25 libraries (2750 – 3020 genes) and the Kapa hyper libraries (2800 genes). GC representation was better in PCR-Free libraries when compared to the TruSeq Nano libraries. Kapa Hyper protocol was optimized on Beckman Coulter’s Biomek FXP liquid handler using 500 ng DNA and can prepare 96 libraries in ~ 6 hours. This protocol also works well with DNA of different integrities. Enhancements have also been made for precise quantification of PCR-Free libraries by qPCR and to eliminate unused adapter molecules in libraries that can impact sequencing.

**Conclusion**
Availability of such robust and automated protocols has positioned us to efficiently work with large sample sets to fully exploit the use of HiSeqX platforms for population level genomic studies and to drive its use in clinical setting.

**Disclosure of interest**
None declared.

**OS5**
Rapid capture methods for clinical sequencing

J. Hu1, K. Walker1, C. Buhay1, X. Liu2, Q. Wang1, R. Sanghvi1, H. Doddapaneni1, Y. Ding1111, N. Veeraraghavan1, Y. Yang1, E. Boerwinkle1111, A. L. Beaudet5, C. M. Eng1, D. M. Muzny4, R. A. Gibbs1

1Human Genome Sequencing Center, Baylor College of Medicine, Houston, TX, USA; 2Department of Molecular and Human Genetics, Baylor College of Medicine, Houston, TX, USA; 3Human Genetics Center, University of Texas Health Science Center at Houston, Houston, TX, USA

**Correspondence:** J. Hu – Human Genome Sequencing Center, Baylor College of Medicine, Houston, TX, USA

**Human Genomics 2016, 10(Suppl 1):OS5**

**Objectives**
Advancement of next generation sequencing in clinical settings has required methods for rapid, robust delivery of high-quality sequencing data. Effective and timely diagnoses or prediction of risk of genetic diseases are important for medical intervention.

**Methods**
We have developed a ‘lightning capture’ process to deliver variant calls in 5–7 days after sample intake. This process includes: quick enrichment library preparation (5–6 hours), capture enrichment (about 8 hours), rapid sequencing (Illumina HiSeq2500) and data analysis via the HGSC-developed Mercury pipeline. The lightning capture protocol has been deployed in BMGL clinic lab for whole exome sequencing (WES) and recent carrier screening with a novel 500kb carrier mutation gene capture panel. Our WES design contains 3643 clinically relevant genes primarily from GeneTests and OMIM, and the carrier panel includes 168 complete genes that contain at least 850 known common genetic variants of clinical relevance. We also employ the genotyping with SNPTrace panel by Fluidigm in order to ensure reliable sample identification, and to test for sample cross-contamination.

**Results**
This method has been validated with ~500 WES and more than 5000 carrier samples. WES samples are processed in single capture or 3-plex co-capture, while carrier samples are in a cost-effective 47plex co-capture format for hybridization followed by sequencing of 94 samples (2 capture pools) per HiSeq 2500 lane. High enrichment efficiency was observed (72-80% reads on target and buffer) and superior coverage metrics across the design with 11 Gb sequencing yield for WES and ~400 Mb for Carrier samples. A detailed analysis of the carrier design performance using 140 de-identified samples found that known carrier mutations were correctly identified with high confidence (98.5%), including large/complex indel mutations.

**Conclusion**
Sample turnaround time for tests is often considered one of the most significant measures of performance for a clinical lab. The lightning capture process we developed enables data delivery in 5–7 days without sacrifice of data quality. This novel method may impact applications in prenatal, neonatal intensive care and other critical settings for clinical and research samples.

**Disclosure of interest**
None declared.

**OS6**
A diploid personal human genome model for better genomes from diverse sequence data

K. C. C. Worley1, Y. Ding1, D. S. T. Hughes1, S. C. Murali1, R. A. Harris3, A. C. English1, X. Qin1, O. A. Hampton1, P. Larsen2, C. Beck3, Y. Han1, M. Wang1, H. Doddapaneni1, C. L. Kovar1, W. J. Salerno1, A. Yoder2, S. Richards1, J. Rogers1, J. R. Lupski1, D. M. Muzny4, R. A. Gibbs1

1Human Genome Sequencing Center, Molecular and Human Genetics, Baylor College of Medicine, Houston, TX, USA; 2Department of Biology, Duke University, Durham, NC, USA; 3Molecular and Human Genetics, Baylor College of Medicine, Houston, TX, USA

**Correspondence:** K. C. C. Worley – Human Genome Sequencing Center, Molecular and Human Genetics, Baylor College of Medicine, Houston, TX, USA

**Human Genomics 2016, 10(Suppl 1):OS6**

**Objectives**
Research into the development of a diploid personal human genome model has been ongoing for many years, with the ultimate aim being to create a personalized genome model that can be used in various medical applications.
Objectives
Generate a high quality reference genome from a single individual to avoid the contribution of different data types to understanding the comprehensive clinical genome.

Methods
Illumina data from a variety of libraries (180 bp, 300 bp and 500 bp paired end data; 3kb, 6.5 kb and 8 kb mate-pair data), as well as Illumina Hi-C data, 20x PacBio RS long read data and BioNano optical mapping data were produced and assembled de novo. Structural variants that are difficult to characterize with exome sequencing or short sequence reads from small fragments were identified using two methods. We identified putative novel insertions in reads that did not map to the GRCh38 reference with calls supported by 6.5 kb mate-pair data, and confirmed in the de novo WGS assembly contigs and 3 kb mate-pair data. We identified tandem duplications with combined signatures of inverted 300 bp to 500 bp read pairs identifying the boundaries and larger read pairs confirming the size of the duplicated region.

Results
We report here the assembly of data from a single individual (HS1011). The data are available at NCBI under BioProject 203659. The released assembly is highly contiguous with a 394 kb Contig N50 and 148 Mb Scaffold N50 with full chromosome scaffolds. Data from the parents of HS1011 and long-read data allow us to phase variants within this genome. Putative novel insertions (78) and tandem duplications (70) were identified.

Conclusion
The assembly and underlying data reported here allow us to optimize methods to combine these data types and explore the utility of the different data types to identify structural variation and define which heterozygous variants are located on the same haplotype for haplotype-aware downstream analyses.

Disclosure of interest
None declared.

O58
Rhesus macaques exhibit more non-synonymous variation but greater impact of purifying selection than humans
1Molecular and Human Genetics, Baylor College of Medicine, Houston, TX, USA; 2Human Genome Sequencing Center, Baylor College of Medicine, Houston, TX, USA; 3Human Genetics, Southwest National Primate Research Center, San Antonio, TX, USA; 4Human Genetics, University of California Los Angeles, Los Angeles, CA, USA; 5Division of Neuroscience, Oregon National Primate Research Center, Beaverton, OR, USA; 6Genomics & Microbiology Research Laboratory, NC Museum of Natural Sciences, Raleigh, NC, USA; 7Yerkes Nonhuman Primate Genomics Core, Yerkes National Primate Research Center, Atlanta, GA, USA; 8Environmental Toxicology, California National Primate Research Center, Davis, CA, USA; 9Physiology, Tulane National Primate Research Center, New Orleans, LA, USA; 10Neuroscience, University of Pennsylvania, Philadelphia, PA, USA; 11Anthropology, University of California Davis, Davis, CA, USA; 12Psychiatry and Human Behavior, University of Mississippi Medical Center, Jackson, MS, USA; 13Genetics, Wisconsin National Primate Research Center, Madison, WI, USA; 14Epidemiology, Human Genetics & Environmental Sciences; 15Epidemiology and Disease Control Human Genetics Center, University of Texas Health Science Center, Houston, TX, USA.

Correspondence: R. A. Harris – Molecular and Human Genetics, Baylor College of Medicine, Houston, TX, USA.

Human Genomics 2016, 10(Suppl 1):O58

Objectives
We generated whole genome sequence data for 133 rhesus macaques (Macaca mulatta), the primary nonhuman primate in biomedical research.

Methods
Using the intersection of GATK and SNPTools SNV calls, we identified 43 million high-quality SNVs, including >126,000 missense and >148,000 synonymous coding variants.

Results
Comparisons with equivalent whole genome data from the Human 1000 Genomes project shows that macaques have 2.5-fold higher levels of overall variation and 20% higher levels of nonsynonymous variation per individual. Comparing the ratio of nonsynonymous to synonymous variants between species shows a lower ratio of N53yn
in macaques, indicating more effective purifying selection, which can be explained by higher effective population size. Looking more specifically at 740 genes from the SFARI autism genetic association database, the ratio of NS:Syn variants among the macaques is lower in the SFARI gene set than in the complete macaque gene set.

**Conclusion**

These data suggest that large effective size in macaques leads to higher levels of both total and nonsynonymous variation than humans, and that purifying selection in macaques is more efficient in restricting mildly deleterious mutations.

**Disclosure of interest**

None declared.

**OS9**

**Assessing RNA structure disruption induced by single-nucleotide variation**

Z. Ouyang, J. Lin, Y. Zhang

1The Jackson Laboratory for Genomic Medicine, Farmington, CT, USA; 2Department of Statistics, University of Connecticut, Storrs, CT, USA

**Correspondence:** Z. Ouyang – The Jackson Laboratory for Genomic Medicine, Farmington, CT, USA

Human Genomics 2016, 10(Suppl 1):OS9

**Objectives**

It has been challenging to interpret noncoding variants in complex traits and human diseases. RiboSNitches, single-nucleotide variants (SNVs) that alter the structures of RNAs, have recently found in many human diseases. RNA structure change mediated by riboSNitches has emerged as a plausible mechanism of pathogenic consequences of mutations. Thus, it is desirable to automatically predict riboSNitches from millions of SNVs of the human genome. However, current computational methods based on in silico RNA-folding algorithms suffer from limited accuracy. We seek to develop a new method for improved riboSNitch detection.

**Methods**

We introduce a new measurement to quantify the structural difference between the wild-type and mutant RNAs in which the two sequences are differed by an SNV. The new measurement is based on assessing the consistency of RNA structure change of individual bases. Using this new measurement, our method automatically selects a region that maximizes the effect of RNA structure disruption induced by an SNV.

**Results**

We applied our method to analyze a genome-scale dataset of riboSNitches and non-riboSNitches determined from the parallel analysis of RNA structure experiments on a family trio of human lymphoblastoid cell lines. The dataset contains rigorously validated subsets of 11 “probed”, 63 “validated”, and 223 “symmetric” riboSNitches. We found that our method consistently outperforms other existing methods on these rigorously validated subsets of riboSNitches.

**Conclusion**

Our new method improves the accuracy of computational prediction of riboSNitches. It facilitates the prioritization of noncoding variants for interpreting personal genomes. It also holds the promise to identify disease-causing variants potentially through RNA structure disruption.

**Disclosure of interest**

None declared.

**P1**

**A meta-analysis of genome-wide association studies of mitochondrial dna copy number**


1National Cancer Institute, Rockville, USA; 2St. Jude Children’s Research Hospital, Memphis, USA; 3National Cancer Institute, NIH, DHHS, Rockville, USA; 4Changhua Christian Hospital, Changhua, Taiwan, Province of China

**Correspondence:** A. Moore – National Cancer Institute, Rockville, USA

Human Genomics 2016, 10(Suppl 1):P1

**Objectives:** Variation in mitochondrial DNA (mtDNA) copy number (CN) has been shown to be related to the risk of several cancers in prospective studies. The inter-individual variability of mtDNA CN is thought to be partially heritable; however, no genome-wide association study (GWAS) of the nuclear genome has yet been performed.

**Methods:** We conducted a meta-analysis of GWAS of peripheral blood mtDNA CN using data from participants of European ancestry from nested case–control studies of prostate cancer and non-Hodgkin lymphoma in the Prostate, Lung, Colorectal, and Ovarian (PLCO) Screening Trial (n=1664). MtDNA CN was natural log-transformed and linear regression was used to evaluate the association, assuming an additive genetic model and adjusting for age at mtDNA blood draw, ancestry, and sex. The three GWAS were combined in a fixed-effects meta-analysis.

**Results:** A quantile-quantile plot of the association results revealed some enrichment for SNPs with small p-values, but no evidence of genomic inflation (λ=1.007). Six loci, defined as +/- 1 Megabase, reached genome-wide significance (p < 5x10^{-8}), but all appeared to be singletons, indicating that they are likely to be false positives. Ten Single Nucleotide Polymorphisms (SNPs) in an intronic region of the long-range sonic Hedgehog signaling gene, DISP1, were found suggestively associated (p < 5x10^{-6}) with mtDNA CN, with consistency in the direction of associations among all three GWAS.

**Conclusion:** Preliminary findings from this meta-analysis suggest that there may be common genetic variants of the nuclear genome associated with mtDNA CN. We are currently augmenting our meta-analysis by including additional GWAS of nested case–control studies in PLCO and the Alpha-Tocopherol, Beta-Carotene Cancer Prevention Study. We expect that the added statistical power will yield novel loci for mtDNA CN and provide new insight into the regulation of mtDNA CN.

**Competing interests**

None declared.

**P2**

**Missense polymorphic genetic combinations underlying down syndrome susceptibility**

E. S. Chen

Biochemistry, National University of Singapore, Singapore, Singapore

Human Genomics 2016, 10(Suppl 1):P2

**Objectives:** Single nucleotide polymorphisms (SNPs) draw much attention as prospective biomolecular markers for human health management and disease therapies. Moreover SNPs have been surmised to constitute unique genetic makeup characteristic to each human individual, which can be utilized to cater therapeutic approaches to personalized medical care. Down syndrome (DS) or trisomy 21 is the most frequently occurring birth-related defects affecting live-born children. Molecular mechanisms that regulate and/or result in the formation of trisomy 21 in DS mothers, remain hitherto unknown. We posit a genetic basis for disposition of DS occurrence. We therefore performed bioinformatics studies of published nonsynonymous SNPs in conjunction with structural information of the proteins encoded by DS risk genes in the attempt to identify novel governing principles of DS risk.

