

---

## Genome Structure and Function

---

**374T ‡** High-throughput functional genomic assessment of known and novel *HNF1A* missense variants to support clinical diagnostic interpretation. S. Althari.

**377T** Primary bilateral macronodular adrenocortical hyperplasia due to mutations in *ARMC5*: New mutations in humans and modeling in zebrafish. A.G. Maria.

**380T** Exome-wide copy number association study for arsenic-induced skin lesions: A prospective study. M.G. Kibriya.

**383T** Age-related structural changes of the olfactory receptor subgenome in human blood cells and autologous brain regions. K. Szigeti.

**386T** Immunotherapy development for *C9ORF72* ALS/FTD using a BAC transgenic mouse model and human antibodies targeting RAN proteins. L. Nguyen.

**389T** Gene discoveries in autism are biased towards intellectual disability. M. Jensen.

**392T** Clinical features in a pediatric population due to chromosome deletions at a third level pediatric Mexican hospital in 24 years period of time: Five case reports. M.D. Hurtado-Hernandez.

**395T** Identification of a novel frameshift mutation in the *MCPH1* gene causes primary microcephaly in a Saudi family. M.I. Naseer.

**398T** Using a combined approach of comparative genomic analysis, luciferase assay and CRISPR/Cas9 to identify and characterize cis-regulatory elements in the critical region of the 9p deletion syndrome. X. Hauge.

**401T** The commitment complex *in vivo* over long intron genes. Y. Leader.

**404T** Comparison of chitinolytic activities among mammalian chitinases and bacterial chitinase. M. Kimura.

**407T** Breakpoint analysis of chromosomes having inverted duplication with terminal deletion by NGS. H. Inagaki.

**410T** Method for deciding detection limit of droplet digital PCR for rare mutations. T. Takahashi.

**413T** Hanwoo-specific structural variations generate genomic diversity in the cattle genome. J. Park.

**416T** Detection of non-reference L1 insertions in the human genome by using a target enrichment method. W. Shin.

**419T** Heterogeneity of human ribosomes inferred from rDNA and rRNA sequencing. R. Nagaraja.

**422T** Extending and improving GENCODE gene annotation. J.E. Loveland.

**425T** The effect and mechanism of inhibiting G6PD activity on the proliferation of *Plasmodium falciparum*. Z. Zhang.

**428T** Detection of rare copy number variants (CNV) in Kaiser cohort using DNA microarray data from Affymetrix axioma array. T. Haldar.

**431T ‡** Pervasive transcriptional dosage compensation buffers impact of autosomal structural variation. R.C. McCoy.

**434T** Characterisation and genotyping structural variation at the malaria-associated human glycophorin A-B-E cluster. W. Algady.

**437T** Human germline mutation hotspots are characterized by a transversion-rich mutation signature. J. Carlson.

---

## Prenatal, Perinatal, and Reproductive Genetics

---

**440T** Do fetal endothelial nitric oxide synthase (eNOS) gene haplotypes influence prolonged preterm rupture of fetal membranes (PPROM)? K. Yanamandra.

**443T** PheWAS analysis of 13,000 individuals detects a common genetic variant that tags the Rh D blood group system in the European population. J. Fadista.

**446T** Genetic diagnosis of disorders of sex development (DSD): A national registry for disease-specific precision health. E.C. Delot.

**449T** Prenatal diagnosis of diastrophic dysplasia: Importance of prenatal approach with NGS panel. M. Tamayo.

**452T** Independent head-to-head comparative diagnostic accuracy of NIPT methods in a prospective Canadian cohort of high-risk and low-risk pregnant women: The PEGASUS study. F. Rousseau.

**455T** The Dutch TRIDENT studies: Implementing NIPT as part of the national prenatal screening program. E.A. Siermans.

**458T** Next generation sequencing based carrier screening study in Chinese population. G. Chen.

**461T** A genomic autopsy of perinatal death: Diagnosis and discovery by whole exome and whole genome sequencing. A.B. Byrne.

**464T** Congenital infection-like phenotypes: Are there any specific particularities available for prenatal diagnosis of rare diseases? N. Bourgon.

**467T** Increased nuchal translucency and Noonan Spectrum Disorders – A Mount Sinai hospital experience. P. Sinajon.

**470T** HDP associated gene analysis in Japanese pregnant women in Maternity Log Study. Y. Tsunemoto.

**473T** Fetal cell-free DNA fraction in maternal plasma is affected by fetal trisomy. N. Suzumori.

**476T** Challenges associated with increasing the predictive power of AMH in controlled ovarian stimulation. S.E. Parets.

**479T** Novel genes for male infertility: Genetic and functional perspectives. D.V.S. Sudhakar.

**482T** Newborn metabolomics: Accurate prediction of gestational age from cord blood. E. Jasper.

**485T** Prenatal screening for 22q11.2 deletions using a targeted microarray-based cell-free DNA (cfDNA) test. J. Shabbeer.

**488T Association between *MTHFR*, *MTHFD1* and *RFC1* gene polymorphisms and unexplained spontaneous pregnancy loss in Korean women.** S. Shim.

**491T Targeted next generation sequencing-based preimplantation genetic screening can enable detection of uniparental isodisomy, familial relationships, and polyploidy.** M. Umbarger.

**494T Broad spectrum of prenatal cultural artifacts detected by microarray.** V. Potluri.

**497T ‡ Novel application of fragile X CCG repeat analysis in a clinical setting: Outcomes and data derived from 716 embryos undergoing preimplantation genetic diagnosis (PGD).** R. Cabey.

---

## Genetic Counseling, ELSI, Education, and Health Services Research

---

**500T Genetic testing in adult cancer patients in palliative care: What they understand, want, and may need.** J. Bodurtha.

**503T ‡ Could population-level genomic screening be cost effective? An economic analysis informed by a large sequencing study.** D.L. Veenstra.

**506T Cancer susceptibility mutations in very young Israeli women with breast cancer.** B. Nehoray.

**509T Hereditary colorectal cancer screening: A 10 year longitudinal study following an educational intervention.** J.C. Carroll.

**512T A reporting of secondary findings in whole exome sequencing in Japan: The Project of HOPE.** Y. Horiuchi.

**515T Assessing the possibility of *RUNX1*, *ETV6* and *GATA2* related germline predisposition in myeloid neoplasms in a somatic cancer setting.** K. Barber.

**518T Potential impact of statin pharmacogenetic testing in an integrated healthcare system: The Integrating Pharmacogenetics in Clinical Care (I-PICC) Study.** S.J. Miller.

**521T Screening African Americans for *APOL1*-associated kidney disease risk: Stakeholder views.** S.M. Fullerton.

**524T Physicians attitudes, knowledge and barriers towards the inborn errors of the metabolism in a university hospital.** F. Suarez.

**527T ‡ Maternal origin of familial 22q11.2 deletions negatively impacts FSIQ scores.** D.E. McGinn.

**530T Early diagnosis of Usher syndrome in non-syndromic young patients with hearing loss, the importance of pretest counseling.** M.F. van Dooren.

**533T Educational approach for TSC families at LeBonheur Children's Hospital Tuberous Sclerosis Center of Excellence.** N. Urraca.

**536T Lessons learned about expanded carrier screening using genome sequencing: Implications for research and practice.** K.A.B. Goddard.

**539T Demystifying biomedical big data analysis through a massive open online course (MOOC).** B.R. Haddad.

**542T Lumping and splitting: An age old dilemma with new age implications for disease classification.** C. Thaxton.

**545T ‡ Fine-scale demography and behavior of male and female human geneticists.** E. Glassberg.

**548T All, some or none: How wanting to learn genomic results differs within a national survey sample.** J.B. McCormick.

**551T Prostate cancer risk follow-up among *BRCA1/2* mutation carriers in Finland.** O. Kajula.

**554T The Rare Genomes Project: Improving our ability to diagnose rare genetic conditions through a nationwide partnership with families.** H. Brooks.

**557T Primary care physician views on direct access pharmacogenomic testing in a community health system.** A.A. Lemke.

**560T Integration of a tool for electronic education and consenting within primary care to enable precision prevention.** M. Moore.

**563T Genotypes associated with phenotypes: A human genetics laboratory exercise.** D. Caporale.

**566T Repatriation of out-of-country molecular testing for disorders targeted by the provincial newborn screening program: Improving access to diagnostic testing in a cost and time efficient manner in Ontario, Canada - Our first year experience.** B. Bélanger.

**569T Phenotate: Crowdsourcing phenotype annotations of genetic disorders through student exercises.** W.H. Chang.

**572T An interactive video vignette successfully teaches pedigree analysis to undergraduates.** D.L. Newman.

**575T Breakthroughs and barriers in secondary/post-secondary partnerships designed to promote research in molecular genetics, human genetics and GMOs.** T.N. Turley-Stoulig.

**578T Evaluating nonresponse bias in a longitudinal study of healthy adults receiving genome sequencing.** S.D. Crawford.