**Methods:** We surveyed all SNPs in the published literature focusing on missense mutations, and superimpose on bioinformatic reconstruction of secondary structural motifs of proteins encoded by DS genes.

**Results:** In our survey, we observed that even the most penetrant SNP implicated in DS is not completely associated with the disease. On the other hand, a combination of co-occurrence of SNPs is important, suggesting a synthetic cooperation between missense mutations to underlie occurrence of DS phenotype. Superimposing documented SNPs from several public databases showed a preferential localization of these SNPs with specific structural motifs within the proteins. Interestingly, we noticed several closely situated SNPs that have not been reported to be associated with DS risk within regulators of the one carbon folate metabolism that included reduced folate carrier 1 (RFC1) and methionine synthase. These may represent
novel SNPs that can be assessed experimentally in a targeted manner in future population studies.

**Conclusion:** Taken together, our analyses showed that SNPs that result in change of protein sequences act synergistically to impact DS phenotype and suggest that SNP combinations to be a more reliable criteria than single SNPs for ascertaining DS risk, at least in the case of missense SNPs. Our study also identified probable secondary structural motifs implicated in DS risk-associating factors. These results will form the basis for future experiments that may hold potential for translation into personalized diagnosis or therapeutic management of DS.

**Competing interests**
None declared.

**P8**

**Differentiating inflammatory bowel diseases by using genomic data: dimension of the problem and network organization**

N. Milli1, R. Molinari, Y. Mar2, S. Guerrier3

1Research Center for Statistics, University of Geneva, Switzerland, Geneva, Switzerland; 2Department of Statistics, University of South Carolina, Columbia, USA; 3Department of Statistics, University of Illinois at Urbana Champaign, Champaign, USA

**Correspondence:** N. Milli – Research Center for Statistics, University of Geneva, Switzerland, Geneva, Switzerland

**Human Genomics 2016, 10(Suppl 1):P8**

**Objectives:** To determine the minimum number of genes (dimension of the problem) and their network organization in the distinction between Crohn’s Disease (CD), Ulcerative Colitis (UC) and normal patients (N).

**Methods:** We relied on the results published by Burczynski et al. where transcriptional profiles in peripheral blood mononuclear cells (PBMC) from 42 healthy individuals, 59 CD patients, and 26 UC patients were assessed. We applied a newly proposed gene selection method, based on statistical and machine-learning principles, which finally delivered a set of models which best predicted the disease class. These models were inserted in a network where the biomarkers were placed in specific positions according to their relevance in discriminating between the diseases.

**Results:** We found that a set of models, each containing only two RNA’s from the PBMC, were sufficient to discriminate CD from UC patients and normal individuals. These RNA’s were organized in networks where the gene in first position could well classify when placed in a model with any of those in the corresponding second position. A summary of these networks is as follows.

**Conclusion:** Our statistical method is a new powerful tool that gives (1) the dimension of the statistical model, (2) the network organization of the selected genomic biomarkers, (3) a set of interchangeable models giving the same information.

Moreover, all the RNA’s in position 1 of the selected networks are known to have a clinical significance in Inflammatory Bowel Diseases. Amyloidosis is a well-known complication of CD and UC (Amyloid beta A4 precursor protein). Chemotaxis and neutrophil activation are fundamental pathways in the pathogenesis of IBD (Chemokine C-X-C beta A4 precursor protein). Chemotaxis and neutrophil activation are

**Competing interests**
None declared.
phenotype-appropriate cell populations. Further, such enhanced datasets make feasible the prediction of functional variants. Presently, we are leveraging our past experiences to generate enhancer catalogues using homogenous populations of dopaminergic (DA) neurons better to understand the role of regulatory variation in Parkinson Disease (PD) and related disorders.

**Methods:** We assayed open chromatin regions using ATAC-seq, producing multiple enhancer catalogues. Each catalogue is generated from 50,000 FACSorted DA neurons from either the forebrain (n=3 libraries) or midbrain (n=3 libraries) of E15.5 transgenic mice. Each ATAC-seq library is of high quality, yields over 30 million reads sequenced, with over 28 million reads mapping, and following filtering of reads, MACS2 calls 50,000 peaks, indicating intervals of open chromatin.

**Results:** Our preliminary analyses indicate that peaks from all libraries show evidence of functional sequence constraint (PhastCons scores>0.3) and significant enrichment for processes and functions appropriate to neuronal function/dysfunction by GO/GREAT. The high quality of these open chromatin signatures also facilitate development of a computational classifier (regulatory vocabulary) of DA neurons. Consequently, we have begun to gain further insight into the transcription factors active in DA neurons and the nature of variation that might influence the function of identified DA enhancers.

**Conclusion:** We are currently validating the DA neuron enhancer catalogues in vivo and are evaluating the shared and unique content of the catalogues and their pertinence to disease. Additionally, we have generated single cell and bulk RNA-seq from these isolated populations to corroborate and inform our chromatin-based findings. With this data in hand, we are able to assay the impact of PD and related movement disorders’ GWAS-implied variation on DA neuron function and disease pathogenesis.

**Competing interests**
None declared.

**P11**
Utilization of a sensitized chemical mutagenesis screen to identify genetic modifiers of retinal dysplasia in homozygous Nr2e3rd7 mice

Y. Kong1, J. R. Charette1, W. L. Hicks1, J. K. Naggert1, L. Zhao1, P. M. Nishina2,2, The Jackson Laboratory, Bar Harbor, USA 1Graduate School of Biomedical Science and Engineering, University of Maine, Orono, USA

**Correspondence:** Y. Kong – The Jackson Laboratory, Bar Harbor, USA

**Human Genomics 2016, 10(Suppl 1):P11**

**Objectives:** To identify and characterize genetic modifiers capable of altering the retinal dysplasia observed in Nr2e3rd7 mutants, a model for human Enhanced S-Cone Syndrome (ESCS).

**Methods:** Nr2e3rd7 mice were chemically mutagenized, and mated to generate a G3 population. The G3 mice were screened by indirect ophthalmoscopy to establish lines bearing genetic modifiers that altered the pan retinal fundus spotting phenotype, characteristic of homozygous Nr2e3rd7 mice. Quantitative trait locus analysis combined with high-throughput sequencing of an exome capture libraries was used to identify the molecular basis of modifiers of the retinal dysplasia in Nr2e3rd7 mutants. Apart from fundus imaging, longitudinal histological studies were carried out to characterize the progression of altered retinal phenotypes. Finally, immunoblotting and marker analyses were performed to reveal the defects that underlie the rd7-retinopathy and how the defects were affected by the modifier(s).

**Results:** Seven heritable modifier mouse lines with an altered retinal phenotype have been established so far. Among them three potential genetic modifiers have been identified, which directly or indirectly are associated with growth and development of neuroretinal cells. For example, the Tvrm222 line bears a nonsense mutation of the Rarb gene, which leads to a vitreal dysplastic phenotype that is more severe in the presence of the Nr2e3rd7 mutation. While a reduced retinal spotting phenotype and suppression of formation of rosette-like structures associated with the rd7 retinopathy in the Tvrm222 line is due to a missense mutation in the Fmd4b gene. The modifying effect of the Fmd4bTvm222 allele is achieved through its effect on cell-cell junctions, revealed by immunoblotting and marker analysis.

**Conclusion:** As an animal model of ESCS, retinal dysplasia in Nr2e3rd7 mouse can be phenotypically altered by multiple genetic modifiers via different pathways. The modifying effects on rd7-associated retinopathies by these particular genetic modifiers, to our knowledge, are the first to be described. They provide novel insights into the pathogenesis of retinal dysplasia as well as degeneration in Nr2e3rd7-associated disease, and may become potential interfering targets for clinical applications against ESCS and related retinopathies.

**Competing interests**
None declared.

**P12**
Ion torrent next generation sequencing of recessive polycystic kidney disease in Saudi patients

B. M. Edrees1, M. Athar1, F. A. Al-Alaifi1, M. M. Taher1, W. Khan2, A. Bouazzouli3, N. A. Harbi2, R. Safar1, H. Al-Edressi3, A. Anazi4, N. Altaye5, M. A. Ahmed2, K. Alansary2, Z. Abduljalil1

1Department of Medical Genetics, Faculty of Medicine, Umm Al-Qura University, Makkah, Saudi Arabia; 2Department of Basic Sciences, College of Science and Health Professions, King Saud Bin Abdulaziz University for Health Sciences, Riyadh, Saudi Arabia; 3Department of Pediatric, King Faisal Specialist Hospital and Research Centre, Jeddah, Saudi Arabia; 4Department of Pediatric, Madinah Maternity and Children’s Hospital, Madinah, Saudi Arabia; 5Pediatric, King Fahad Medical City, Riyadh, Saudi Arabia; 6Molecular Diagnostics Unit, Department of Laboratory and Blood Bank, King Abdullah Medical City, Makkah, Saudi Arabia; 7Medical Genetics, King Salman Armed Forces Hospital, Tabuk, Saudi Arabia; 8Medical Genetics, King Fahad Medical City, Riyadh, Saudi Arabia

**Correspondence:** Z. Abduljalil – Department of Medical Genetics, Faculty of Medicine, Umm Al-Qura University, Makkah, Saudi Arabia

**Human Genomics 2016, 10(Suppl 1):P12**

**Objectives:** Targeted customized sequencing of genes implicated in the Autosomal recessive polycystic kidney disease (ARPKD) phenotype to identify candidate variants using next-generation sequencing by Ion torrent PGM.

**Methods:** Eighteen unrelated ARPKD probands and healthy human adult control samples were recruited for genetic screening of ARPKD at a referral hospital from northern region of Saudi Arabia. Probands had survived the neonatal period and had age range in between 2 months to 13 years.

**Ion-Torrent PGM sequencing:** We have customized primers and a targeting scheme for targeting of the ARPKD candidate gene (PKHDI), and also included the PKD1 and PKD2 genes that may mimic the phenotype of the ARPKD. The NGS protocol involves three steps (1) Library preparation (2) Template preparation, finally sequencing was performed on PGM using Ion PGM 200 sequencing kit.

**Mapping assembly and variants discovery from NGS data:** For each resulted deleterious variants identified by NGS were also confirmed by Capillary sequencing.

**Results:** We identified five potential pathogenic missense variants in PKHDI gene in 12 ARPKD Saudi patients. One missense variant was novel and other four had been reported in other ethnic groups but not in Saudis. The rest of the patient’s samples have few variants in PKD1 and PKD2 genes that were not in damage but two causative variants observed. One missense homoyozygous variant c.4870C>T, p.Arg1624Trp was common in eight patients in PKHDI1 gene derived from a male proband. Our results showed that the deleterious missense variant detected in PKHDI1 gene was pathological significant or damaged were identified by computational predictions Sorting Intolerant From Tolerant (SIFT) and Polyphen2 Phenotyping (PolyPhen2). Taken together, this strategy significantly lowers the cost and time for simultaneous targeted genes sequence analysis, and facilitating routine genetic diagnostics of ARPKD.

**Conclusion:** Overall, the NGS TargetSeq exome sequencing may prove to be advantageous in the early diagnosis in patients with ARPKD disease.
Competing interests
None declared.

P13
Digital expression profiling of Purkinje neurons and dendrites in different subcellular compartments
A. Kratz1, P. Beguin1, S. Poullain1, M. Kaneko1, C. Takahiko1, A. Matsuanga2, S. Kato2, A. M. Suzuki2, N. Bertin3, T. Lassmann4, R. Vigot4, P. Carninci1, C. Plessy5, T. Launey6
1Center for Life Science Technologies, RIKEN Yokohama, Yokohama City, Kanagawa, Japan; 2Brain Science Institute (BSI), Launey Research Unit, RIKEN Wako, Wako, Japan
Correspondence: A. Kratz – Center for Life Science Technologies, RIKEN Yokohama, Yokohama City, Kanagawa, Japan
Human Genomics 2016, 10(Suppl 1):P13

Objectives: Neuronal cells are not homogeneously distributed and subtypes are intermingled with each other as well as with non-neuronal cells such as glia and blood vessel cells. When attempting to digitally profile the expression of a specific type of neuron, retrieving the RNA only of that cell type therefore poses a considerable challenge. Our aim was to isolate RNA specifically from Purkinje neurons in different parts of the cell body: soma (in different subcellular compartments, cytoplasm and rough endoplasmic reticulum) and dendrites.

Methods: In previous work, we used a technology called translating ribosome affinity purification (TRAP) to isolate the ribosome-associated transcriptome — the translatome. We modified it to target any cell type that can be specifically infected by a modified adeno-associated virus, and applied it to Purkinje cells (PCs) in the rat cerebellum. We obtained quantitative expression data in single-base-pair resolution by profiling the ribosome-associated, isolated RNA using the nanoCAGE protocol.

Results: Subsequent data analysis revealed the landscape of ribosome-associated RNA of PCs in different subcellular compartments: cytoplasm and rough endoplasmic reticulum in the soma. We published these results in [1]. Building on this work, we have now successfully retrieved RNA from dendrites in the same model system with replicated libraries, and thus obtained a deep sequencing using a newly developed protocol employing unique molecular identifiers (UMI) for a more precise measurement of expression.

Conclusion: In neurons, protein translation occurs not only in the soma but also distally in dendrites near or within the dendritic spines. This distal translation is thought to be regulated in response to external stimuli including long-term depression and memory formation. We have applied TRAP to Purkinje dendrites and sequenced the isolated RNA with an improved nanoCAGE protocol including a tagmentation step, to address the increased difficulty of sequencing from dendrites, which contain even less RNA than Purkinje cell soma.

References

Competing interests
None declared.

P14
The evolution of imperfection and imperfection of evolution: the functional and functionless fractions of the human genome
D. Graur
Biology and Biochemistry, University of Houston, Houston, USA
Human Genomics 2016, 10(Suppl 1):P14

Objectives: Genomes are products of natural processes. Hence all genomes contain functional and nonfunctional parts. Here, I present a functional classification of genomic elements and estimate the functional fraction within the human genome.

Methods: The classification into different categories of functionality were based on the concept of selected-effect function. Intraspecific and interspecific genomic comparisons and standard evolutionary methodology were used to infer the functional fraction within the human genome.

Results: According to their selected-effect function, the genome is divided into functional and rubbish DNA. Functional DNA is further subdivided into literal and indifferent DNA. In literal DNA, the order of nucleotides is under selection; in indifferent DNA, only the presence or absence of the sequence is under selection. Rubbish DNA is further subdivided into junk and garbage DNA. Junk DNA neither contributes to nor detracts from the fitness and, hence, evolves under selective neutrality. Garbage DNA, on the other hand, decreases the fitness of its carriers; it exists in the genome because natural selection is neither omnipotent nor instantaneous. Each of these four functional categories can be transcribed and translated, transcribed but not translated, or not transcribed. The affiliation to a particular functional category may change during evolution: Functional DNA may become junk DNA, junk DNA may become garbage DNA, and so on; however, in the absence of prophetic powers determining the functionality or nonfunctionality of a genomic sequence must be based on its present status rather than on its potential to change in the future. Changes in functional affiliation are categorized into pseudogenes, Lazarus DNA, zombie DNA, and Jekyll-to-Hyde DNA. Intraspecific and interspecific genomic comparisons indicate that the functional fraction in the human genome ranges from 8% to 15%.

Conclusion: A common misconception exists according to which evolutionary processes can produce a genome that is wholly functional. Actually, evolution can only produce such a genome if and only if the effective population size is infinite, the deleterious effects of increasing genome size by even one nucleotide are considerable, and the generation time is short. Not even in the commonest of bacterial species are these conditions met. In species with small effective population sizes and long generation time, such as humans, a genome that is ~100% functional is contrary to reason.

Competing interests
None declared.

P16
Species-independent identification of known and novel recurrent genomic entities in multiple cancer patients
J. Friis-Nielsen, J. M. Izarzugaza, S. Brunak
Technical University of Denmark, Center for Biological Sequence Analysis, Lyngby, Denmark
Correspondence: J. M. Izarzugaza – Technical University of Denmark, Center for Biological Sequence Analysis, Lyngby, Denmark
Human Genomics 2016, 10(Suppl 1):P16

Objectives: Here we present a new method for the identification of recurrent genomic entities that play a causative role in the onset of disease. Our approach is particularly amenable for the analyses high-throughput sequencing data. Existing approaches often follow a bottom-up approach where taxonomic determination necessarily takes place before associations to disease can be determined; naturally failing to establish the causality of novel pathogens not present in reference databases.

Methods: To overcome this intrinsic limitation, we have developed a species-agnostic top-bottom approach that clusters sequences and identifies co-occurrence in multiple patients, associates recurrent sequences to disease and, finally, determines the taxonomic context where existing knowledge permits.

Results: We analysed 686 sequencing libraries from 252 cancer specimens and 56 controls. Recurrent sequences were statistically associated to biological, methodological and technical features to identify novel pathogens and contaminants stemming from laboratory reagents.

Conclusion: We provide examples of identified inhabitants of the healthy tissue flora, known experimental contaminants and
uncharacterised sequences that co-occur with high statistical significance with disease. The latter represent a category that can only be addressed by a species-independent approach. Thus, our method helps to chart the unknown sequence-space where novel pathogens can be identified.

Competing interests
None declared.

P18
Discovery of active gene modules which are densely conserved across multiple cancer types reveal their prognostic power and mutually exclusive mutation patterns
B. S. Soibam
University of Houston-Downtown, Houston, USA
Human Genomics 2016, 10(Suppl 1):P18

Objectives: An active module which is densely conserved across multiple gene networks exhibit strong and conserved interactions among its active member genes across all the networks. Identification of such modules across multiple species using gene networks in stem cell differentiation has provided new insights into evolutionary conserved developmental pathways and conserved pioneer factors. Similarly in cancer, such modules (if exists) will represent core common carcinogenesis-driving pathways in multiple types of cancer. These common pathways can have the same prognosis in cancers stemming from different tissues. Even though, a comprehensive amount of gene expression data can have the same prognosis in cancers stemming from different tissues. Even though, a comprehensive amount of gene expression data can have the same prognosis in cancers stemming from different tissues.

Methods: We developed a computational framework to identify active modules of genes which are densely conserved across 8 different types of cancer by extending a previous tool called neXus to allow it to work on more than 2 cancer gene networks. We identified 174 modules of genes satisfying these three strict criteria – 1) member genes were differentially expressed between normal and cancer tissues (FDR < 0.05) in at least 7 cancer types of cancer of interest, 2) average fold change of 2 in the member genes across all 8 cancer types and 3) the clustering coefficient of at least 0.5 in all the 8 cancer gene networks.

Results: The identified modules represented some known pathways associated with multiple cancers such as the RAS pathway, but several new genes which may play important in triggering cancer in multiple types of tissues were discovered. We found that these conserved modules of genes have high prognostic power in all the 8 types of cancer of interest. We also found that these active and conserved modules exhibit similar mutually exclusive mutation patterns among the gene members and these patterns were also conserved across the majority of the types of cancer.

Conclusion: These findings reveal a new set of previously unknown pathways, which most likely run as a common thread during carcinogenesis in many cancer types and hence are worth investigating further for experimental validation.

Competing interests
None declared.

P19
Whole exome sequencing of dysplastic leukoplakia tissue indicates sequential accumulation of somatic mutations from oral precancer to cancer
D. Das1, N. Biswas1, S. Das1, S. Sarkar2, A. Maitra1, C. Panda2, P. Majumder1
1National Institute of Biomedical Genomics, Kalyani, India; 2Chittaranjan National Cancer Institute, Kolkata, India
Correspondence: D. Das – National Institute of Biomedical Genomics, Kalyani, India
Human Genomics 2016, 10(Suppl 1):P19

Objectives: Oral leukoplakia (OL) is the most common precancerous lesion in the oral cavity. The percentage of individuals with dysplastic OL in whom there is malignant transformation to oral squamous cell carcinoma (OSCC) is high, up to 36%. Germline and somatic copy number variations in mitochondrial DNA of OL patients have earlier been noted. We sought to test the hypothesis that about 36% of patients with the pre-cancerous lesion (OL) will possess somatic mutations in genes that are recurrently mutated in OSCC.

Methods: Whole exome sequencing of DNA isolated from the affected oral tissue and from peripheral blood of twelve OL patients with dysplasia, was used to profile the landscape of autosomal somatic recurrent mutations in OL and to investigate whether mutations in the genes that drive OSCC are present in OL patients or whether the mutational landscapes of OL and OSCC are largely disjoint.

Results: We have detected mutations in some genes that drive both oral leukoplakia and oral cancer. TGFB2 is recurrently mutated in OL as well as in head and neck squamous cell carcinoma (HNSCC). Some significantly mutated genes in OSCC or HNSCC, viz., FAT1, NOTCH1 and CDKN2A are also found to be mutated in OL patients. Further, we have identified that MAPK signalling and oxidative phosphorylation (OXPHOS) pathways are significantly altered in OL patients.

Conclusion: We have found that the proportion of OL patients with epithelial dysplasia among whom mutations were found in the set of genes that is also recurrently mutated in OSCC/HNSCC, closely corresponds to the fraction (~36%) of patients with dysplastic leukoplakia who develop oral cancer. The leukoplakia patients recruited in this study were free of malignancy in the oral cavity; our results are, therefore, not influenced by field cancerization.

Competing interests
None declared.

P21
Epigenetic mechanisms of carcinogenesis by hereditary breast cancer genes
J. J. Gruber, N. Jaeger, M. Snyder
Genetics, Stanford University, Palo Alto, USA
Correspondence: J. J. Gruber – Genetics, Stanford University, Palo Alto, USA
Human Genomics 2016, 10(Suppl 1):P21

Objectives: BRCA2-induced breast cancers share a predominant histologic and molecular phenotype (ER+, luminal B) that distinguishes them from most sporadic breast cancers and breast cancers arising in other inherited disorders. This suggests that breast cancers arising in BRCA2-mutation carriers have essential shared properties that drive carcinogenesis and can be targeted for intervention. To investigate this observation, we performed a cell biological screen in non-transformed breast epithelial cells for phenotypes specific to BRCA2 loss-of-function.

Methods: Non-transformed breast epithelial cells were treated with siRNAs targeting hereditary breast cancer genes. Growth curves were obtained in complete growth media and growth factor-withdrawal media. Whole genome sequencing and transcriptomics were performed. Functional cell biological assays including treatment with recombinant cytokines and inhibitors were performed.

Results: Despite the role of BRCA2 in homologous recombination-mediated DNA repair, no recurrent de novo mutations were recovered. Instead, we discovered a novel pathway whereby BRCA2 depletion induces strong, persistent transcriptional activation of the chemokines on chromosome 4q13 (CXCL1, CXCL3, CXCL5, CXCL8). Surprisingly, these chemokines were sufficient to stimulate EGF-independent growth of non-transformed breast cells. Furthermore, inhibitors of the receptors of the chemokines impaired cell proliferation after BRCA2 depletion.

Conclusion: Altogether, these findings indicate that transcriptional activation of the 4q13 chemokine locus induces an early cell-autonomous autocrine signaling pathway in BRCA2-mediated carcinogenesis that could be exploited to prevent cancer onset.

Competing interests
None declared.
RNA Direct: a novel RNA enrichment strategy applied to transcripts associated with solid tumors

K. Patel1, S. Bowman1, T. Davis3, D. Kraushaar1, A. Emerman1, S. Russello1, N. Henig1, C. Hendrickson1

1Directed Genomics, USA; 2New England Biolabs, Ipswich, USA

Objectives: RNA sequencing (RNA-Seq) is a powerful tool used for the interrogation of transcripts that enables the analysis of gene expression and the identification of nucleotide or structural variations. RNA-Seq, however, can be cost prohibitive due to the size and complexity of most transcriptomes, which require deep sequencing coverage to achieve the necessary sensitivity for a reliable analysis. By combining targeted enrichment strategies with next-generation sequencing (NGS), a subset of transcript regions or sequences can be enriched and analyzed with the resolution required for both research and clinical applications. Here, we applied a novel RNA enrichment strategy, RNA DIRECT, to the capture of targets commonly associated with solid tumors.

Methods: RNA DIRECT target enrichment utilizes cDNA and probe-based hybridization to capture only desired cDNA sequences with removal of off-target regions via enzymatic digestion. Targeted sequences are then ligated to NGS platform specific adapters and amplified by PCR.

Results: RNA converted to cDNA was used for targeted enrichment with RNA DIRECT. Analysis of sequenced reads showed at least 97% alignment to the transcriptome with greater than 90% aligning to targeted regions. We also report the identification and detection of variants and gene fusions associated with solid tumors with high specificity and sensitivity.

Conclusion: The RNA DIRECT strategy provides a robust and cost-effective method for the enrichment of targeted transcript sequences for the identification and detection of known or novel variants and gene fusions.

Competing interests
None declared.

RNA sequencing identifies gene mutations for neuroblastoma

K. Zhang
Pathology, University of North Dakota, Grand Forks, USA

Objectives: Neuroblastomas are the most common of all malignancies in infants and the most common extracranial malignancy of childhood. With 650 new cases each year it accounts for over 15% of childhood cancer mortality. This neuroectodermally derived malignancy is most often found in the adrenal glands but can be found throughout the body in sympathetic ganglia. Though a small number of cases are familial (1-2%) with known genetic causes, most cases are sporadic with little known about what causes them or what causes the diverse outcomes of this disease.

Methods: The current study used transcriptome sequencing to locate possible genetic mutations from a small cohort of neuroblastoma samples. The mutations were used to construct a phylogenetic tree that demonstrated the tumor progression and predicted the outcome.

Results: Using this method a handful of associated mutations have been found, but few effect disease outcome. In this study we used next generation RNA sequencing to fully sequence 249 neuroblastoma samples. Using these samples and focusing on indel mutations we located 1247 mutated genes that affect the favorable or unfavorable outcome of the disease. Due to the large number of mutations, online databases were used to identify genes associated with neuroblastomas. Comparing these genes to our sample we found a subset of genes that when mutated affected the survival rate of patients.

Conclusion: This study suggests the importance of a few genes that drive the progression of neuroblastomas and determine the clinical outcomes.

Competing interests
None declared.
sensitivity is achieved through a greater read depth, further increasing sequencing costs. Therefore, we utilize a targeted bisulfite sequencing method for the comprehensive analysis of genomic regions relevant to cancer, comprising 8 megabases (~3% of the human genome), covering 3.7 million CpGs, including most RefSeq and GENCODE gene promoters, all known cancer genes, CpG islands, and their shores. Up to 100-fold read depth can be achieved on average by pooling four human prostate samples on one Illumina HiSeq4000 lane.

Results: Of the differentially methylated regions (DMRs) we detected, the majority is hypermethylated in the aggressive versus the indolent prostate tumor. Most DMRs overlap a CpG island and are predominately found in or close to gene promoters, as well as the promoter regions of long non-coding RNAs, and to a lesser extent within gene bodies or intergenic. Often, we find strong hypermethylation of the up- and downstream CpG islands surrounding the transcription start site (TSS), while the TSS itself stays unmethylated. Furthermore, ~70% of the hypermethylated DMRs overlap regions reported to be a bivalent promoter in various cell types from the ENCODE project. The DMRs that can be associated with RefSeq genes are enriched for transcription factors, and more than half of those contain a homeodomain, such as different members of the HOX, SOX and FOX gene families.

Conclusion: The overarching theme for DMRs called in this set of prostate cancers using a targeted deep Methylation- Sequencing approach is hypermethylation of regions within bivalent CpG islands, presenting a prognostic methylation signature that warrants further investigation.

Competing interests
None declared.