**581T Special considerations for genomic sequencing research in the United States Air Force: Development of the MilSeq Project.** M.D. Maxwell.

**584T A legal analysis of the loss of chance doctrine in the context of genomics and precision medicine.** J. Wagner.

**587T ‡ Experience and specialty impact processes for interpretation and clinical application of genetic test results.** C. Berrios.

**590T Measuring health outcomes in telegenetics.** J. Stock.

**593T Targeted genomic screening in unselected adults.** K.R. Muesig.

---

## Cancer Genetics

---

**596T Male breast cancer susceptibility due to *FANCM* mutation: A case report.** R. Janavicius.

**599T Muir-Torre syndrome presenting with juvenile astrocytoma.** G.E. Tiller.

‡ Indicates Reviewers' Choice Abstract; "ES" Indicates Epstein Trainee Award Semifinalist; "EF" indicates Epstein Trainee Award Finalists

Photographing and recording posters are strictly prohibited if the author has displayed the no photography symbol. You agreed to adhere to this policy when you registered.

- 602T** Evaluation of QIAGEN Clinical Insight as a content resource for variant curation in a CLIA laboratory. K. Karimi.
- 605T** Screening of over 1000 Indian patients with breast and/or ovarian cancer with a multi-gene panel: Prevalence of *BRCA1/2* and non-*BRCA* mutations. A.U. Mannan.
- 608T** Unexpected cancer-predisposition gene mutations in Cowden syndrome and Bannayan-Riley-Ruvalcaba syndrome patients without underlying germline *PTEN* mutations. L. Yehia.
- 611T** Identification of three novel loss of function mutations within *APC*, the causal gene for classical familial adenomatous polyposis. A. Gupta.
- 614T** The HBV receptor gene *SLC10A1* is frequently down-regulated in hepatocellular carcinoma and is associated with poor survival. P. An.
- 617T** The progression of global gene expression in melanoma: From normal skin to metastatic disease. L. Cordeiro.
- 620T** Multi-gene hereditary cancer panel testing for *BAP1*. S. Hiraki.
- 623T** Birth order affects risk of multiple lymphoid cancers in lymphoid cancer families. S.J. Jones.
- 626T** Analysis of circulating tumor cells in multiple myeloma patients reveals mutations in proto-oncogenes and tumor suppressor genes of NF- $\kappa$ B, Ras/MAPK, and PI3K/Akt pathways. D.S. Manjogowda.
- 629T** Gene environment interactions in the context of lobular breast cancer. C. Petridis.
- 632T** Exome sequencing provides evidence of novel genes associated with colorectal cancer and polyps. E.A. Rosenthal.
- 635T** A rare variant in *GOLM1* predisposes to cutaneous malignant melanoma. C. Teerlink.
- 638T** Cisplatin induced gene expression in lung and ovarian cancer cell lines reveal tissue specificity. S.W. Williams.
- 641T** A genetic analysis of the change in prostate-specific antigen concentrations over time. S. Rashkin.
- 644T** Fine-mapping analysis of 152 breast cancer risk loci from OncoArray and iCOGS data. L. Fachal.
- 647T** Melanoma genetics: Larger sample size identifies novel loci and enables causal inference. S. Macgregor.
- 650T** Genome-wide association study identifies novel loci for mammographic breast density. W. Sieh.
- 653T** Prognostic inherited genetic variation in non-small cell lung cancer. F. Abbas Aghababazadeh.
- 656T** Impact of interaction between single nucleotide polymorphisms (SNPs) in neural repair genes and patient characteristics on cognitive outcomes in patients with hematological malignancies treated with hematopoietic cell transplantation (HCT). N. Sharafeldin.
- 659T** Integrative genomic analyses revealed candidate susceptibility genes in GWAS identified loci for colorectal cancer risk. J. Bao.
- 662T** Familial-aggregation of somatic mutations in lung cancers. Y. Chang.
- 665T** Fine mapping of the 6q25 breast cancer risk locus among Latinas reveals additional variants associated with risk. J. Hoffman.
- 668T** Results of *BRCA1/2* testing in 1339 high risk Israeli patients with breast and/or ovarian cancer who were tested negative for the founder mutations. I.M. Kedar.
- 671T** Identification of genetic variants associated with lung cancer risk among European and African Americans with COPD. V.L. Martucci.
- 674T** Height and body mass index as modifiers of breast cancer risk among 22,588 carriers of *BRCA1* or *BRCA2* mutations: A Mendelian randomization study. F. Qian.
- 677T** Genetic variants in the 8q24 region are associated with prostate cancer risk in Mexican men. B. Silva.
- 680T** SNP-SNP interactions associated with prostate cancer aggressiveness in African Americans. H. Tung.
- 683T** Tumor profiling of separated carcinomatous and sarcomatous components from uterine carcinosarcoma biopsies provides insights into their development. Z. Weber.
- 686T** Rare germline variants in the promoter region of *CDKN2B* may cause melanoma predisposition. R. Yang.
- 689T** A esophageal adenocarcinoma susceptibility locus at 9q22 also confers risk to esophageal squamous cell carcinoma by regulating the function of *BARX1*. C.W. Yan.
- 692T** Type 2 diabetes susceptibility variants contribute to breast cancer risk. M.H. Black.
- 695T** Genes associated with pancreatic cancer predict survival and prognosis. A. Gonzalez-Reymundez.
- 698T** HPV16 genomic insights into cervical carcinogenesis: Viral oncogene E7 conservation is critical to carcinogenesis, and relation to human APOBEC3 activity. L. Mirabello.
- 701T** Mosaic truncating *PPM1D* mutations are age-related but lack a strong association with breast cancer risk. T.A. Myers.
- 704T** Inflated genome-wide *de novo* mutation rate in carriers of *TP53* germline mutations. X. Pan.
- 707T** Population-based breast cancer risk estimates associated with mutations in cancer predisposition genes from the CARRIERS study. F.J. Couch.
- 710T** The early evolutionary signatures of clonal hematopoiesis leading to blood based cancers and cardiometabolic conditions. K. Skead.
- 713T** ‡ Functional role of intragenic methylation in alternative splicing in cancer. Y. Lee.
- 716T** NGSEA: Network-augmented Gene Set Enrichment Analysis. H. Han.