P26
Mutant TPMT alleles in children with acute lymphoblastic leukemia from México City and Yucatán, Mexico
S. Jiménez-Morales1, M. Ramírez2, J. Nuñez2, V. Bekker4, Y. Leal5, E. Jiménez2, A. Medina1, A. Hidalgo6, J. Mejía9
1Cancer Genetic Laboratory, National Institute of Genomic Medicine (INMEGEN), Mexico; 2Biològía, FES -Iztacala, UNAM, Mexico; 3Hospital de Pediatría, CMN XXI; IMSS, Mexico; 4Investigación Médica en Inmunología, CMN La Raza, IMSS, Mexico; 5Diagnóstico Molecular H1N1-Influenza, UMAE-IMSS, Mérida, Yucatán, Mexico; 6Hematología Pediatrica, CMN La Raza, IMSS, Mexico; 7Hemato-Oncologia, Hospital Infantil de México, Mexico; 8Cancer Genomics Laboratory, INMEGEN, Mexico; 9Coordinación de Investigación en Salud, IMSS, Mexico

Correspondence: S. Jiménez-Morales – Cancer Genetic Laboratory, National Institute of Genomic Medicine (INMEGEN), Mexico Human Genomics 2016, 10(Suppl 1):P26

Objectives: To know the frequency of the TPMT deficient alleles in children with acute lymphoblastic leukemia and healthy subjects from two Mexican populations

Methods: We included 813 unrelated subjects, 392 were children with ALL and 421 were healthy subjects. Genotyping of the rs1800462, rs1800460 and rs1142345 SNPs was performed by TaqMan assays. To genetically dissect modifier loci of AS, we performed a phenotypic screen of 135 Alms1Gt/Gt backcross progeny from two backcrosses: ((C57BL6/Ei X Balb/cJF1-Alms1+/Gt) X C57BL6/Ei-Alms1+/Gt) and (C57BL6/Ei X Balb/cJF1-Alms1+/Gt X Balb/cJ/Ei-Alms1+/Gt). DNA of the backcross progeny was typed using evenly spaced microsatellite markers throughout the genome and quantitative trait locus (QTL) analysis was performed. Recombinational fine mapping and characterization of subcongeneric lines was used to refine a retinal degeneration QTL on Chr. 2.

Results: QTL for body weight, plasma insulin and triglyceride levels, alanine aminotransferase levels, hepatic steatosis, hepatic fibrosis, and retinal degeneration were mapped to regions on five chromosomes. The location of a major modifier locus on Chr. 2 in which the B6 allele protects Alms1GtGt retinas from rapid photoreceptor degeneration was refined to a 12 Mb region. A candidate mutation in the glutamylation TTTL9 was identified and is associated with reduced glutamylation of tubulin in Balb/cJ-Alms1GtGt retinas.

Conclusion: Elucidation of the genetic networks of Alms1 may lead to a better understanding of the role of Alms1 in metabolic and neurosensoric disease and may provide novel targets for therapeutic intervention.

Competing interests
None declared.

P31
Association of genomic variants with the occurrence of angiotensin-converting-enzyme inhibitor (ACEI)-induced coughing among Filipinos
1National Institutes of Health, University of the Philippines, Manila, Philippines; 2Philippine Genome Center, University of the Philippines, Quezon City, Philippines; 3College of Medicine, University of the Philippines, Manila, Philippines; 4Department of Molecular and Human Genetics, Baylor College of Medicine, Houston, TX, United States; 5Philippine General Hospital, University of the Philippines, Manila, Philippines

Correspondence: E. M. Cutongco De La Paz – National Institutes of Health, University of the Philippines, Manila, Philippines Human Genomics 2016, 10(Suppl 1):P31

Objectives: To genetically dissect modifier loci of AS, we performed a phenotypic screen of 135 Alms1Gt/Gt backcross progeny from two backcrosses: ((C57BL6/Ei X Balb/cJF1-Alms1+/Gt) X C57BL6/Ei-Alms1+/Gt) and (C57BL6/Ei X Balb/cJF1-Alms1+/Gt X Balb/cJ/Ei-Alms1+/Gt). DNA of the backcross progeny was typed using evenly spaced microsatellite markers throughout the genome and quantitative trait locus (QTL) analysis was performed. Recombinational fine mapping and characterization of subcongeneric lines was used to refine a retinal degeneration QTL on Chr. 2.

Results: QTL for body weight, plasma insulin and triglyceride levels, alanine aminotransferase levels, hepatic steatosis, hepatic fibrosis, and retinal degeneration were mapped to regions on five chromosomes. The location of a major modifier locus on Chr. 2 in which the B6 allele protects Alms1GtGt retinas from rapid photoreceptor degeneration was refined to a 12 Mb region. A candidate mutation in the glutamylation TTTL9 was identified and is associated with reduced glutamylation of tubulin in Balb/cJ-Alms1GtGt retinas.

Conclusion: Elucidation of the genetic networks of Alms1 may lead to a better understanding of the role of Alms1 in metabolic and neurosensoric disease and may provide novel targets for therapeutic intervention.

Competing interests
None declared.
Objectives: Angiotensin-converting-enzyme inhibitors (ACEIs) are among the most commonly used drugs in the management of cardiovascular disease. It is used as an antihypertensive and for the alleviation of progressive vascular injury. However, intake of ACEIs may lead to an adverse side effect, uncomfortable dry cough that occur in about 20-25% of patients. Although several genomic variants have been found to be associated with ACEI-induced coughing, there are no published data to adequately address pharmacogenetic utility among Filipino patients. This was undertaken to determine the prevalence and clinical association of candidate genomic variants among Filipinos.

Methods: A case-control study involving 186 unrelated patients who were taking ACEI for at least 6 months was done (101 males, 85 females; 62 cases, 124 controls). DNA from blood samples were extracted and were genotyped using customized Illumina GoldenGate microarray chips for 384 gene variants.

Results: Results show that allelic variants of the genes ZPR1, ADAMTS7, CTB-129P6.7 and LOC157273 are significantly associated with ACEI-induced coughing (OR: 2.34, 3.120, 2.49 and 2.64, respectively, p<0.01). Using genotypic modeling, ZPR1 shows a dominant trend, while ADAMTS7 and CTB-129P6.7 manifest genotypic patterns (Cochran-Armitage test, p<0.01). Further, an intergenic loci in chromosome 4 is also significant. Interestingly, using logistic regression, in addition to ZPR1, ADAMTS7 and CTB-129P6.7, eight variants located proximal to each other in the X chromosome have been associated with the ACEI-induced coughing.

Conclusion: The study presents possible pharmacogenetic markers for Filipinos, as well as genomic regions of interest that may further shed light on the mechanisms of ACEI-induced coughing.

Competing interests None declared.

P32
The use of “humanized” mouse models to validate disease association of a de novo GARS variant and to test a novel gene therapy strategy for Charcot-Marie-Tooth disease type 2D
K. H. Morelli1,2, J. S. Domire3, N. Pyne3, S. Harper2, R. Burgess1
1The Jackson Laboratory, Bar Harbor, USA; 2Graduate School of Biomedical Sciences & Engineering, The University of Maine, Orono, USA; 3Center For Gene Therapy, The Research Institute at Nationwide Children’s Hospital, Columbus, Ohio, USA

Correspondence: K. H. Morelli – The Jackson Laboratory, Bar Harbor, USA

Human Genomics 2016, 10(Suppl 1):P32

Objectives: Mutations in GARS (glycyl tRNA synthetase) cause autosomal dominant Charcot-Marie-Tooth disease type 2D (CMT2D). Thirteen GARS variants have been previously linked to CMT2D. Recently, diagnostic whole exome sequencing revealed heterozygosity for a novel, de novo, 12 base-pair deletion in exon 8 of GARS (c.894_904del12) in a one-year-old female showing symptoms including hypotonia and weakness. This variant causes an in-frame deletion of four amino acids (E299-S302del, referred to as ΔETAQ) within the catalytic domain of the enzyme and is thus likely deleterious. To validate ΔETAQ as the causative mutation, we are currently engineering a “humanized” mouse model in which both the normally functioning human sequence of exon 8 and the mutant ΔETAQ variant sequence of exon 8 have been introduced into the mouse genome.

Methods: We have successfully engineered a mouse that expresses the wild-type human sequence of GARS exon 8 using CRISPR/Cas genome editing technology and are currently engineering a mouse that will express the mutant sequence. Once both strains are verified we will cross them to produce a compound heterozygote with the same putatively pathogenic DNA sequences as the patient (GarsΔETAQ/Δ ETAQ). Once established as stocks, the GarsΔETAQ/Δ ETAQ mice will be evaluated for features of neuropathy observed in other established mouse models of GARS-linked CMT2D. The GarsΔETAQ mice will also provide a humanized disease model for preclinical studies. Previous studies predict that knockdown of mutant GARS should be therapeutically beneficial for patients with CMT2D, provided wild type GARS is preserved. Therefore, we developed a gene therapy strategy that involves the allele-specific knockdown of mutant GARS transcripts by virally delivered RNAi. RNAi vectors designed to target the ΔETAQ variant as well as other confirmed CMT2D-linked GARS variants have been developed and tested in vitro for knockdown efficacy and specificity.

Results: The results of our in vitro studies confirm that we have developed several RNAi sequences that specifically target several GARS variants but not wild type GARS.

Conclusion: Success with this novel gene therapy approach will provide a promising avenue for treatment of CMT2D and other dominantly inherited neuropudemal diseases.

Competing interests None declared.

P34
Molecular regulation of chondrogenic human induced pluripotent stem cells
M. A. Gari1, A. Daila2, H. Alsehli2, A. Gar2, M. Gari3, A. Abuzenanad3
1Medical Laboratory Technology, Saudi Arabia; 2Center of Innovation in Personalized Medicine, King Abdulaziz University, Jeddah, Saudi Arabia

Correspondence: M. A. Gari – Medical Laboratory Technology, Saudi Arabia
Human Genomics 2016, 10(Suppl 1):P34

Objectives: Human induced pluripotent stem cells (hiPSC) are a promising source for chondrogenic stem cells. Sequential differentiation of hiPSC provides a platform for dissecting the molecular pathways associated with chondrogenesis in vivo and could reveal targets for better control of chondrocyte fate for cartilage repair applications. The aim of this study was to use next generation sequencing (NGS) to investigate the transcriptome and the methylome of chondrogenic hiPSCs.

Methods: The hiPSC line (C19) was derived through reprogramming of human dermal fibroblasts using viral vectors expressing Oct4, Sox2 and Klf4. A protocol of sequential growth factors including Activin A, FGF2 and BMP4 was used to drive the formation of chondrogenic progenitors directly from hiPSC colonies. The chondrogenic hiPSCs were characterised exhaustively by tissue engineering, histochimical analysis and biochemical analysis. The transcriptome of undifferentiated hiPSCs, hiPSC derived chondrocytes and native chondrocytes was interrogated utilizing RNAseq on the SOLID S500 XL platform where the polyA fraction was sequenced at a coverage level of at least 25 million reads.

Results: Differential gene expression revealed the induction of several collagen genes including type 1 to type 12, type 14 and type 18 during transition from the pluripotent state to the chondrogenic state (Fig. 7). Collagen regulatory genes such as PCOLCE which drives the endopeptidase cleavage of procollagen as well as regulators of collagen glycosylation were upregulated. The expression of various fibroblasts growth factors (FGFs) including FGF11, FGF22 and insulin growth factor2 (IGF2) was upregulated as well as the Wnt induced secreted protein, WISP2. Mitotic genes were downregulated in derived and differentiated chondrocytes. Integrated methylome and transcriptome analysis revealed the step-wise differentiation process. Conclusion: NGS analysis demonstrated the recapitulation of early events in cartilage development during hiPSC chondrogenesis. The upregulation of many members of the collagen family indicate the intricate nature of collagen expression during chondrogenesis. Further analysis of nonchondrogenic targets may reveal novel pathways for controlling the fate of chondrogenic hiPSCs.

Competing interests None declared.

References
Methods: Blood or bone marrow DNA from 260 patients recruited from tumour-only analysis of NGS in hematological malignancies. We describe a triaging algorithm to identify clinically relevant variants for accurate diagnosis, prognostic risk stratification, and identification of therapeutic targets for genotype-phenotype correlation. Our objective was to design methods for efficient prioritization of variants for interpretation and reporting. We matched trials in cancer. Our objective was to design methods for efficient prioritization of variants for interpretation and reporting. We describe a triaging algorithm to identify clinically relevant variants for accurate diagnosis, prognostic risk stratification, and identification of therapeutic targets for genotype-phenotype correlation.

Results: Of all variants detected by NGS (median 427, range 338–643 variants/case), 35% (median 150, range 125–172 variants/case) passed all MSR quality criteria. Applying a variant allele frequency threshold refined the data to 7.4% of the original dataset (median 30, range 16–48 variants/case). Reporting was restricted to well-covered, exonic nonsynonymous, intronic splice site, and known pathogenic synonymous variants, resulting in a median of 4 variants/case for manual review (range 0–13). When combined with our dataset of >600 interpretations across 8 hematological malignancies, this approach enabled rapid review and interpretation of previously known variants, and an effective system to prioritize novel variants in order of clinical actionability (Sukhai et al., 2015). We excluded variants with high germline population frequencies (median 50, range 42–62 variants/case) through the use of multiple reference population databases.

Conclusion: We describe our approach to prioritize NGS derived variants, based on data quality, functional effects, allele frequency, coverage depth, and coding effects. This approach iteratively utilizes our lab-developed variant knowledge base, and enables us organize and use variant interpretations to generate clinical reports.

References

Competing interests
None declared.

P36
Accessing genomic evidence for clinical variants at NCBI
NCBI, NIH, Bethesda, USA
Correspondence: S. Sherry – NCBI, NIH, Bethesda, USA
Human Genomics 2016, 10(Suppl 1):P36

Objectives: NCBI provides many resources for evaluating and declaring evidence of pathogenicity for an increasing number of human sequence variants. Primary details about a genetic test’s analytical validity and clinical utility are reported in the Genetic Test Repository, and evidence for inferences of variant pathogenicity are summarized in ClinVar. NCBI has developed several tools that integrate these high level records with the more basic factual data describing them as population level variants (dbSNP/dbVar), and deeper still as individual-level observations with called genotypes (the NCBI Genotype Server), phenotypes (dbGaP), whole genome/exome sequences (SRA) and finally as positions on the reference genome (GRCh human reference assemblies).

Methods: Traversing the connections between variant-level records, e.g. GTR, ClinVar and dbSNP, and individual-level data (e.g. genotypes, sequences, samples, and phenotypes) is a computationally intensive activity, and NCBI has developed several new services to precompute these relationships and permit users to quickly move from summary records to individual level data.

Results: This presentation will introduce several of these services including allele registry, the ClinVar beacon search, and the dbGaP genome browser with particular emphasis on how users can access and review individual level data for clinical variants or ad hoc genomic positions of particular interest.

Conclusion: Examples of use include the review of ClinVar records by expert panels, identify research into the existence of specific sequence alleles, automatic notification when new data for specific potential alleles of interest are submitted to NCBI, confirmation of variant properties during manuscript review, and research in general questions of human genetic architecture.

Competing interests
None declared.

P37
NGS-SWIFT: a cloud-based variant analysis framework using control-accessed sequencing data from DBGAP/SRA
C. Xiao, E. Yaschenko, S. Sherry
National Institutes of Health, Bethesda, USA
Correspondence: C. Xiao – National Institutes of Health, Bethesda, USA
Human Genomics 2016, 10(Suppl 1):P37

Objectives: Genetic variation analysis plays an important role in elucidating the causes of various human diseases. The drastically reduced costs of genome sequencing driven by next generation sequence technologies now make it possible to analyze genetic variations with hundreds or thousands of samples simultaneously, but with the cost of ever increasing local storage requirements. The tera- and peta-byte scale footprint for sequence data imposes significant technical challenges for data management and analysis, including...
the tasks of collection, storage, transfer, sharing, and privacy protec-
tion. Currently, each analysis group must download all the relevant
sequence data into a local file system before variation analysis is initi-
ated. This heavy-weight transaction not only slows down the pace of the
analysis, but also creates financial burdens for researchers due to the
cost of hardware and time required to transfer the data over typ-
ical academic internet connections.

Methods: To overcome such limitations and explore the feasibility of
analyzing control-accessed sequencing data in cloud environ-
ment while maintaining data privacy and security, here we intro-
duce a cloud-based analysis framework that facilitates variation
analysis using direct access to the NCBI Sequence Read Archive
through SRA Toolkit, which allows the users to programmatically ac-
cess data housed within SRA with encryption and decryption cap-
abilities and converts it from the SRA format to the desired format
for data analysis.

Results: A customized machine image (ngs-swift) with preconfigured
tools, including SRA Toolkit and NGS Software Development Kit, and
resources essential for variant analysis has been created for instanti-
ating an EC2 instance or instance cluster on Amazon cloud. Perform-
ance of this framework has been evaluated using dbGaP study
phs000710.v1.p1, and compared with that from traditional analysis
pipeline, and security handling in cloud environment when dealing
with control-accessed sequence data has been addressed. We dem-
onstrate that with this framework, it is cost effective to make variant
calls without first transferring the entire set of aligned sequence data
into a local storage environment.

Conclusion: This direct data access approach using NCBI SRA Toolkit
from cloud for next generation sequencing analysis is more cost-
effective in terms of time and disc spaces being used for the analysis,
and thus will accelerate variation discovery using control-accessed
sequencing data.

Competing interests
None declared.

P38
Computational assessment of drug induced hepatotoxicity
through gene expression profiling
C. Rangel-Escareño, H. Rueda-Zarate
Computational Genomics, National Institute of Genomic Medicine,
Mexico City, Mexico
Correspondence: C. Rangel-Escareño – Computational Genomics,
National Institute of Genomic Medicine, Mexico City, Mexico
Human Genomics 2016, 10(Suppl 1):P38

Objectives: Liver is the primary organ responsible for drug metaboli-
ization process. Many currently and normally used drugs could affect
the liver adversely in any combination of the reactions described.
Gene expression profiling can be used to identify the mechanisms
that underlie the potential toxicity of chemicals. This technology has
also been applied to identify biomarkers of toxicity to predict poten-
tial hazardous chemicals. We propose a strategy that allows to com-
pare models (Hu, Rat), protocols (iVV, iVT), dosages (None, Low,
toxicity of 131 compounds, mainly medical drugs and their effect in
the liver.

Methods: The strategy involves differential expression by group con-
trasts or ranking genes based on absolute or relative amounts of
change over time as a function of the drug concentration in relation
to their replicate variances. Once genes are classified, a series of
class discovery methods are applied to identify and analyze pat-
terns of chemical structure, gene profiles over time or gene pro-
files by compound dose. We used the Japanese toxicogenomics
project, data contains a collection of 17,657 Affymetrix® microar-
rays from human in vitro and animal samples. Data are pre-processed
in the R statistical environment using a collection of libraries from
Bioconductor.

Results: Due to the dynamic nature of the data, we implemented a
time course analysis for each species in all dosages and for all
compounds. For every subset, genes are classified according to a
multivariate empirical Bayes statistic for replicated microarray
time course data. Genes were ranked based on large absolute or
relative amounts of change over time as a function of the drug
concentration in relation to their replicate variances. A hierarch-
ical clustering analysis to identify patterns of gene profiles was
performed. Genes were selected based on top ranking according to
their MB statistic.

Conclusion: Our approach involves the development of a pipeline
that involves involves analyses that are hypothesis free or hypothesis
driven. Hepatotoxicity caused by drugs, in particular idiosyncratic re-
actions, is a major challenge to the pharmaceutical industry and phy-
sicians. The application of new technologies, such as genomics,
offers the potential to identify risk factors and clarify the pathogen-
esis of idiosyncratic hepatotoxicity. Even with these technologies the
data mining process is the real challenge.

Competing interests
None declared.

P40
Flowr: robust and efficient pipelines using a simple language-
agnostic approach;ultrasq; fast modular pipeline for somatic
variation calling using flowr
S. Seth1, S. Amin2, X. Song1, X. Mao3, H. Sun1, R. G. Verhaak2, A. Futreal2, J. Zhang1
1Institute of Applied Cancer Science, USA; 2Genomic Medicine,
University of Texas; 3MD Anderson Cancer Center, Houston, USA
Correspondence: S. Seth – Institute of Applied Cancer Science, USA
Human Genomics 2016, 10(Suppl 1):P40

Objectives: Bioinformatics analyses have increasingly become com-
pute intensive processes, with lowering costs of data production and
increasing numbers of samples. Each laboratory spends time creating
and maintaining a set of pipelines, which may not be robust, scalable,
or efficient. Further, the existence of different computing environ-
ments across institutions hinders both collaboration and the portability of ana-
lysis pipelines.

Methods: Flowr is a robust and scalable framework for designing and
deploying computing pipelines in an easy-to-use fashion. It implements
a scatter-gather approach using computing clusters, simplifying the
concept to the use of five simple terms (in submission and dependency
types). Most importantly, it is flexible, such that customizing existing
pipelines is easy, and since it works across several computing environ-
ments (LSF, SGE, Torque, and SLURM), it is portable.

Results: Ultrasq; Using flowr's framework we have created a flexible
pipeline for somatic variant calling. This aligns raw reads, splitting
the processing across multiple nodes of a computing cluster. Results
are gathered, creating a merged bam; which is then split according to
the contigs in the genome. Further steps including de-duplication,
indel-realignment and base-quality recalibration and variant calling
are performed at the contig level, using a scatter-gather approach.
This enables complete processing of a typical whole-exome in about
two hours, and whole-genome in a few hours (depending on the li-
brary size).

Conclusion: Flowr follows the “design once” principle, enabling
the user to develop robust, portable pipelines that can be run on a
host of computing platforms. Further, the same pipeline can be
run on a local machine, computing cluster, or cloud-based envi-
ronment. With automatic logging of each step and the preserva-
tion of the exact commands run to produce the output, the
system allows users to generate an easy-to-use, efficient, and re-
producible analysis pipeline. Ultrasq provides a fast and robust
and modular pipeline for somatic variation calling. This enables
users to easily add new tools and methods are they are released,
and possibly share with other users in a format, which is robust,
efficient and portable.

Availability: http://docs.flowr.space

Competing interests
None declared.
P41
Applying “Big data” technologies to the rapid analysis of heterogenous large cohort data
S. J. White1, T. Chiang1, A. English1, J. Farek1, Z. Kahn1, W. Salerno1, N. Veeraraghavan1, E. Boenink2, R. Gibbs1
1Human Genome Sequencing Center, Baylor College of Medicine, USA; 2Human Genetics Center, University of Texas Health Science Center at Houston, Houston, USA
Correspondence: S. J. White – Human Genome Sequencing Center, Baylor College of Medicine, USA
Human Genomics 2016, 10(Suppl 1):P41

Objectives: Analysis of large cohort genomic data is a complex task, typical bioinformatics approaches use collections of scripts and R code, this becomes difficult to manage as sample numbers grow to 10’s of thousands and file sizes grow to terabytes. We applied “Big data” technologies to the analysis of 578 Hi-seq X whole genomes (WGS) and 10,913 exomes (WES), in both cases we QC’d and integrated billions of variant calls from Atlas and GATK to provide concordant and consensus genotypes.

Methods: Raw variant data was pre-processed to produce key value pairs; keys representing variants and values representing sample specific data stored as JSON. Using a modest Hadoop test cluster (88 cores 512 Gb memory 7tb disk), we imported the data into Hbase tables. WGS data was stored as 578 columns, one column per sample. WES data was stored as a single column due to the large number of samples.

QC and analysis were performed by first building normalised summary tables in Hive, this process required a full Hbase table scan and took several hours to complete. However, once the data was processed, we were able to perform rapid analysis (minutes) on both the WGS and WES data sets using identical SQL queries regardless of how the underlying data was structured.

In this way we were able to perform QC filtering such as Ti/Tv, mappability, monomorphic sites, missingness rates and Hardy-Weinberg by leveraging the power of map-reduce and the rich ecosystem of tools around Hadoop we were able to streamline the analysis of these large genomic data sets, rapidly processing billions of genotypes using simple SQL queries to provide accurate, reproducible QC statistics without the need to track and manage thousands of files.

Competing interests
None declared.

Table 2 (abstract P41). Example of summary statistics comparing Atlas genotype calls with differing allele fraction thresholds with GATK calls.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>GATK Atlas (ORIGINALS)</th>
<th>ATLASDP&gt;=1.0</th>
<th>GATK Atlas (0.25&lt;df&lt;1.0)</th>
<th>ATLASDP&gt;=1.0</th>
<th>GATK Atlas (0.1&lt;df&lt;1.0)</th>
<th>ATLASDP&gt;=1.0</th>
</tr>
</thead>
<tbody>
<tr>
<td>0/0</td>
<td>1,793,94,356</td>
<td>1,788,666,240</td>
<td>1,788,666,240</td>
<td>1,776,686,240</td>
<td>1,776,686,240</td>
<td>1,776,686,240</td>
</tr>
<tr>
<td>0/1</td>
<td>138,744,203</td>
<td>69,153,666</td>
<td>112,165,710</td>
<td>147,763,797</td>
<td>124,056,567</td>
<td>124,056,567</td>
</tr>
<tr>
<td>1/1</td>
<td>79,407,733</td>
<td>60,398,312</td>
<td>73,417,546</td>
<td>49,710,016</td>
<td>73,432,295</td>
<td>73,432,295</td>
</tr>
<tr>
<td>Het/hom</td>
<td>1.75</td>
<td>1.14</td>
<td>1.53</td>
<td>2.97</td>
<td>1.69</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>2,011,546,292</td>
<td>1,908,220,218</td>
<td></td>
<td>1,964,251,496</td>
<td>1,976,142,053</td>
<td>1,976,147,802</td>
</tr>
</tbody>
</table>

P42
FANTOMS web resource for the large-scale genome-wide transcription start site activity profiles of wide-range of mammalian cells
T. Kasukawa1, M. Lizio1, J. Harshbarger1, S. Hisashi1,2, J. Severin1, A. Imad1, S. Sahin1, T. C. Freeman3, A. Sandelin4, P. Carninci1, A. R. R. Forrest1, H. Kawaji1,2, The FANTOM Consortium1
1Center for Life Science Technologies, RIKEN, Yokohama, Japan; 2Preventive Medicine and Diagnosis Innovation Program, RIKEN, Wako, Japan; 3The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Edinburgh, United Kingdom; 4Department of Biology & Biotech Research and Innovation Centre, University of Copenhagen, Copenhagen, Denmark
Correspondence: T. Kasukawa – Center for Life Science Technologies, RIKEN, Yokohama, Japan
Human Genomics 2016, 10(Suppl 1):P42

Objectives: To identify genome-wide transcription start site activities in various mammalian cells, a worldwide collaborative project, FANTOMS (Functional Annotation of Mammalian Cells 5) was organized. In this project, diverse range of mammalian samples (~2000 for human and ~1200 for mouse, including primary cells, cancer cell lines, tissues, and transiting cells in time courses) was profiled to obtain promoter-level transcriptional atlas using high-throughput sequencers. To provide this large-scale data collection to the scientific community, we developed an integrated web resource, the FANTOMS web resource.

Methods: To support various sort of inspections and analyses, the web resource contains several tools. SSTAR (Semantic catalogue of Samples, Transcription initiation And Regulators) provides a wide range of analysis results as well as detailed information of individual samples; ZENBU, a data integration, data processing, and expression enhanced visualization system designed for big data genomics projects, provides interactive way to inspect the entire promoter activities measured in FANTOMS interactively; and Table Extraction Tool (TET) provides an easy-to-use interface to download subsets of the overall FANTOMS expression table in an efficient way. A BioMart instance and a track hub for UCSC genome browser enable us to access our TSS resources with widely used interfaces. Furthermore, PressTo provides an interface to browse human enhancers identified in the FANTOMS project, and Biolayout enable us to visualize biological states in a three dimensional expression space with interactive interface.