- 719T **A tailored topic model integrates both nucleotide context and genomic location heterogeneity in mutational process profiling.** S. Li.
- 722T ‡ **Identification of germline copy number variations (CNVs) using targeted sequencing data on 6q in hereditary lung cancer families.** D. Mandal.
- 725T **Identification and characterization of novel oncogene candidates in invasive breast carcinoma.** D.G. Piqué.
- 728T **Telomere length dynamics from whole genome sequencing using Telomeasure in progressing and non-progressing Barrett's esophagus.** J.M. Shelton.
- 731T **Integrated somatic mutation detection from tumor-normal sequencing data using multiple calling methods.** Y. Wang.
- 734T **Optimal design of single cell studies for detecting and quantifying clonal subpopulations.** J. Yu.
- 737T **Incorporating multiple NGS read features enables detection of transposon insertions across the genome.** A. Zimmer.
- 740T **Tumor mutation burden (TMB) as a marker for DDR and IO combination.** Z. Lai.
- 743T **Tissue-specific feature of whole genome sequencing aids tissue-mapping in plasma.** H. Liang.
- 746T **Expression variability is associated with breast tumour subtype.** J.F. Pearson.
- 749T ‡ **Multiregion high-depth whole exome sequencing of matched primary and metastatic tumors revealed inter- and intra-individual genomic heterogeneity and polyclonal seeding in colorectal cancer metastasis.** Q. Wei.
- 752T **Dissecting tumor-immune system interaction in non-small cell lung cancer using TCGA data.** X. Yu.
- 755T **Integrative approach to cancer driver gene discovery from somatic mutations.** S. Zhao.
- 758T **GATK4 adds germline and somatic copy number variant plus somatic SNV and indel calling.** S.H. Lee.
- 761T **MicroRNA eQTL analysis in pancreatic cancer with efforts towards functional validation.** A. Jermusyk.
- 764T ‡ **Developing validated phenotypic cancer cohorts for molecular stratification and susceptibility assessment, a use case: Patients diagnosed with early versus late stage non-small cell lung cancer.** B.R. Johnson.
- 767T **Subtype-specific expression of long noncoding RNAs in b-cell acute lymphoblastic leukemia.** C. Nodzak.
- 770T **Negative binomial model-based clustering: Discover novel molecular subtypes of ovarian cancer.** Q. Li.
- 773T **Expression-based Variant Impact Phenotyping (eVIP) for determination of somatic mutation function in cancer.** A. Berger.
- 776T **Obtaining high quality transcriptome data from formalin-fixed, paraffin-embedded diagnostic prostate tumour specimens.** L.M. FitzGerald.
- 779T **Development of a lysate-based multiplex proteomics platform using nCounter.** J. Lee.
- 782T **Genomic features of gastric cancer patient-derived xenograft (PDX) models.** C. Zhang.
- 785T **Functional integration of genomic and transcriptomic data using Strand NGS explains drug resistance in basal cell carcinoma.** S. Kapoor.
- 788T **Use of Bionano Optical Maps to identify medically-relevant genomic variation.** A.W.C. Pang.
- 791T **Novel sequencing adapters resolve index-hopping with unique, dual-matched barcoding and enable low frequency mutation detection with consensus analysis.** M. Light.
- 794T **Cell cycle specific copy number profiling from parallel single cell genomics and transcriptomics.** R. Rahbari.
- 797T **Exome sequencing reveals a novel germline gain-of-function EGFR mutation in a young adult with bilateral adrenocortical carcinoma.** S. Akhavanfard.
- 800T **Ion AmpliSeq™ TERT promoter sequencing.** J.M. Kilzer.
- 803T **Effects of 744ins20 - ter240 BRCA1 mutation on breast/ovarian carcinogenesis and role of curcumin in telomerase inhibition.** M. Pongsavee.
- 806T **An integrative detection and analysis of structural variation in cancer genomes.** J. Xu.
- 809T **Comprehensive whole-genome analysis of the primary ENCODE cell line K562.** B. Zhou.
- 812T **Epigenetic regulation of POLG1 in breast cancer.** P. Bajpai.
- 815T **Epigenetic regulation of the Runx2 gene in lung cancer.** A. Herrero.
- 818T **The effect of expression of glycosylation genes, regulators, and targets on cancer cell line sensitivity to drug treatment.** J. Krushkal.
- 821T **Evaluation of circulating cell free DNA in bisulfite sequencing applications.** M. Poulin.
- 824T **Epigenetics modification and gene expression studies upon human amniotic fluid stem cells treated with chemotherapeutic drugs.** P. Upadhyaya.
- 827T **The genetic diversity affects the cell-fate in genotoxicity test.** C.C. Lin.
- 830T **In silico reanalysis reveals novel prognostic miRNAs in pancreatic neuroendocrine tumors.** V.K. Grolmusz.
- 833T **Single cell RNA sequencing identifies novel gene expression signatures in a mouse model of multiple myeloma treated with the cIAP antagonist LCL161.** N.E. Banovich.
- 836T **Genetic variations in alcohol-metabolizing genes (GSTM1, GSTT1, CYP2E1, ADH2 and ADH3) and pancreatitis risk in alcoholics.** V. Aaren.
- 839T **MiR-450a and miR-450b-5p negatively impact the tumorigenic potential of ovarian epithelial cancer cells.** B.R. Muys.

**842T** Whole exome sequencing of patient cell lines with high-persensitivity to radiation exposure identifies ATIC as a novel target for chemoradiosensitization. X. Liu.

**845T** Modeling human cancer syndromes using TALEN and CRISPR/Cas9 mediated genome editing in *Xenopus tropicalis*. K. Vleminckx.

---

## Mendelian Phenotypes

---

**848T** CPT1A p.P479L and long QT syndrome in Northern BC: Evidence for an increased risk for symptomatic hypoglycemia and implications for management. S.A. Collins.

**851T** Blue genes or red genes: Using large scale sequencing cohorts to reassess the pathogenicity of monogenic diabetes genes. T.W. Laver.

**854T** Case report of congenital disorder of glycosylation caused by novel variant on COG6 gene diagnosed in early infancy. Z. Wei.

**857T** Teeth loss and ungueal dysplasia as atypical features in Hunter syndrome. P. Garavito.

**860T** Evaluation of intracerebroventricular enzyme replacement therapy treatment with rhNAGLU-IGF2 from birth onwards in MPS IIIB mice. S.-h. Kan.

**863T** Monoallelic mutations in *OXCT1* in clinically and biochemically proven SCOT deficiency: Evidence of deep intronic mutations? C. Murali.

**866T** ‡ Increased expression of *SLC26A9* delays age at onset of diabetes in cystic fibrosis. A. Lam.

**869T** Biallelic mutations in *GPD1* gene in a Chinese boy mainly presented with obesity, insulin resistance, fatty liver, and short stature. N. Li.

**872T** Very early-onset inflammatory bowel disease in a Mexican patient with an IL10 receptor deficiency due to a novel homozygous *IL10RB* mutation. D.E. Cervantes-Barragan.

**875T** ‡ Genomic characterization of *F8* and *F9* copy number variants in the My Life, Our Future TOPMed hemophilia cohort. M.M. Wheeler.

**878T** ‡ Factor (F)VIII gene mutation type and type of FVIII therapeutic influence the risk of developing neutralizing anti-FVIII antibodies independent of genetic relatedness, age, race, hemophilia A (HA) severity, therapeutic exposure days, and haplotype in HA patients of the PATH Study. T.E. Howard.

**881T** Novel truncating variant in single immunoglobulin Interleukin-1 receptor related (*SIGIRR*) gene in a dominant family with early-onset inflammatory bowel disease. J.E. Horowitz.

**884T** Case report of a patient with uncharacterized IFN- $\gamma$  mediated autoinflammatory disorder. O. Schnappauf.

**887T** Variants in *FOXP1* cause syndromic genitourinary tract defects. N. Bekheirnia.

**890T** Rapid paediatric sequencing (RaPS) from patient to variant: A step-by-step workflow and case report. L. Boukhibar.

**893T** A case of vitamin D-dependent rickets type 1a with a novel-pathogenic variant in a Mexican patient. M. Abreu-González.

**896T** Novel genotype-phenotype correlations in X-linked Alport syndrome: Serum albumin level, age at onset of hematuria and hypertension. L.I. Shagam.

**899T** *CFTR* gene mutations in the São Miguel island (Azores, Portugal): 20 years follow-up study. L. Mota-Vieira.

**902T** A novel mutation in the C-Terminal Associated Peptide (TCAP) region of Teneurin 3 found to co-segregate in all affecteds in a multi-generation family with developmental dysplasia of the hip. G.J. Feldman.

**905T** Potential pathogenic variants identified in a Turkish tooth agenesis cohort via whole exome sequencing. R. Du.

**908T** Dyggve-Melchior-Clausen syndrome, a case report with typical family tree. L. Mora.

**911T** ‡ Multi-center cohorts with animal model and genotype-phenotype analyses: deciphering a new and undefined subtype of congenital scoliosis, *TBX6*-associated congenital scoliosis (TACS). N. Wu.

**914T** Case report of a mild skeletal phenotype secondary to mutations in *LBR* gene. M.D.F. Carvalho.

**917T** Spinal manifestations of patients with musculocontractural Ehlers-Danlos syndrome caused by *CHST14/D4ST1* deficiency (mcEDS-*CHST14*). T. Kosho.

**920T** Investigation of the molecular basis of familial and isolated Tarlov cysts. M. Muriello.

**923T** Early oro-dental manifestations as a clue for the clinical diagnosis of infantile systemic hyalinosis. I.S.M. Sayed.

**926T** Delineation of musculocontractural Ehlers-Danlos syndrome caused by dermatan sulfate epimerase deficiency (mcEDS-*DSE*): Report of additional patients and comprehensive review of reported cases. A. Unzaki.

**929T** Cutaneous neurofibromas in neurofibromatosis type 1: A quantitative natural history study. A. Cannon.

**932T** Synonymous variant in *KCTD7* causes alternative splicing in siblings with progressive epilepsy. D.B. Zastrow.

**935T** Comparison of the mutations that cause Alzheimer's disease on secondary protein misfolding on transgenic mouse models. G. Xu.

**938T** A novel *PRRT2* pathogenic variant in a family with paroxysmal kinesigenic dyskinesia and benign familial infantile seizures. J.G. Lu.

**941T** Japan Consortium of Ataxias (J-CAT): A cloud-based national registry for degenerative ataxias providing comprehensive genetic diagnosis and prospective natural history researches. Y. Takahashi.

**944T** *Tmlhe* and *Bbox1* null mouse models of carnitine deficiency. A. Ye.

---

‡ Indicates Reviewers' Choice Abstract; "ES" Indicates Epstein Trainee Award Semifinalist; "EF" indicates Epstein Trainee Award Finalists

The author listed is the first/presenting author of the abstract. The letter following each poster number indicates the day that the author will present at their posters. W=Wednesday; T=Thursday; F=Friday.