Results: The web resource is accessible from the FANTOMS portal page: http://fantom.gsc.riken.jp/S/.
Conclusion: The resource is continuously updating, for example, the data remapped to the recent genomes was added. The FANTOMS web resource is a gateway to access the large expression atlas in mammalian and we describes our challenges to provide large-scale genomic data to the scientific community from multiple aspects.

Competing interests
None declared.

P43
Rapid and scalable typing of structural variants for disease cohorts
W. Salerno1, A. English1, S. N. Shekar2, A. Mangubat2, J. Bruestle2, E. Boerwinkle1,3, R. A. Gibbs1
1Human Genome Sequencing Center, Baylor College of Medicine, Houston, Texas, USA; 2Spiral Genetics, Seattle, Washington, USA; 3Human Genetics Center and Department of Epidemiology, UT School of Public Health, Houston, Texas, USA
Correspondence: W. Salerno – Human Genome Sequencing Center, Baylor College of Medicine, Houston, Texas, USA
Human Genomics 2016, 10(Suppl 1):P43

Objectives: For studies such as the Alzheimer’s Disease Sequencing Project and the CHARGE Consortium, disease complexity manifests as data heterogeneity, requiring informatics that can additively scale to thousands of samples and analytics that go beyond identifying small variants in capture data. Specifically, whole-genome sequencing (WGS) can assess large, complex genomic variation in both coding and non-coding regions. At scale, the challenge of evaluating these structural variants (SVs) becomes the “N+1” problem of incrementally adding samples without having to perpetually reevaluate petabytes of population read data stored in BAM files.

Methods: The Biograph Analysis Format (BAF) is a novel method of indexing NGS data that allows rapid, at-scale queries by coordinate and genomic sequence. A BAF of HiSeq X 30x WGS data is 8.3 Gb, 95% smaller than the corresponding BAM. Generated from the BAM and genomic sequence. A BAF of HiSeq X 30x WGS data for the Alzheimer’s Disease Sequencing Project and the CHARGE Consortium, disease complexity manifests as data heterogeneity, requiring informatics that can additively scale to thousands of samples and analytics that go beyond identifying small variants in capture data. Specifically, whole-genome sequencing (WGS) can assess large, complex genomic variation in both coding and non-coding regions. At scale, the challenge of evaluating these structural variants (SVs) becomes the “N+1” problem of incrementally adding samples without having to perpetually reevaluate petabytes of population read data stored in BAM files.

Results: To evaluate the BAF, we indexed the HS1011 reference genome sequence with 60x coverage on the HiSeq X. The HS1011 individual has previously been characterized for SV content, identifying ~10,000 high-confidence SVs from ~30,000 putative sites. These sites were BAF-queried in less than 60 seconds. SV-tying these sites across 10,000 HiSeq X WGS samples in BAM would require less than 100 TB, 166 CPU hours, and 2.5 total hours. Because the BAF can be batched across individuals, query time grows less than linearly with the number of individuals.

Conclusion: We will describe how the BAF API allows users to query SV data, how these queries inform SV typing, and how BQF typing performs on a pilot set of 100 30x HiSeq X samples from a disease cohort, providing counts and allele frequencies for multiple SV types.

Competing interests
None declared.

P46
Genetic divergence of CYP3A5*3 pharmacogenomic marker for native and admixed Mexican populations
J. C. Fernandez-Lopez1, V. Bonifaz-Peña1, C. Rangel-Escareño1, A. Hidalgo-Miranda2, A. V. Contreras3
1Computational Genomics, Nacional de Medicina Genomica, Mexico City, Mexico; 2Cancer Genomics Laboratory, Nacional de Medicina Genomica, Mexico City, Mexico; 3Nutrigenetics and Nutrigenomics Laboratory, Instituto Nacional de Medicina Genomica, Mexico City, Mexico
Correspondence: J. C. Fernandez-Lopez – Computational Genomics, Nacional de Medicina Genomica, Mexico City, Mexico
Human Genomics 2016, 10(Suppl 1):P46

Objectives: Glutathione S-transferases (GSTs) play a major role in the detoxification of various compounds. Similarly, human sulfotransferases (SULTs) are involved in the metabolism of many drugs, xenobiotics, neurotransmitters and hormones. Polymorphic variants in GST and SULT1A genes were reported for different populations. The objectives of this study were to determine the frequencies of GSTM1 and GSTT1 null genotypes, and the genotype and allele frequencies of SULT1A1 (G638A) gene polymorphism in the Sudanese population.

Methods: GST genotyping was carried out using multiplex PCR while SULT1A1 genotyping was done using PCR-RFLP. Study population included 114 (GST genotyping) and 142 (SULT1A1 genotyping) unrelated healthy Sudanese subjects.

Results: The prevalence of GSTM1 and GSTT1 deletion homozygosity were 54.7% and 42.1%, respectively. The genotype frequencies of SULT1A1 gene polymorphism showed that 40.8% of Sudanese were homozygous for the GG genotype, 50.7% were heterozygous for the GA genotype and 8.5% were homozygous for the AA genotype. The frequencies of the SULT1A1*1 and SULT1A1*2 alleles in the SULT1A1 Gene were found to be 0.66 and 0.34, respectively. There are no significant differences in allelic distribution of GSTM1 gene between the Sudanese and other ethnic groups except for sub-Saharan Africans. As regards the allelic distribution of GSTT1 gene, the Sudanese population is similar to sub-Saharan Africans but significantly different from Europeans. Combined analysis of both genes revealed that 24.6% of Sudanese harbor the deleted genotype of both genes and it is the highest reported so far for an Arab and African population. The frequency of the SULT1A1*2 allele did not differ significantly from Caucasians and African-Americans, but it was much higher than in Asians.

Conclusion: This is the first study that addresses polymorphism of GST and SULT1A1 genes in Sudanese. We provide a reference database of allelic frequencies of the genotypes of these genes among Sudanese.

Competing interests
None declared.

P44
Polymorphism of glutathione S-transferases and sulphotransferases genes in an Arab population
A. H. Salem1, M. Ali1, A. Ibrahim1, M. Ibrahim1
1Anatomy, Arabian Gulf University, Manama, Bahrain; 2Biochemistry, Arabian Gulf University, Manama, Bahrain; 3Central Laboratory, Ministry of Science and Technology, Sudan; 4College of Animal Production Science and Technology, Sudan University of Science and Technology, Khartoum, Sudan
Correspondence: A. H. Salem – Anatomy, Arabian Gulf University, Manama, Bahrain
Human Genomics 2016, 10(Suppl 1):P44

Objectives: Glutathione S-transferases (GSTs) play a major role in the detoxification of various compounds. Similarly, human sulfotransferases (SULTs) are involved in the metabolism of many drugs, xenobiotics, neurotransmitters and hormones. Polymorphic variants in GST and SULT1A genes were reported for different populations. The objectives of this study were to determine the frequencies of GSTM1 and GSTT1 null genotypes, and the genotype and allele frequencies of SULT1A1 (G638A) gene polymorphism in the Sudanese population.

Methods: GST genotyping was carried out using multiplex PCR while SULT1A1 genotyping was done using PCR-RFLP. Study population included 114 (GST genotyping) and 142 (SULT1A1 genotyping) unrelated healthy Sudanese subjects.

Results: The prevalence of GSTM1 and GSTT1 deletion homozygosity were 54.7% and 42.1%, respectively. The genotype frequencies of SULT1A1 gene polymorphism showed that 40.8% of Sudanese were homozygous for the GG genotype, 50.7% were heterozygous for the GA genotype and 8.5% were homozygous for the AA genotype. The frequencies of the SULT1A1*1 and SULT1A1*2 alleles in the SULT1A1 Gene were found to be 0.66 and 0.34, respectively. There are no significant differences in allelic distribution of GSTM1 gene between the Sudanese and other ethnic groups except for sub-Saharan Africans. As regards the allelic distribution of GSTT1 gene, the Sudanese population is similar to sub-Saharan Africans but significantly different from Europeans. Combined analysis of both genes revealed that 24.6% of Sudanese harbor the deleted genotype of both genes and it is the highest reported so far for an Arab and African population. The frequency of the SULT1A1*2 allele did not differ significantly from Caucasians and African-Americans, but it was much higher than in Asians.

Conclusion: This is the first study that addresses polymorphism of GST and SULT1A1 genes in Sudanese. We provide a reference database of allelic frequencies of the genotypes of these genes among Sudanese.

Competing interests
None declared.
and 60 European, 60 African, 90 East Asian from the HapMap project. The Fst statistic was analyzed as measure of the degree of genetic differentiation pairwise populations.

Results: Extreme genetic differentiation among HapMap populations for was observed for CYP3A5*3 (rs776746) as one would expect, particularly for the comparisons of African and European ancestry populations. However, the largest Fst statistic and allele frequencies values was found among Native Americans. For example, the allele frequency of CYP3A5*3 allele is more than 6-fold higher in Tepehuanes (0.43) than Zapotecas (0.07) with Fst value of 0.1746 (largest divergence).

Conclusion: We identified novel CASR variants that have a potential to be related to serum calcium levels in Korean population. Inter-ethnic differences were suggested in some associated SNPs. Given the significant role played by calcium in many diseases and cell signalling, further studies with more East Asian subjects or meta-analyses on them may enable validation of our results and identification of novel genetic loci associated with serum calcium levels.

Competing interests
None declared.

| Table 3 (abstract P46). Genetic differentiation among Native and admixed Mexican populations |
|---------------------------------|-----------------|----------------|----------------|----------------|----------------|
| POP1_name | POP2_name | POP1频率 | POP2频率 | Fst (Pop1vsPop2) |
|----------------|----------------|----------------|----------------|----------------|----------------|
| ZAPOTECAS | CEU(hapmap) | 0.07143 | 0.036 | 0.0062 |
| ZAPOTECAS | YRI(hapmap) | 0.07143 | 0.845 | 0.6026 |
| ZAPOTECAS | JPT+CHB | 0.07143 | 0.2921 | 0.0011 |
| ZAPOTECAS | MEXICAN MESTIZOS | 0.07143 | 0.2263 | 0.0473 |
| ZAPOTECAS | MIXTECOS | 0.07143 | 0.23333 | 0.0507 |
| ZAPOTECAS | MAYAS | 0.07143 | 0.1481 | 0.0150 |
| ZAPOTECAS | TEPEHUANES | 0.07143 | 0.4384 | 0.1746 |
| MAYAS | CEU(hapmap) | 0.1481 | 0.036 | 0.0376 |
| MAYAS | YRI(hapmap) | 0.1481 | 0.845 | 0.4857 |
| MAYAS | JPT+CHB | 0.1481 | 0.2921 | 0.0302 |
| MAYAS | MIXTECOS | 0.1481 | 0.23333 | 0.01188 |
| MAYAS | TEPEHUANES | 0.1481 | 0.4348 | 0.0995 |
| MAYAS | MEXICAN MESTIZOS | 0.1481 | 0.2263 | 0.0100 |
| TEPEHUANES | CEU(hapmap) | 0.4384 | 0.036 | 0.2209 |
| TEPEHUANES | YRI(hapmap) | 0.4384 | 0.845 | 0.1826 |
| TEPEHUANES | JPT+CHB | 0.4384 | 0.2921 | 0.0220 |
| TEPEHUANES | MIXTECOS | 0.4384 | 0.23333 | 0.0456 |
| TEPEHUANES | MEXICAN MESTIZOS | 0.4384 | 0.2263 | 0.0456 |
| MIXTECOS | CEU(hapmap) | 0.23333 | 0.036 | 0.0835 |
| MIXTECOS | YRI(hapmap) | 0.23333 | 0.845 | 0.3764 |
| MIXTECOS | JPT+CHB | 0.23333 | 0.2921 | 0.0045 |
| MIXTECOS | MEXICAN MESTIZOS | 0.23333 | 0.2263 | 0.0011 |
| MEXICAN MESTIZOS | CEU(hapmap) | 0.2263 | 0.036 | 0.0795 |
| MEXICAN MESTIZOS | YRI(hapmap) | 0.2263 | 0.845 | 0.3847 |
| MEXICAN MESTIZOS | JPT+CHB | 0.2263 | 0.2921 | 0.0056 |

P47

Whole exome sequence meta-analysis of 13 white blood cell, red blood cell, and platelet traits

L. Polfus, CHARGE and NHLBI Exome Sequence Project Working Groups Human Genetics Center, University of Texas Health Science Center, Houston, USA

Correspondence: L. Polfus – Human Genetics Center, University of Texas Health Science Center, Houston, USA

Human Genomics 2016, 10(Suppl 1)1

Objectives: Blood cell counts and erythrocyte indices are clinically important indicators of a variety of disease states. The ability to detect and include novel rare variants in gene-based tests is best accomplished via sequencing.

Methods: In order to identify novel genes influencing hematologic traits, we analyzed whole exome sequencing data in 15,459 participants of 6 population-based cohort studies for 13 traits in European descent (EU) and African Americans (AA), analyzed together and separately, in fixed-effects meta-analyses. We analyzed variants individually and aggregated functional and loss-of-function (LOF) variants with MAF<5% within genes using SKAT and T5 burden tests. CRISPR/Cas9 genome editing was performed to functionally follow up a replicated novel finding.