- 947T ‡** The novel aldehyde trap ADX-102 reduces accumulations of GHB and GABA in brain tissue from succinic semialdehyde dehydrogenase-deficient mice. S.G. Macdonald.
- 950T** Novel mutations in *CLN6* cause late-infantile neuronal ceroid lipofuscinosis in two unrelated patients. B. Behnam.
- 953T** Genetic, clinical, and imaging study of Pelizaeus-Merzbacher disease using the Integrative Brain Imaging Support System (IBISS). K. Inoue.
- 956T** Characterizing genetic causes of neurodevelopmental disorders with brain malformations in a predominantly Turkish cohort. J. Punetha.
- 959T** Exome sequencing identifies a novel *FBXO38* variant inherited from a mosaic mother to cause distal hereditary motor neuropathy Type IID with distinct features. S.A. Ugur Iseri.
- 962T** *BICD2*-related arthrogryposis with unexplained cardiomyopathy. R.D. Kastury.
- 965T** Clinical presentation and genotype-phenotype correlation of a complex neurodevelopmental disorder caused by mutations in *ADNP*. F. Kooy.
- 968T** Case report of a patient with a *TANGO2* deletion that provides additional phenotype information. R. Godshalk.
- 971T** *CAD* mutations and uridine-responsive epileptic encephalopathy. I. Bader.
- 974T** New epilepsy genes and variants discovered utilizing patients referred for clinical genetic testing. K. McCarty.
- 977T** *STXBP1* encephalopathy with epilepsy: 6-year-old girl with de novo missense variant in *STXBP1* expands the phenotype. J. Pappas.
- 980T** Whole exome sequencing reveals potential oligogenic inheritance and candidate novel genes in patients with arthrogryposis. Y. Bayram.
- 983T** Clinical and molecular insights into developmental abnormalities of corpus callosum. M. Hebbbar.
- 986T** A novel *de novo* alteration in *SLC12A6* in a patient with early-onset severe progressive sensorimotor polyneuropathy and abnormal EEG. M. Rossi.
- 989T** Expanding the clinical spectrum of *ARL6IP1*-associated hereditary spastic paraplegia. S. Majid.
- 992T ‡** Integrative omics analysis of a cohort of 198 singletons with cerebral palsy. J. Gecz.
- 995T** Heterozygous *COG4* variant causes a non-lethal type of *COG4*-CDG (formerly CDG-IIj). R. Hamid.
- 998T ‡** Mutations of the *ZNF292* gene are a novel cause of neurodevelopmental disability, behavioral problems, and autism spectrum disorders (ASD). G. Mirzaa.
- 1001T** Magnetic resonance spectroscopy and lipid profiling of myelin composition in corpus callosum of mucopolysaccharidosis I mice. S. Le.
- 1004T** The Lysosomal Disease Network. C.B. Whitley.
- 1007T** Further clinical and molecular characterization of the novel autosomal recessive neurodegenerative disorder related to the *ATP8A2* gene. A. Telegrafi.
- 1010T** Myotonia congenita with a novel missense mutation in *CLCN1* gene (c.680T>A, p.Ile227Asn). A. Kiraz.
- 1013T** Search for target genes of transcriptional regulation by dentatorubral-pallidoluysian atrophy protein (DRPLA) that acts as transcriptional co-regulator. K. Hatano.
- 1016T** Mutant human proteins linked to familial neurodegeneration cause secondary protein misfolding in the spinal cord. M.C. Pace.
- 1019T** An autopsy case of familial amyloid polyneuropathy (FAP) with novel transthyretin (TTR) mutation (TTR, Lys80Arg). H. Furuya.
- 1022T** Spastic paraplegia type 4: A novel *SPAST* splice site donor mutation and expansion of the phenotype variability. A. Orlacchio.
- 1025T** Phenotypical features and genetic findings in Lithuanian patients with *CMTX1*. B. Burnyte.
- 1028T** A rare male patient with classic Rett Syndrome caused by *MeCP2\_e1* mutation. A. Goji.
- 1031T** Sensory, behavioral, and social phenotypes observed in individuals with Williams syndrome in Japan. T. Awaya.
- 1034T** Expansion of the molecular and phenotypic spectrum of *CAMTA1*-related neurological disorders. L.B. Henderson.
- 1037T ‡** *De novo* *TCF20* pathogenic variants are associated with intellectual disability, dysmorphic features, hypotonia, and neurological deficits with similarities to Smith-Magenis syndrome: Seven new cases further delineate the phenotypic presentation of this new syndrome. F. Vetrini.
- 1040T ‡** Novel *de novo* *TAOK1* variants associated with a neurodevelopmental phenotype, macrocephaly, and joint hypermobility. H.M. McLaughlin.
- 1043T** *De novo* missense variant in *CSNK2A1* can cause intellectual disability, behavioral problem, and dysmorphic features: The first male child with Okur-Chung neurodevelopmental syndrome. M. Akahira-Azuma.
- 1046T** Alpha-thalassemia X-linked intellectual disability (*ATRX*) syndrome in a Colombian patient. A. Paredes.
- 1049T** Exploring the therapeutic potential of CRISPR/Cas9 technology for the treatment of *MeCP2* duplication syndrome. E. Maino.
- 1052T** Novel *AHDC1* mutations cause intellectual disability and developmental delay. Y. Tsurusaki.
- 1055T** Attempts to elucidate role of *ZBTB11* gene as a novel candidate gene in intellectual disability. Z. Fattahi.
- 1058T** *De novo* LoF mutations in *MED12* cause a syndromic form of X-linked ID in females. D.L. Polla.
- 1061T** Intellectual disability and macrocephaly in three sisters from a consanguineous marriage with a novel *SZT2* homozygous mutation. C. Trujillo.

- 1064T Exome Pool-Seq in neurodevelopmental disorders.** C. Zweier.
- 1067T A new X-linked form of syndromic intellectual disability on Xp11.22.** D.A. Scott.
- 1070T Mutational spectrum of Duchene Muscular Dystrophy in Colombian patients.** P. Ayala-Ramírez.
- 1073T A zebrafish *mut*<sup>0</sup> model recapitulates key aspects of severe methylmalonic acidemia.** K.T. Ellis.
- 1076T Identification of the genetic causes of mitochondrial oxidative phosphorylation (OXPHOS) disease.** S.C. Lim.
- 1079T Severe leukodystrophy with complete clinical recovery caused by recessive *BOLA3* mutations.** C.A. Stutterd.
- 1082T Identification of large effect variants underlying non-syndromic MA in families segregating the disease.** G.A. Arenas-Perez.
- 1085T ‡ Leveraging consanguinity in inherited retinal diseases uncovers missing genetic variation: Rare novel disease genes and a multitude of novel variants in known disease genes.** K. Van Schil.
- 1088T Unique mutation spectrums in hearing-impaired Mongolian patients reveal possible migration events and founder effects of common deafness mutations.** Y.H. Lin.
- 1091T *SLC6A6*: Nutritional therapeutic potential of a novel autosomal recessive gene for progressive retinal degeneration and cardiomyopathy.** E. Ranza.
- 1094T Unexpected difficulties in discovery of genes involved in hearing loss.** S. Naz.
- 1097T A novel homozygous deletion in last exon of *CYP1B1* gene cause primary congenital glaucoma in an Iranian female patient.** M. Noruzinia.
- 1100T Identification of novel candidate genes for recessive visual impairment by analyzing 132 consanguineous families.** M. Ansar.
- 1103T A homozygous truncating variant of *KCNE1* (p.Tyr46\*) associated with deafness in the absence of a long QT interval reveals a novel genotype-phenotype correlation.** R. Faridi.
- 1106T Novel *PXDN* mutations cause microphthalmia and anterior segment dysgenesis.** N. Chassaing.
- 1109T First systematic molecular analysis of 45 Greek patients with retinal dystrophies by next generation sequencing reveals 21 novel mutations in 30 genes and establishes a wide spectrum of distinct retinal degenerative diseases.** S. Kamakari.
- 1112T Unclassifiable brachydactyly (brachydactyly E+A2) due to a novel missense mutation in *IHH*.** H. Numabe.
- 1115T Craniosynostosis: Expanding the phenotype of 3 rare syndromes.** E.H. Zackai.
- 1118T Phenotypic and genotypic spectrum in Richieri-Costa-Pereira syndrome.** D. Bertola.
- 1121T A novel mutation in *PDE3A* gene in a 7-year-old female patient with dysmorphic features, developmental delay, short stature, and unilateral brachydactyly without high blood pressure.** A. Alali.
- 1124T Identification of *AFF4* missense mutation in a girl with Cornelia de Lange syndrome (CdLS) like phenotype and obesity.** E. Nishi.
- 1127T *SATB2*-associated syndrome: Differential diagnosis and genotype-phenotype correlations by detailed facial dysmorphism analysis using facial recognition technology in 38 individuals.** Y. Zarate.
- 1130T Redefining phenotypic spectrum of constitutional *CDK13* mutations: Three patients without cardiac defects.** T. Uehara.
- 1133T The expansion of heterotopic bone in fibrodysplasia ossificans progressiva is Activin A-dependent.** A.N. Economides.
- 1136T A growing need for reverse clinical genomics: Demonstrated by phenotypic characterization of *CDK13*-related disorders.** B. Bostwick.
- 1139T Case report Kleefstra syndrome in a Colombian patient.** A. Nova.
- 1142T Rare syndrome: First reported Egyptian sibs with 3MC(1) syndrome and detection of novel *MASP1* gene mutation in the family.** A.N. Khalaf.
- 1145T Genetic diagnosis and clinical characteristic reviews in neonate patients of *KMT2D* gene mutation caused Kabuki syndrome.** B. Wu.
- 1148T Exome-first approach identified two novel indels and gene deletions in Mowat-Wilson Syndrome cases previously diagnosed as clinical Angelman syndrome.** F. Gosso.
- 1151T Frontonasal dysplasia with facial skin polyps: From Pai syndrome to differential diagnosis through a series of 25 patients.** D. Lehalle.
- 1154T Ovotesticular DSD associated with a pathogenic mutation in the *BMP15* gene.** S. Albanyan.
- 1157T Exome sequencing in a family with autosomal recessive amelogenesis imperfecta.** G. Chavarria-Soley.
- 1160T Twelve novel *GUSB* mutations and genotype-phenotype correlation in mucopolysaccharidosis VII (MPS VII) patients.** Q. Abu Ali.
- 1163T ‡ Frequency of germline pathogenic variation in *NF1* and eight other RASopathy genes in the Exome Aggregation Consortium (ExAC) database: A pilot study.** A. Pemov.
- 1166T Germline mutations associated with polycomb repressive complex 2 cause Weaver syndrome.** E. Imagawa.
- 1169T SOPH syndrome: Multisystem disorder with facial dysmorphism, skeletal dysplasia, episodic liver failure, immune dysfunction and intellectual disability.** A. Yadav.
- 1172T ‡ An integrated clinical program and crowdsourcing strategy for genomic sequencing and Mendelian disease-gene discovery.** A. Haghighi.
- 1175T Oral cavity findings in *A2ML1*-related otitis media.** R.L.P. Santos-Cortez.

1178T **A combinatorial approach for the selection of novel bioactive peptides.** R.R. Handley.

---

## Bioinformatics and Computational Approaches

---

1181T **The ET-HPN highlights a potential ALS-related disease cluster.** B.E. Graham.

1184T ‡ **LabWAS: A catalog of real-world associations between genetic variants and lab values.** J.A. Goldstein.

1187T **Retrospective electronic medical record analysis to identify patients at risk of hypophosphatasia.** C. Peroutka.

1190T ***In-silico* characterization of cell-type composition in adipose tissue: Implications for 'omic analyses and associations to adiposity measures.** C.A. Glastonbury.

1193T **Identification of genes alternatively spliced in HIV-infected CD4+ T-cells.** S. Han.

1196T **A high-throughput deep sequencing approach for CRISPR off-target assessment in therapeutic genome editing applications.** A. Ajetunmobi.

1199T **Understanding chronic fatigue syndrome using immune cell specific RNA-seq in a time series after an exercise perturbation.** P. Comella.

1202T **Hunting rare variants in chronic kidney disease.** S.R. Cameron-Christie.

1205T **The gene expression signature associated with rheumatoid arthritis is altered during pregnancy.** D. Jawaheer.

1208T ***In silico* screening for potentially aberrant novel essential splice sites (PANESS) created by single nucleotide variants (SNVs) in the human genome.** C.C. Bruels.

1211T **NIA Genetics of Alzheimer's Disease Data Storage Site (NI-AGADS) Genomics Database.** E. Greenfest-Allen.

1214T **NIA Genetics of Alzheimer's Disease Data Storage Site (NI-AGADS): Update 2017.** H. Lin.

1217T ‡ **Omic-based machine learning modeling of monogenic neurological diseases.** J.A. Botía.

1220T **Evaluation of basic massive parallel sequencing parameters in relation to true/false positivity's findings of rare variants from an isolated population from South-Eastern Moravia in the Czech Republic with high incidence of Parkinsonism.** R. Vodicka.

1223T **Accurate identification of de novo structural variants in a trio using a reference agnostic, rapidly queryable format to reduce the proportion of unsolved cases.** S.N. Shekar.

1226T ‡ **Neuron-squared ( $N^2$ ): An industrial-scale iPSC disease-modeling project for neuropsychiatric disorders.** R. Randhawa.

1229T **Novel pathway transcriptomics method greatly increases detection of molecular pathways associated with the trait.** C. Chatzinakos.

1232T **The Registry of Candidate Regulatory Elements: Integrating human and mouse epigenomic data to fine map and annotate genetic variants.** J. Moore.

1235T **Augmenting multi-ethnic image signals to enhance schizophrenia prediction.** H. Qin.

1238T **Exomerate: A machine-learning approach to identify high-confidence CNVs from exome sequencing data.** V. Pounraja.

1241T **A paradigm for using human GWAS summary statistics to accurately test gene expression correlation networks derived from model organisms or post-mortem tissues.** S. Bacanu.

1244T **Sample-specific background correction leveraging vast historical patient cohort maximizes sensitivity of noninvasive prenatal screening.** D. Muzzey.

1247T **Assessment of the performance of splicing predictors at non-canonical intronic sites and implications for variant classification.** D.H. Tran.

1250T **MiRMed: Therapeutic recommendation and drug repositioning framework for rare and common diseases using micro-RNA signatures.** K. Shameer.

1253T **Age-related changes in abundance of extracellular RNA in human serum.** D.F. Dluzen.

1256T **CookHLA: Accurate, efficient, and memory-efficient HLA imputation.** S. Cook.

1259T **Improving sequence read mapping and allele calling for the polymorphic *PRDM9* gene using a reference graph approach.** H. Gibling.

1262T **A high-throughput pipeline for genotyping within primary health care to enable precision prevention.** S. Jai Kumar Ahuja.

1265T **Limits of indel detection using CLC alignment and variant calling.** T. Koganti.

1268T **Accurate radiation biodosimetry through automation of metaphase cell image selection and chromosome segmentation.** Y. Li.

1271T **LRSim: A linked reads simulator generating insights for better genome partitioning.** R. Luo.

1274T **The predictive power of RNA-Seq: Modeling blood chemistry and hematology test results.** M. Naymik.

1277T ‡ ***Indexcov*: Whole-genome coverage in <1 second per BAM.** B.S. Pedersen.

1280T **Precision phenotyping of sample biopsies of kidney transplants by leveraging public microarray data and cell types enrichment analysis.** D. Rychkov.

1283T **Unprogrammed presentation number**

1286T ‡ **Bayesian multiple eQTL detection with control for population structure and sample relatedness.** B. Zeng.

1289T **Leveraging allele-specific expression to refine fine-mapping for eQTL studies.** J. Zou.