Results: Discovery phase associations identified 4 novel gene-based results and 3 novel single variants meeting exome-wide Bonferroni corrected thresholds (P<2.6x10^-6 and P<1.6x10^-7). Rare functional variants in MYOM2 were associated with mean corpuscular hemoglobin concentration (SKAT EU=AA=2.2x10^-6). In EUs, rare variants in MRPL43 were associated with hemoglobin (TS EU=AA=1.2x10^-5). LOF Variants in MMAHC were associated with hemoglobin (SKAT P EU=AA=1.3x10^-6). MMAHC regulates vitamin B12 metabolism and known variants cause a Mendelian syndrome including anemia. In AAs, rare functional variants in ACTN4 were associated with mean corpuscular volume (SKAT P EU=AA=1.5x10^-6). ACTN4 variants were previously associated with focal segmental glomerulosclerosis of the kidney. Among the single variant tests, we found low-frequency variant rs9565446 (MAF=0.03, P EU=AA=1.5x10^-6) in AGBL3 to be associated with basophil count. A common variant in CPS1 (rs1047891, MAF=0.33, P EU=AA=5.7x10^-6) was associated with platelet count. We also identified an association of platelet count with a low-frequency (MAF=0.009) synonymous variant (rs150813342, P EU=AA=4.7x10^-4) in GFI1B, a gene known to cause gray platelet syndrome. In silico algorithms predict rs150813342 to affect exon 5 splicing. Replication in up to 52,024 individuals were significantly associated with lower platelet count for CPS1 (rs1047891 (MAF EU=AA=0.328, P=1.02x10^-6)) and GFI1B (rs150813342 (P=5.71x10^-21)).

Conclusion: In this exome sequencing study, we identified a novel low frequency loci. We demonstrate an alternative splicing mechanism by which the GFI1B rs150813342 variant suppresses formation of a GFI1B isoform that preferentially promotes megakaryocyte differentiation and platelet production.

Competing interests
None declared.

P48

Association of adipok gene with type 2 diabetes and related phenotypes in african american men and women: The Jackson heart study

S. Davis1, R. Xu2, S. Gebeab1, P Riestra1, A Gaye1, R. Khan1, J. Wilson2, A. Bidulescu3
1Cardiovascular Section/Metabolic, Cardiovascular and Inflammatory Disease Genomics Branch, National Human Genome Research Institute/National Institutes of Health, Bethesda; 2University of Mississippi Medical Center, Jackson; 3Department of Epidemiology and Biostatistics, Indiana University School of Public Health, Bloomington, United States

Correspondence: R. Xu – Cardiovascular Section/Metabolic, Cardiovascular and Inflammatory Disease Genomics Branch, National Human Genome Research Institute/National Institutes of Health, Bethesda

Human Genomics 2016, 10(Suppl 1)
Objectives: African Americans experience disproportionately higher prevalence of type 2 diabetes and related risk factors. Little research has been done on the association of ADIPOQ gene on type 2 diabetes, plasma adiponectin, blood glucose, HOMA-IR and body mass index (BMI) in African Americans. The objective of our research was to assess such associations with selected SNPs. The study included a sample of 3,020 men and women from the Jackson Heart Study who had ADIPOQ genotyping information.

Methods: Unadjusted and adjusted regression models with covariates were used with type 2 diabetes and related phenotypes as the outcome stratified by sex. There was no association between selected ADIPOQ SNPs with type 2 diabetes, blood glucose, or BMI in men or women.

Results: There was a significant association between variant rs16861205 and lower adiponectin in women with minor allele A in the fully adjusted model ($\beta$SE) p = -.13(0.05), 0.003. There was also a significant association with variant rs7627128 and lower HOMA-IR among men with minor allele A in the fully adjusted model ($\beta$SE) p = -0.74(0.20), 0.0002.

Conclusion: These findings represent new insights regarding the association of ADIPOQ gene and type 2 diabetes and related phenotypes in African American men and women.

Competing interests
None declared.

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
Integrated Research Center for Genome Polymorphism, The Catholic University of Korea, Seoul, Korea, Republic Of
Correspondence: S. H. Jung – Integrated Research Center for Genome Polymorphism, The Catholic University of Korea, Seoul, Korea, Republic Of
Human Genomics 2016, 10(Suppl 1):P49

Objectives: Calcium is a universal intracellular messenger that has an important role in controlling various cellular processes. In this study, we attempts to evaluate the genetic polymorphisms that affect serum calcium levels in Korean population through a two-stage genome-wide association study with the sample of 8642 unrelated Koreans (4558 for discovery and 4093 for replication).

Methods: Study subjects were selected from an ongoing population-based study known as the Korean Genome and Epidemiology Study (KoGES) and genotyped using the Affymetrix Genome-Wide Human SNP Array 5.0. We applied standard quality control parameters such as SNP call rate >95%, minor allele frequency >5% and HWE P>0.001. After this quality control process, genotypes of 4558 individuals for 1219546 autosomal SNPs were used for stage 1 association analysis.

Results: Using SNP arrays, we discovered 963 associated SNPs in stage 1, and replicated 105 SNPs among them in stage 2. We examined them in a combined set of stage 1 and 2 samples and observed that 65 SNPs were significantly associated with serum calcium levels. Among them, rs13068893 in the CASR gene showed the strongest significance (P=3.85x10–8). Considering the high allele frequency and significance level of the rs13068893 C>G in the CASR gene, this SNP may have a key role in regulating the serum calcium level. We also successfully replicated the four loci (CASR, CSTA, DGKD and GCKR) using our data set that have been previously reported to be significantly associated with calcium levels in Europeans and Indians.

Conclusion: In this exome sequencing study, we identified a novel low frequency loci. We demonstrate an alternative splicing mechanism by which the GFI1B rs150813342 variant suppresses formation of a GFI1B isoform that preferentially promotes megakaryocyte differentiation and platelet production.

References

Competing interests
None declared.

P50
Inference of multiple-wave population admixture by modeling decay of linkage disequilibrium with multiple exponential functions
Y. Zhou, S. Xu
Max-Planck Independent Research Group on Population Genomics, CAS-MPG PARTNER INSTITUTE FOR COMPUTATIONAL BIOLOGY, Shanghai, China
Correspondence: S. Xu – Max-Planck Independent Research Group on Population Genomics, CAS-MPG PARTNER INSTITUTE FOR COMPUTATIONAL BIOLOGY, Shanghai, China
Human Genomics 2016, 10(Suppl 1):P50

Objectives: To infer the histories of complex admixture, two important challenges stand out with methods based on the admixture-introduced linkage disequilibrium (LD): getting rid of the effect of confounding LD (CLD) brought by source populations and fitting LD decay induced by admixture. In previous studies, the decay curve of weighted LD between pairs of sites whose genetic distance were bigger than a certain starting distance was fitted by single or multiple exponential functions, for the inference of single- or multiple-wave of admixture.

Methods: In this study, we developed a new LD based algorithm, named MALDmef, to date the multiple-wave admixtures. Different from previous software, MALDmef takes advantage of derived source populations to reduce the effect of CLD and fits the remaining weighted LD decay curves with hundreds of exponential functions.

Results: The performance of MALDmef was evaluated by simulation and it was shown to be more accurate than MALDER, a state-of-the-art LD based method that was recently developed for similar purposes, under various admixture models. We further applied MALDmef to analyzing genome-wide data from the Human Genome Diversity Project (HGDP) and the HapMap Project. Interestingly, we were able to identify more than one admixture events in several populations, which have yet to be reported. For example, two major admixture events were identified in Xinjiang Uygur, occurring around 27–30 generations ago and 182–195 generations ago, respectively. In an African population (MKK), three recent major admixture events occurring 13–16, 50–67, and 107–139 generations ago were detected.

Conclusion: Our method is a considerable improvement over other current methods and further facilitates the inference of the histories of complex population admixtures.

References
1. Ying Zhou, Kai Yuan, Yaoliang Yu, Xumin Ni, Pengtao Xie, Eric P Xing, Shuhua Xu*. Inference of multiple-wave population admixture by modeling decay of linkage disequilibrium with multiple exponential functions. doi: http://dx.doi.org/10.1101/026757

Competing interests
None declared.

P51
A Bayesian framework for generalized linear mixed models in genome-wide association studies
X. Wang, V. Philip, G. Carter
System Genetics, The Jackson Laboratory, Bar Harbor, USA
Correspondence: X. Wang – System Genetics, The Jackson Laboratory, Bar Harbor, USA
Human Genomics 2016, 10(Suppl 1):P51

Objectives: Recent technical and methodological advances have greatly expanded genome-wide association studies (GWAS). The advent of low-cost whole-genome sequencing facilitates high-resolution variant identification, and the development of linear mixed models (LMM) improves identification of putatively causal variants. While essential for correcting false positive associations due to population
stratification, LMMs have been restricted to numerical variables. However, phenotypic traits in association studies are often categorical, coded as binary case-control or ordered variables describing disease stages. Furthermore, optimally integrating the results of prior studies remains a methodological challenge.

Methods: To address these issues, we have devised a method for genomic association studies that implements a generalized linear mixed model (GLMM) in a Bayesian framework, called Bayes-GLMM. Bayes-GLMM has four major features: support of categorical variables; cohesive integration of previous GWAS results for related traits by Bayesian modeling; correction for sample relatedness by mixed modeling; and model estimation by both MCMC sampling and maximal likelihood estimation.

Results: To demonstrate our method, we applied Bayes-GLMM to the whole-genome sequencing cohort in the Alzheimer's Disease Sequencing Project (ADSP). This study contains 576 individuals distributed across 111 families, each with Alzheimer's disease diagnosed at four confidence levels. The profound population structure in these data required a mixed model approach, and the categorical trait necessitated a generalized model.

Conclusion: In summary, this work provides the first implementation of a flexible, generalized mixed model approach in a Bayesian framework.

Competing interests
None declared.

P52
Targeted sequencing approach for the identification of the genetic causes of hereditary hearing impairment
A. A. Abuzenadah1, M. Gari 1, R. Turki2, A. Dallol1
1Center of Innovation in Personalized Medicine, Faculty of Applied Medical Sciences, King Abdulaziz University, Saudi Arabia; 2Ob/Gyn, King Abdulaziz University Hospital, Jeddah, Saudi Arabia
Correspondence: A. A. Abuzenadah – Center of Innovation in Personalized Medicine, Faculty of Applied Medical Sciences, King Abdulaziz University, Saudi Arabia
Human Genomics 2016, 10(Suppl 1):P52

Objectives: Hearing loss is one of the most common afflictions in the world affecting about one in every 1000 newborns (Petersen and Willems 2006). Genetic factors are estimated to be the underlining cause of more than half of the hearing loss cases. The majority of hereditary hearing loss cases is not associated with syndromes (nonsyndromic hearing loss; NSHL) which can be transmitted in an autosomal recessive, autosomal dominant or X-linked modes of inheritance (Petersen and Willems 2006). At least half of the hereditary NSHL cases are caused by mutations in the GJB2/CONNEXIN26 gene (Hereditary Hearing Loss Home Page, http://webh01.uu.ac.be/ hhh/). However, the contribution of GJB2 mutation to NSHL in the Kingdom of Saudi Arabia is minimal (Al-Qahtani et al. 2009) where the rate of children affected with sensoneural hearing loss was estimated to be approximately 26 children out of 1000 (Bafaqeeh et al. 1994). NSHL can be caused by mutations affecting any one of over 80 deafness loci identified so far making NSHL a very heterogenous trait and complicates diagnosis and genetic counseling (Hilgert et al. 2009).

Methods: The recent advancements in targeted sequencing technologies have made it feasible to sequence multiple genes at a reasonably low cost. Therefore we have designed a targeted sequencing panel using the Ampliseq technology to amplify and sequence 84 genes known to cause NSHL. Genes were selected and custom primers were designed and manufactured through the Ampliseq portal (http://ampiseq.com).

Results: The design resulted in a coverage of 97.42% generating 2697 amplicons with a size range of 125–275 bp in two pools and generating 500.44 kb of DNA sequence.

Conclusion: This panel, which we termed OtoScan will be a useful front line genetic screening tool that will speed up the identification of many genetic causes of hereditary deafness in the Kingdom of Saudi Arabia.

Competing interests
None declared.

P53
Identification of enhancer sequences by ATAC-seq open chromatin profiling
A. Uyar1, A. Kaygun2, S. Zaman1, E. Marquez1, J. George1, D. Ucar1
1The Jackson Laboratory for Genomic Medicine, Farmington, USA; 2Department of Mathematical Engineering, Istanbul Technical University, Istanbul, Turkey
Correspondence: A. Uyar – The Jackson Laboratory for Genomic Medicine, Farmington, USA
Human Genomics 2016, 10(Suppl 1):P53

Objectives: Enhancers are cis-regulatory elements that regulate gene expression in the control of cell type-specific functions, developmental fate and evolution. Recent studies revealed the importance of enhancer misregulation for the pathogenesis of certain diseases including cancer through point mutations in either regulatory elements or factors modulating enhancer-promoter communication. Enhancers are often located far from their target gene promoters within the noncoding genome, which makes their identification challenging. Using statistical models, such as ChromHMM, we can infer enhancer locations by studying multiple histone modifications obtained by the ChIP-seq technology. However, ChIP-seq requires large cell numbers (~10M), which is not compatible with clinical samples. The Assay for Transposase Accessible Chromatin (ATAC-seq) is an alternative assay to generate chromatin accessibility maps from 500–5,000 cells, making this an ideal approach to study enhancers in clinical samples. Here we developed a machine-learning model to infer the entire repertoire of enhancers from ATAC-seq open chromatin profiles.

Methods: We conduct our analysis on ATAC-seq data generated from GM12878 human lymphoblastoid cell line and CD4+ T-cells. From these samples, we extracted i) ATAC-seq features, e.g., peak strength; ii) DNA sequence based features, e.g., conservation scores; and iii) TF binding features using footprinting algorithms and compiled a comprehensive dataset. We applied Random Forest algorithm on this data to predict reference enhancers obtained from ChromHMM models.

Results: Our final data include ~60K ATAC-seq peaks and 490 features and a class indicating chromatin state obtained via ChromHMM. Random Forest based model predicted enhancer sequences with 74.8% sensitivity and 73.8% specificity. We also showed that the most important features for accurately predicting enhancer sequences include ATAC-seq based features and certain TF binding profiles.