- 1292T** Showing your work: Combining genetic variant interpretations with evidence to enable reanalysis and reuse. B.C. Powell.
- 1295T** Detecting copy number variants in 200,000 individuals: The Department of Veterans Affairs Million Veterans Program (MVP). M. Li.
- 1298T** Illuminating the Druggable Genome (IDG): An NIH Common Fund program. J. Baker.
- 1301T** Controlled-access databases for genetic and phenotypic human data in Japan. Y. Kodama.
- 1304T** Improved phenotype-based computational methods to support diagnosis of genetic disease. J. Chen.
- 1307T** QRank: A novel quantile regression tool for eQTL discovery. X. Song.
- 1310T** User-driven prioritisation of study addition to the NHGRI-EBI Genome-Wide Association Study (GWAS) Catalog. J.A.L. MacArthur.
- 1313T** Genomic multilateration. K. Kim.
- 1316T** Scaling workflows for growing microbiome applications. J. Lai.
- 1319T** Stargazer: A software tool for calling star alleles from next-generation sequencing data using *CYP2D6* as a model. S. Lee.
- 1322T** ‡ Quickly determining subject ancestries in large datasets using genotypes of dbGaP fingerprint SNPs. Y. Jin.
- 1325T** Search Candidate Regulatory Elements by ENCODE (SCREEN): A web-based tool for visualizing genomic annotations. H.E. Pratt.
- 1328T** The Mega2R suite of R packages: Tools for accessing and processing common genetic data formats in R. D.E. Weeks.
- 1331T** 1000 Genomes Project data and additional openly consented data resources can be accessed via the International Genome Sample Resource (IGSR). S. Fairley.
- 1334T** Multi-sample isoform quantification from RNA-seq for known and novel transcripts. A.E. Byrnes.
- 1337T** NGS based CNV calling in a clinical diagnostic setting. D. Becker.
- 1340T** Faster genotype phasing and imputation for large-scale data. B.L. Browning.
- 1343T** Accurate quantification of allele-specific methylation from genetically diverse population. K. Choi.
- 1346T** Gene identifiers: More than just a number. P. Denny.
- 1349T** Minerva & Me: Public participation in research: Crowdsourcing for computational phenotyping method development. M. Ferlaino.
- 1352T** The European Variation Archive: A repository for short and structural genomic variation. C.Y. Gonzalez Garcia.
- 1355T** PathwayMatcher: Direct mapping of omics data to the Reactome pathway knowledgebase. L.F. Hernández Sánchez.
- 1358T** Target Gene Notebook: Connecting genetics and drug discovery through enabling computational and logistical tools. J. Hutz.
- 1361T** ‡ High-performance whole genome sequence variant analysis in the TOPMed project using cloud environments. R. Kuraisa.
- 1364T** A graph remapping framework for in silico adjudication of SNVs, indels, and structural genetic variants from genetic sequencing data. D.H. Lee.
- 1367T** Optimal workflow for next generation sequencing data processing using existing technology. J.E. Martin.
- 1370T** Use of a metadata-driven architecture for tools and techniques to enhance methods for data sharing and facilitate meta-analysis for genetic association. M.C. O'Leary.
- 1373T** Hail: Scaling statistical genetics to tens of thousands of whole genomes. C. Seed.
- 1376T** Cloud computing environment for hosting federated genomic databases. W. Souza.
- 1379T** GA4GH Genomic Beacon Network: Security challenges and mitigation. S. Ur-Rehman.
- 1382T** Integrated breakpoint analysis and structural variation detection using sequencing reads from multiple sequencing technologies for an Ashkenazi trio. C. Xiao.
- 1385T** An alignment-based method to trim adapter and filtrate low-quality reads from pair-end FASTQ files. R. Ye.
- 1388T** Gene set comparison analysis using both first and second moment information. L. Zhang.
- 1391T** Organize and share your bioinformatics analysis with the R package workflow. J.D. Blischak.
- 1394T** ‡ From quantity to quality: A population-based approach for building reference panel imputation. M. Cocca.
- 1397T** A unified web platform for network-based analyses of genomic data. T. Li.
- 1400T** Comparative analysis of methods for discovery of germline copy-number variants from exome data. B.D. O'Fallon.
- 1403T** Graph embedding and visualization of genetic data using paired factor analysis. G.T. Wang.
- 1406T** The quantity of detected copy number variation (CNV) deletions substantially increases when coverage of whole-genome sequencing (WGS) data increases from 30x to 91x. Y.S. Huang.
- 1409T** Robust identification of deletions in next generation trio sequence data based on clustering of Mendelian errors. K.B. Manheimer.
- 1412T** CNVs from targeted NGS data: Building a cohort for validation and semiautomatic regression testing in a diagnostic setting. M. Ziegler.
- 1415T** ClinGen Allele Registry: Linking information about human genetic variation across the web. P. Pawliczek.
- 1418T** Insights into the performance of whole-exome sequencing technologies. Y. Yu.

**1421T** Factorbook: ENCODE ChIP-seq and DNase-seq data visualizer. M. Purcaro.

**1424T** CRISPinator: A web-based sgRNA design tool that accounts for post-transcriptional influences on protein translation. Y. Yeu.

**1427T** ‡ A map of highly constrained coding regions in the human genome. J. Havrilla.

**1430T** ‡ Impact of polygenic risk on changes in biomarkers over time due to lifestyle intervention and aging. M. Conomos.

**1433T** ‡ Unsupervised pattern discovery in noncoding variants enables identify their potential functional consequences. H. Yang.

**1436T** High-speed mosaicism detection for agnostic genome-wide detection, using the DGX-1 array processor on an NHGRI website for the genetic community. T. Markello.

**1439T** A novel method of phenotype similarities of rare-disease patients using gene-pathway-phenotype relationships. S. Ogishima.

**1442T** Automated abstraction of phenotypes from electronic health records facilitates genetic diagnosis. K. Wang.

**1445T** Modeling and analysis of RNA structures. Z. Ouyang.

**1448T** Leveraging genomic data for Bayesian analysis of high-throughput regulatory functionalization assays. A. Ghazi.

**1451T** RNASeqFPro, a full processing pipeline for RNA-Seq differential gene expression analysis. M. Pjanic.

**1454T** General validation framework using semi-supervised learning on complex cfDNA clinical assays. K.R. Haas.

**1457T** A reference haplotype panel for genome-wide imputation of short tandem repeat variants. S. Saini.

---

## Omics Technologies

---

**1460T** Elucidation of the complex metabolic profile of cerebrospinal fluid using an untargeted biochemical profiling assay. L. Hubert.

**1463T** RNA sequencing analysis identifies differentially expressed genes in Lymphoblastoid Cell Lines (LCLs) generated from diabetic retinopathy patients. Y. Cho.

**1466T** Novel human T cell receptor variable gene alleles revealed by long-amplicon TCR $\beta$  repertoire sequencing with Ion Torrent. T. Looney.

**1469T** ‡ Modulation of Notch pathway in adult mouse airways by antisense oligonucleotides. T.R. Grossman.

**1472T** Tau phosphorylation is impacted by rare AD-associated AKAP9 mutations specific to African Americans. T. Ikezu.

**1475T** RNA sequencing and proteomics approaches reveal novel multi-cellular deficits in the cortex of Rett syndrome mice. N.L. Pacheco.

**1478T** Bridging the therapy gap for rare genetic disorders: Comprehensive high-throughput drug repurposing screening to identify potential new treatment opportunities. C.M. Maher.

**1481T** Novel treatment approaches for autism spectrum disorder: An in vitro model. L. Boccuto.

**1484T** Personalized dosing of dichloroacetate by clinical genotyping assay. T. Langae.

**1487T** Disease relevant structural variation analysis by next-generation mapping. A. Hastie.

**1490T** Sequence read length effects on differential gene expression analyses using RNA-sequencing technologies. A.C. Shetty.

**1493T** Enrichment of long reads for Mendelian disease using the Oxford Nanopore MinION. E. Farrow.

**1496T** Performance comparison of two exome enrichment systems for enhanced coverage of disease-associated regions. L. Tian.

**1499T** NEBNext Ultra II FS DNA: An enzyme-based, single tube fragmentation system for library construction. V. Panchapakesa.

**1502T** Detection of small exonic CNVs, SNPs and INDELs in a single assay. S. Melo.

**1505T** A spin column and magnetic bead-based approach for the isolation of host and bacterial DNA from human feces. D. Wiczorek.

**1508T** Complete, streamlined, reduced-bias workflow for RNA extraction and small RNA library preparation from serum and plasma samples. R. Wong.

**1511T** ‡ Pathogenic variants that alter protein code often disrupt splicing. R. Soemedi.

**1514T** Highly efficient transcriptome profiling method for single-cell or low input RNA. K. Krishnan.

**1517T** Evaluation of NXType™ NGS high-resolution HLA typing kit. S. Khor.

**1520T** Automation of ultra-high molecular weight DNA isolation and labeling for genome mapping. P. Lynch.

**1523T** Implementation of an automated sample quality control tool in a whole exome sequencing workflow. A. Regala.

**1526T** Monitoring guide RNA synthesis for CRISPR/Cas9 genome editing workflow. M. Liu.

**1529T** An optimal long-read workflow for human genome sequencing. J. Lenhart.

**1532T** Genomic DNA analysis using automated pulsed-field capillary electrophoresis. J. Uthe.

**1535T** iMETHYL: An integrative database of whole genome DNA methylation analysis combined with whole genome and whole transcriptome analyses of over 100 Japanese individuals. S. Komaki.

**1538T** Evaluation of PCR followed by high-resolution melting analysis and synthetic constructs on four commercial thermocyclers. K. Dawkins.

---

‡ Indicates Reviewers' Choice Abstract; "ES" Indicates Epstein Trainee Award Semifinalist; "EF" indicates Epstein Trainee Award Finalists

Photographing and recording posters are strictly prohibited if the author has displayed the no photography symbol. You agreed to adhere to this policy when you registered.

1541T Use of a molecular inversion probe (MIP) system for the detection of copy number variants. K. Jefferson.

---

## Epigenetics and Gene Regulation

---

1544T ‡ Physical interaction in human beta-cells between islet eQTL sites and target gene promoters at loci associated with type 2 diabetes risk and glycaemic traits. J. Torres.

1547T ‡ Dissecting features of epigenetic variants underlying cardiometabolic risk using full-resolution epigenome maps. F. Allum.

1550T Methylation-wide association study of sex-specific methylation effects on central adiposity. A. Justice.

1553T A multi-tissue transcriptome association analysis of BMI provides a whole-body view into the impacts of adiposity. T. Tukiainen.

1556T Transcriptomic profiles of duodenal biopsies in cholesterol gallstone diseases. E. Riveras.

1559T Identification of hypermethylated T- and B-cell receptor signaling molecule clusters in systemic lupus erythematosus (SLE) patients by integrative analysis. M.B. Guo.

1562T ‡ An epigenome-guided approach to causal variant discovery in autoimmune disease. R.C. Pelikan.

1565T ‡ Integrative analysis identified pervasive long-range regulation mediated by super-enhancers shared in multiple autoimmune diseases. X.F. Chen.

1568T An atlas of immune chromatin accessibility and gene expression. D. Calderon.

1571T Blood cell type-specific genome-wide DNA methylation analysis of Chinese patients with early-onset systemic lupus erythematosus identifies loss of DNA methylation in genes related to the Type I Interferon pathway. H.Y.B. Chung.

1574T Using clustering analysis and meQTLs to probe differential methylation in females with multiple sclerosis. B. Reinstadler.

1577T Long-range regulation of *IRF5* expression mediated by a functional SNP associated with systemic lupus erythematosus and systemic sclerosis. H.N. Thynn.

1580T Integrative analysis of transcriptional regulation unveils regulatory modules that stratify SLE transcriptome. T. Wang.

1583T Transcriptome analysis of cystic fibrosis molecular signatures. J.E. Ideozu.

1586T Hippocampus and blood *APOE* locus DNA methylation in Alzheimer's disease. L. Bekris.

1589T Haploinsufficiency models of *CHD8* in neuronal cells display alterations in chromatin landscape and regulatory consequences in Wnt signaling. E. Kerschbamer.

1592T Epigenetic silencing in Friedreich ataxia is caused by hypermethylation of the *FXN* promoter CpG island shore. L.N. Rodden.

1595T Decreased expression of *Beclin2* and *LC3* genes in PGRN deficiency: A CRISPR-Cas9 neuronal cell model. S. Napoletano.

1598T Interpreting regulatory effects of disease-associated variants: A lesson from *SNCA* rs356168. O. Glenn.

1601T Genome-wide analyses of DNA methylation in autism brains suggest epigenetic-mediated dysfunction in GABA signaling. J.I. Young.

1604T DNA methylation profiles in a cohort of Brazilian children with ADHD. T.V.M.M. Costa.

1607T The role of DNA methylation and the 5-HTTLPR long/short variant of the serotonin transporter gene (*SLC6A4*) in antidepressant treatment response. A.J. Lisoway.

1610T Methylomic profiling and replication implicates deregulation of PCSK9 in alcohol use disorder. F.W. Lohoff.

1613T Transcriptional profiling of long noncoding RNA in PTSD patients reveals a potential early biomarker of trauma-induced alterations in the acute phase after exposure. G. Guffanti.

1616T Small non-coding RNAs in major depression and antidepressant response. R. Lin.

1619T G-quadruplex binding chemicals may ameliorate the cognitive function of ATR-X syndrome. T. Wada.

1622T C-to-U RNA editing of osteopontin in mouse retina with laser-induced choroidal neovascularization. J. Chen.

1625T Disruption of a remote putative novel enhancer in the cis-regulatory domain of *FOXL2* in a multigenerational Polynesian family with BPES. H. Verdin.

1628T Genome-wide miRNA profiling in plasma of pregnant women with Down syndrome fetuses. I. Svobodova.

1631T Aging and subregion specific transcriptional changes in the rat hippocampus. I.S. Piras.

1634T Testing a stochastic model of epigenetic drift in longitudinal DNA methylation data. C. Robins.

1637T Better statistical methods to predict age from DNA methylation. Q. Zhang.

1640T Discover regulatory grammar across 127 human cell types using tree-based recurrent neural network. Z. Zhang.

1643T Common DNA sequence variation leads to variation in 3D genome organization. Y. Qiu.

1646T Fine mapping of interacting functional elements in Hi-C peaks. A.T. Jaroszewicz.

1649T X-chromosome epigenetic markers for age-prediction. I.C.T. Mello.

1652T Shared household environment makes an important contribution to variation in the human methylome. Y. Zeng.

1655T Glomerular and tubulointerstitial eQTLs of patients with nephrotic syndrome. R. Putler.

**1658T** DNA methylation of *PPARGC1A* is associated with cycling performance. D.J. Hunter.

**1661T** Nanopore full length mRNA sequencing resolves transcript structure in single auditory hair cells. P. Ranum.

**1664T** The 5-HTTLPR polymorphism does not moderate the effect of sleep loss on neural responses to implicit threat and fear learning and memory. V.C. Kodavali.

**1667T** RIPK3-dependent regulation of cell death switch (live or dye) as major determinant in incontinentia pigmenti. A. Pescatore.

**1670T** Furthering the GTEx project legacy through the GTEx bio-specimen resource. E. Gelfand.

**1673T** DNA methylation changes as an exposure signature of cigarette smoking. E. Kim.

**1676T** ‡ Novel deep learning approaches reveal sophisticated epigenetic regulation in eukaryotes. Z. Wei.

**1679T** Regulatory role of conserved non-coding elements. B. Ambrose.

**1682T** A novel computational and experimental approach for allele-specific expression analysis in high-throughput reporter assays. C. Kalita.

**1685T** Determining blood cell-type composition using DNA methylation sequencing. W.A. Cheung.

**1688T** ‡ The landscape of short RNAs in human cell types and tissues. Y.Y. Leung.

**1691T** Recognition of human elements regulating escape from X-chromosome inactivation in mouse. S.B. Peeters.

---

## Developmental Genetics and Gene Function

---

**1694T** Haploinsufficiency of a histone modifier, *Kmt2d*, in a mouse model of Kabuki syndrome leads to widespread defects in the B cell lineage. G. Pilarowski.

**1697T** *Xenopus* as a model of precision medicine: Application of CRISPR to mimic the mutations of human CSBS syndrome patients. S. Cha.

**1700T** Identification of novel candidate genes for 46,XY disorders of sex development (DSD) using a C57BL/6J-Y<sup>POS</sup> mouse model. E. Vilain.

**1703T** Novel pathogenic variant in *OFD1* results in male lethal oral facial digital syndrome type 1 with pituitary aplasia. D. Aljeaid.

**1706T** Investigating phosphatidylserine metabolism in Lenz-Majewski syndrome. C. Demetriou.

**1709T** Missense and splicing mutations in the retinoic acid catabolizing enzyme *CYP26C1* in idiopathic short stature. G. Rappold.

**1712T** Familial dysautonomia: The regulation of *IKBKAP* in the nervous system and therapeutic approaches. S. Yannai.

**1715T** A *Drosophila* model of essential tremor. L.N. Clark.

**1718T** ‡ Evolutionary conserved ARX-regulatory pathway in mammals and nematode to find a convergent druggable pathway damaged in neurodevelopmental disorders. L. Poeta.

**1721T** Functional evaluation of rare variants in glutamate receptor *GRIN*, *GRIA*, *GRIK*, and *GRID* genes reveals a diversity of effects on receptor activity. S.J. Myers.

**1724T** Genetics of congenital megacolon in East Asians. C. Tang.

**1727T** *PEA15* deficiency is associated with striking neurologic and motor abnormalities in *Felis catus*. J.N. Cochran.

**1730T** IBGC mouse model with *SLC20A2* mutation and potential prevention and therapeutics. J.Y. Liu.

**1733T** The binding of RNA regulates the formation of nuclear membraneless structures by *Matrin 3* and *TDP43* in myocytes. M.C. Gallego Iradi.

**1736T** Genetic analysis of Japanese patients with neurofibromatosis type 1 and the neuronal complications. K. Fujita.

**1739T** The chr14.232.a pseudogene in the 14q21.2 region regulates the expression of the contiguous *LRFN5* gene and is deleted in a patient with autism. G. Cappuccio.

**1742T** Further evidence supporting the involvement of *ERC1* gene variation in ASD. S. Raskin.

**1745T** ‡ Changes of open chromatin regions reveal stage-specific transcriptional network dynamics in human iPSC-derived neurons. W. Moy.

**1748T** Behavioral characterization in a mouse model of Bohring–Opitz syndrome. K. Walz.

**1751T** Cytoplasmic FMRP-Interacting Protein 2 (*CYFIP2*) causes syndromic intellectual disability. A. Begtrup.

**1754T** MeCP2 AT-hook1 mutations disrupt DNA binding and chromatin compaction in patients with intellectual disability and schizophrenia. T.I. Sheikh.

**1757T** ‡ Regulating transcriptional activity by phosphorylation of the intellectual disability and seizure associated ARX homeodomain transcription factor. C. Shoubridge.

**1760T** Custom capture high-throughput sequencing for mutation detection: Results from 217 coloboma subjects across 196 genes identifies novel mutations in genes associated with ocular coloboma. V.K. Kalaskar.

**1763T** Integration of whole exome sequencing, expression profiling, and pathway analysis for the identification of novel genes in familial exudative vitreoretinopathy. M.-Y. Chung.

**1766T** Bardet-Biedl syndrome, postaxial polydactyly, Shh signaling pathway and a founder effect in a Libyan extended consanguineous family from Tarhunah Berber tribe. N.Bouayed. Abdelmoula.