Conclusion: The present study demonstrated that prediction of regulatory elements using ATAC-seq data alone is comparable to ChromHMM predictions. It is noteworthy that ChromHMM states are also predictions and the actual performance of ATAC-seq based model needs to be tested on experimentally validated enhancers. Our future work includes comparing our predictions with known enhancers from public databases such as FANTOMS and Vista enhancers.

Competing interests
None declared.

P54
Direct enrichment for the rapid preparation of targeted NGS libraries
C. L. Hendrickson1, A. Emerman 1, D. Kraushaar 1, S. Bowman 1, N. Henig1, T. Davis1, S. Russello 2, K. Patel1
1Directed Genomics, Ipswich, USA; 2New England Biolabs, Ipswich, USA
Correspondence: C. L. Hendrickson – Directed Genomics, Ipswich, USA
Human Genomics 2016, 10(Suppl 1):P54

Objectives: Target enrichment, coupled with next-generation sequencing, enables the interrogation of specific targets of interest at a level of sensitivity that is typically cost-prohibitive with whole genome sequencing. However, the drawbacks to target enrichment generally include longer and more complex library preparation workflows or a loss of the ability to detect PCR duplicates. Here we present DIRECT target
enrichment, a unique and highly specific method for hybridization-based target enrichment that incorporates the use of unique molecular indexes in a simple, one-day protocol.

**Methods:** DNA was isolated from fresh frozen tissue, FFPE samples, and liquid biopsies followed by enrichment of 36 kb of cancer-related targets with the DIRECT enrichment method. Combined with unique molecule barcoding and Illumina sequencing, variants were detected and frequencies reported using common variant callers.

**Results:** Application of DIRECT target enrichment across different DNA sample types show similar results, with no loss in specificity or sensitivity across DNA isolated from different sources. Somatic variations can be detected with high sensitivity using as little as 50 ng of input DNA, and libraries can be made with as little as 10 ng of starting material for the detection of genetic variations.

**Conclusion:** DIRECT target enrichment enables the highly specific capture of regions of interest within 7 hours and with low amounts of starting material. As a result, this method can easily be applied to a variety of applications for which time and sample amount may be limiting.

**Competing interests**
None declared.

**P56**

**Performance of the Agilent D5000 and High Sensitivity D5000 ScreenTape assays for the Agilent 4200 TapeStation System**

R. Nitsche, L. Prieto-Lafuente


**Correspondence:** R. Nitsche – Agilent Technologies, Agilent Technologies, Waldbronn, Germany

**Human Genomics 2016, 10(Suppl 1):P56**

**Objectives:** This Poster focuses on the performance of both D5000 ScreenTape assays with respect to the accuracy and precision of quantification and sizing, as well as the sensitivity of these assays. Data analysis for quantification and molarity determination was compared against the corresponding assay for the Agilent 2100 Bioanalyzer system. Additionally, performance of both the D5000 and High Sensitivity D5000 assays on the 4200 TapeStation was compared to the 2200 TapeStation system.

**Methods:** The 4200 and 2200 TapeStation systems were used with the D5000 and High Sensitivity D5000 ScreenTape assays.

**Results:** Data is presented that prove the specifications of sensitivity, reproducibility, accuracy and linearity of the new D5000 assay for the Agilent 4200 TapeStation system.

**Conclusion:** This Poster shows that the Agilent D5000 ScreenTape and Agilent High Sensitivity D5000 ScreenTape assays for the Agilent 4200 TapeStation system provide highly accurate and reproducible sizing and quantification of DNA fragments ranging from 100 to 5,000 bp. Furthermore, it demonstrates that the assays can also be applied to determine the DNA average region size, molarity, and concentration of distributed DNA smears. The sizing, concentration, and molarity results highly correlate with the data obtained from equivalent assays on the Agilent 2100 Bioanalyzer system. In addition, D5000 and High Sensitivity D5000 ScreenTape assays show equivalent performance in the 4200 and Agilent 2200 TapeStation systems.

**Competing interests**

**P57**

**ClinVar: a multi-source archive for variant interpretation**

M. Landrum, J. Lee, W. Rubinstein, D. Maglott

NHG/NLM/NCBI, Bethesda, USA

**Correspondence:** M. Landrum – NHG/NLM/NCBI, Bethesda, USA

**Human Genomics 2016, 10(Suppl 1):P57**

**Objectives:** ClinVar archives submitted interpretations of the medical importance of human variants, standardizes content, and aggregates data from multiple sources to facilitate peer review and track revisions.

**Methods:** Interpretations are provided by clinical testing laboratories, research laboratories, OMIM®, GeneReviews®, locus-specific databases, expert panels and organizations that provide practice guidelines. ClinVar integrates those data with information from other NCBI databases such as dbSNP, dbVar, Gene, and MedGen.

**Results:** The ClinVar website can be searched with gene symbols, variant names including HGVS expressions, rs numbers, and diseases or phenotypes. Searches with many results may be narrowed with filters, such as restricting to a clinical significance, type of variant, and more. Searching by location is facilitated by Variation Viewer, a browser to view all NCBI variation data in a region of interest, such as a region of structural variation. Each row of the search results table in ClinVar links to a page for that variant(s), which has two major sections: aggregate data and submitter-specific data. The aggregate data section provides a summary of information about the interpreted variant(s). The summary includes the review status for the variant(s), represented with a description and a number of gold stars, and a variation identifier, which is a unique identifier that represents the variant(s) that were interpreted. The summary also displays an overall clinical significance, which is calculated based on interpretations provided by submitters; ClinVar staff do not curate or review clinical significance. A list of conditions for which the variant was interpreted is provided, as well as general information about the variant including links to other public databases. The submitter-specific section includes details of the assertions of clinical significance and evidence provided by each submitter. Evidence may include citations, counts of individuals with the variant, free text descriptions of the evidence, and more. Data is updated only by the submitter; thus maintenance of an interpretation and the supporting evidence is the responsibility of each submitter.

**Conclusion:** Those with new evidence and interpretations are encouraged to contribute their own data to improve content for all. An online Submission Portal is available to upload data to ClinVar, as a single submission or in batch. ClinVar provides monthly releases available via FTP, and API to access specific records.

**Competing interests**
None declared.

**P59**

**Association of functional variants and protein physical interactions of human MUTY homolog linked with familial adenomatous polyposis and colorectal cancer syndrome**

Z. Abduljaleel, W. Khan, F. A. Al-Alaf, M. Athar, M. M. Taher, N. Shahzad

1. Department of Medical Genetics, Faculty of Medicine, Umm Al-Qura University, Makka, Saudi Arabia; 2. Department of Basic Sciences, College of Science and Health Professions, King Saud Bin Abdul Aziz University for Health Sciences, Riyadh, Saudi Arabia

**Correspondence:** Z. Abduljaleel – Department of Medical Genetics, Faculty of Medicine, Umm Al-Qura University, Makka, Saudi Arabia

**Human Genomics 2016, 10(Suppl 1):P59**

**Objectives:** To the best of our knowledge, this is the first report confirming the structural and functional association of MUTYH mutations (Y165C; G382D; P54S; A22V; Q63R; G45D; S136P and N435) through In-silico approach.

**Methods:** We retrieved clinical records of MUTYH for multiple adenomas, test unit Code 84304 from the Mayo Medical Laboratory, USA. The nonsynonymous single nucleotide polymorphisms (nsSNPs) may alter the structure or function of expressed proteins, and therefore have an effect on disease outcome. In order to evaluate the phenotypic effects of nsSNPs in human DNA repair genes, we studied the polymorphism in terms of various functional properties. The molecular origin of disease-related phenotypes was caused by six mutations in MUTYH, and that were associated with heritable predisposition of colon and stomach cancer syndrome of FAP.

**Results:** We confirmed that MAP was inherited in an autosomal recessive pattern due to the mutations in MutY (P54S, A22V, Q63R, G45D, S136P and N435), hence both copies of the gene become inactivated during disease occurrence. The parents of an individual with an
Correspondence: Regensburg, Regensburg, Germany

In-silico the identified important features of the HMUTYH mutations through a fresh avenue for the FAP researchers. We also strongly believe that the identified important features of the HMUTYH mutations through our In-silico study will support further in vitro studies in future.

Competing interests
None declared.

P60
Modification of the microbiom constitution in the gut using chicken IgY antibodies resulted in a reduction of acute graft-versus-host disease after experimental bone marrow transplantation

A. Bouazzouli1,2, E. Huber1, A. Dan1, F. A. Al-Allaf1, W. Herr1, G. Sprotte2, J. Kostler2, A. Hieregeist2, A. Gassner4, R. Andreessen4, E. Holler4, 
1Science and Technology Unit, Umm Al-Qura University, Mecca, Saudi Arabia; 2Department of Medical Genetics, Umm Al-Qura University, Mecca, Saudi Arabia; 3Medical Clinic 3 – Hematology/Oncology, University Hospital Regensburg, Regensburg, Germany; 4Department of Pathology, University Hospital Regensburg, Regensburg, Germany;

IgNova Gmbh, Oberuern, Germany; 5Department of Medical Genetics, Faculty of Medicine, Umm Al-Qura University, Mecca, Saudi Arabia; 6Department of Anesthesiology, University of Würzburg Medical School, Würzburg, Germany; 7Department of microbiology, University Hospital Regensburg, Regensburg, Germany

Correspondence: F. A. Al-Allaf - Science and Technology Unit, Umm Al Qura University, Mecca, Saudi Arabia

Human Genomics 2016, 10(Suppl 1):P60

Objectives: GVHD remains the major cause of morbidity and mortality after allogeneic stem cell transplantation. This is particularly true for intestinal GVHD, therefore new methods are urgently needed. One approach is the reduction of pathogenic bacteria.

Methods: Using a haploidentical murine model, B6D2F1 mice conditioned with total body irradiation (TBI) received bone marrow cells and splenocytes from either syngeneic (B6D2F1) or allogeneic (C57BL/6) donors. After that, animals received from day -2 until day +28 chow with egg yolk (IgY) containing antibodies against E. coli, S. typhimurium and C. perfringens (in alternative protocol, mice received chow from day -2 until day 15). As control the mice received chow without egg yolk. After treatment the effect on the severity of aGVHD, cytokines, chemokines and pathogen-associated molecular patterns products (PAMP) were analyzed. Furthermore the bacterial load and microbial constitution in the stool were determined using real time PCR and new generation sequencing method.

Results: Animals received IgY chow showed reduced GVHD severity, improved survival and less organ damages compared to control animals. The improvement was associated with significantly diminished expression of TNF, IL-2 and IL-6 levels in the serum and correlated with decreased bacteria load in the stool, especially E. coli. Interestingly, the bacterium L. reuteri showed increased load in IgY treated animals. This result is in line with early works showed that Lactobacillus mediated protection again aGVHD (1, 2). The expression of TLR2, 4 and NOD2 was also reduced in the gut of IgY mice.

Conclusion: Feed pellets with egg yolk containing chicken antibodies (IgY) improved GVHD and reduced the cytokine, chemokine and PAMP expression. Furthermore IgY antibodies decreased the pathogenic and improved the probiotic bacteria in the colon.

References

Disclosure of interest
None declared.

P61
Compound heterozygous mutation in the LDLR gene in Saudi patients suffering severe hypercholesterolemia

F. Al-Allaf1–2, A. Alashwafi3, Z. Abduljaaleel1–2, M. Tahan1,2, A. Bouazzouli1,2, H. Abalkhail3, A. Al-Allaf2, R. Barmardadh3, M. Athar1,2
1Department of Medical Genetics, Faculty of Medicine, Umm Al-Qura University, Saudi Arabia; 2Science and Technology Unit, Umm Al-Qura University, Saudi Arabia; 3Molecular Diagnostics Unit, Department of Laboratory and Blood Bank, King Abdullah Medical City, Makka, Saudi Arabia; 4King Faisal Specialist Hospital and Research Centre, Saudi Arabia; 5Faculty of Medicine, Alfaisal University, Riyadh, Saudi Arabia

Correspondence: F. Al-Allaf - Department of Medical Genetics, Faculty of Medicine, Umm Al-Qura University, Saudi Arabia

Human Genomics 2016, 10(Suppl 1):P61

Objectives: Familial hypercholesterolemia (FH) is most commonly caused by variants in the LDL receptor (LDLR) gene. Herein, we describe a severely affected FH proband and their first-degree blood relatives, the proband was resistant to statin therapy and was managed on an apheresis program.

Methods: Genetic screening for the LDLR variants was performed by exon sequencing analysis. Using a bioinformatics approach we theoretically explored the putative structure of the wild type and mutant LDLR protein and the implication of structural changes on the possibility of LDLR dimer formation.

Results: We identified a compound heterozygous mutation with missense c.1731G>T, p.(W577C) and frameshift c.2027delG, p.(G676Afs*33) variants at exons 12 and 14 of the LDLR gene respectively in a proband of a Saudi family. DNA sequencing of LDLR from the parents demonstrated that the missense variant was inherited from the mother and frameshift variant was inherited from the father. The frameshift variant resulted in a stop signal 33 codons downstream of the deletion, which most likely lead to a truncated protein that lacks important functional domains, including the transmembrane domain and the cytoplasmic tail domain. The missense variant is also predicted to be likely pathogenic and affect EGF-precursor homology domain of the LDLR protein. The segregation pattern of the variants is consistent with the lipid profile, suggesting a more severe FH phenotype when the variants are in the compound heterozygous state. We also describe a three dimensional homology model of LDLR structure and examine the consequence of the missense and frameshift variants, as this could affect the LDLR structure in a region involved in dimer formation, and protein stability.

Conclusion: The finding of a compound heterozygous mutation causing severe FH phenotype is important for the genotype-phenotype correlation. Furthermore, provided bioinformatics based structural analysis of the mutant protein and its molecular consequences on the physiology of FH that could facilitate developing mechanistic models of LDLR function. These results also enlarge the spectrum of FH-causative LDLR variants in the Arab population, including the Saudi population.

Disclosure of interest
None declared.