**1769T** A dog model of non-syndromic cleft palate. B. Schutte.

**1772T** Multidisciplinary assessment of 49, XXXYY, a rare X and Y chromosomal variation (XYV). P. Lasutschinkow.

---

‡ Indicates Reviewers' Choice Abstract; "ES" Indicates Epstein Trainee Award Semifinalist; "EF" indicates Epstein Trainee Award Finalists

Photographing and recording posters are strictly prohibited if the author has displayed the no photography symbol. You agreed to adhere to this policy when you registered.

**1775T** 11q terminal deletion associated with mild phenotype of Jacobsen syndrome. C. da Silva-Camargo.

**1778T** Expanding the phenotypic spectrum of *de novo* *KAT6A* mutations and their impact on biological pathways through functional genomics. V. Arboleda.

**1781T** Defining requirements for cleavage of prelamin A by the zinc metalloprotease *ZMPSTE24*. T. Babatz.

**1784T** Mechanistic insight of inactivation of mouse chitinase-like protein *Ym1*. F. Oyama.

**1787T** An iPSC approach to examine the molecular mechanisms underlying *SRCAP* mutations in Floating-Harbor syndrome. R.L. Hood.

**1790T** The association of haploinsufficiency of *ARID2* with Ras-MAPK signaling pathway. M. Kang.

**1793T** *ARMC5* and PMAH: From human genetic defects to the *Armc5*<sup>+/-</sup> mouse. F.R. Faucz.

---

## Complex Traits and Polygenic Disorders

---

**1796T** Assessment of the impact of variants in constrained non-essential splice sites in fifty-two thousand type 2 diabetes cases and controls. J.M. Mercader.

**1799T** Genetic variability in energy expenditure and the risk of severe obesity. A.C.P. Fonseca.

**1802T** Impact of genetic variants identified in genome-wide association studies of diabetic retinopathy in Chinese patients with type 2 diabetes. C.Y.Y. Cheung.

**1805T** Whole exome sequencing and exome array genotyping in 3,943 Korean type 2 diabetes cases and controls. S. Kwak.

**1808T** ‡ Glucose challenge metabolomics identifies C10- and C12-carnitines as possible contributors to insulin resistance. C. Nowak.

**1811T** Diabetome: A comprehensive collection of diabetes phenotype and genotype data. S. Shah.

**1814T** Systemic approach to understand human non-alcoholic fatty liver disease. T. Yoo.

**1817T** Multifactor dimensionality reduction (MDR) method to study association of type 2 diabetes mellitus with *ENPP1* (K121Q), *TCF7L2* (G>T) and *GYS1* (A1>A2) gene variants in Punjabi population, India. B. Doza.

**1820T** Association study of *ENPP1* (K121Q), *TCF7L2* (G>T), *GYS1* (A1/A2) variants with type 2 diabetes mellitus (T2DM) in north Indian Punjabi population. M. Kaur.

**1823T** Glucose metabolism in pregnancy: Analysis of diabetes related genetic risk scores against glucose curve trajectories. G.H. Moen.

**1826T** Replication of 93 T2D associated SNPs in Jat Sikhs, population of Punjab, India. G. Singh.

**1829T** Characterization of potential regulatory variants at the *SH2B1* body-mass index GWAS locus. M.E. Cannon.

**1832T** Transient genetic effects important for early growth programming. O. Helgeland.

**1835T** Genome-wide study suggests a parent-of-origin effect on birth weight at *ANK1-NKX6-3* type 2 diabetes locus. R.N. Beaumont.

**1838T** Phenome-wide association study of exome data from childhood obesity cohort reveals pleiotropic loci for 13 obesity-related traits. S.B. Cho.

**1841T** Genotype determination: Analysis of *PNPLA3*, *GC*, and *LCP1* genes in nonalcoholic fatty liver disease in south of Iran. S.S. Tabei.

**1844T** ‡ Causality links between gut microbiome and glucose/insulin metabolism and type 2 diabetes. S. Sanna.

**1847T** Genetic evidence that early carbohydrate-stimulated insulin secretion affects accumulation and distribution of adiposity. C.M. Astley.

**1850T** Copy number variation and mutation analysis indicate a possible interesting role of *POU3F2* in the Prader Willi like phenotype. E. Geets.

**1853T** ‡ Contrasting the genetic architecture of human thinness and severe obesity. F. Riveros McKay Aguilera.

**1856T** Effects of long noncoding RNA regulation of gene expression on type 2 diabetes. A.J. Payne.

**1859T** Meta-analysis of >150 genome-wide studies for association with blood lipid levels. S.E. Graham.

**1862T** Heritability and genetic correlation of 25 complex traits in Taiwanese population. C. Lin.

**1865T** A multi-trait genetic association approach to identify genetic loci not identified before in single-trait GWAS of lipid traits. M. Preuss.

**1868T** ‡ Novel genetic variants associated with lipid levels in a multi-ethnic population from the Population Architecture using Genomics and Epidemiology (PAGE) Study. Y. Hu.

**1871T** *TM6SF2* rs58542926 impacts lipid processing in liver and small intestine. N.A. Zaghoul.

**1874T** Genetic effects of familial hypercholesterolemia variants on LDL cholesterol levels among multi-ethnic veterans: The Million Veteran Program Study. Y.V. Sun.

**1877T** Genetic regulation of adipose tissue transcript expression is involved in modulating serum triglyceride and HDL-cholesterol. S.K. Das.

**1880T** Multi-omic approaches to identifying clinical biomarkers of asthma exacerbations in African Americans. H. Gui.

**1883T** Unraveling the genetic architecture of generalized vitiligo in a homogeneous, isolated Romanian village. G. Andersen.

**1886T** Admixture mapping of 13,569 individuals provides evidence for increased European origin of the major histocompatibility complex class I region in multiple sclerosis. C. Chi.

---

‡ Indicates Reviewers' Choice Abstract; "ES" Indicates Epstein Trainee Award Semifinalist; "EF" indicates Epstein Trainee Award Finalists

The author listed is the first/presenting author of the abstract. The letter following each poster number indicates the day that the author will present at their posters. W=Wednesday; T=Thursday; F=Friday.

- 1889T** Lupus-associated functional polymorphism in *PNP* causes cell cycle abnormalities and interferon pathway activation in human immune cells. Y. Ghodke-Puranik.
- 1892T** Identification of the primary functional variants in primary biliary cholangitis susceptibility gene loci *NFKB1/MANBA*. Y. Hitomi.
- 1895T** Genetic variation in the estrogen receptor alpha gene (*ESR1*) and susceptibility to rheumatoid arthritis. S.E. Lofgren.
- 1898T** Variants near *HLA-DQA1* contribute to the development of antibodies to anti-TNF in Crohn's disease. A. Sazonovs.
- 1901T** Identification of one novel IBD susceptibility locus through a genome-wide association study in Korean populations. B.D. Ye.
- 1904T** First report of the mutational and phenotypic spectrum of hereditary spherocytosis in Indian patients. A. Aggarwal.
- 1907T** An intergenic variant between HLA-DRA and HLA-DRB contributes to the clinical course and long-term outcome of ulcerative colitis in Asians. H.S. Lee.
- 1910T** ‡ Transcriptome analysis of systemic lupus erythematosus reveals distinct susceptibility, activity and severity signatures. N. Panousis.
- 1913T** Characterising copy number variation at the Crohn disease-associated gene intelectin 1 (*ITLN1*). F. Almalki.
- 1916T** *De novo* mutations implicate novel genes with burden of rare variants in systemic lupus erythematosus. A. Roberts.
- 1919T** Trans-ethnic meta-analysis of the Korean, East Asian and European ImmunoChip data identifies three novel IBD susceptibility loci. S. Jung.
- 1922T** Pleiotropy analysis of penicillin and sulfa drug allergy in the Kaiser GERA cohort. A. Majumdar.
- 1925T** A genome-wide association analysis identifies *NMNA2* and *HCP5* as susceptibility loci for Kawasaki disease. J. Kim.
- 1928T** Reduced severity of collagen-induced arthritis in peptidyl-larginine deiminase type 4 knockout mice. A. Suzuki.
- 1931T** Targeted sequencing in 1000 SLE patients discovers regulatory alleles that downregulate DAP expression and promote autoimmunity. P. Raj.
- 1934T** Assessing the mechanisms of thymic involution in an animal model of multiple sclerosis. S.G. Gregory.
- 1937T** Deciphering genetic susceptibility to tuberculous meningitis: Exome sequencing and a GWAS in a South African population. M. Möller.
- 1940T** High density imputation genome wide association study of spontaneous resolution of hepatitis C virus. C.I. Vergara.
- 1943T** ‡ Location, location, location: Single cell gene expression of mucosal T cells vs peripheral blood T cells in Crohn's disease. E.A.M. Festen.
- 1946T** Local ancestry interaction models reveal a novel asthma association with asthma on chromosome 1q23.1 specific to people of African ancestry. M.P. Boorgula.
- 1949T** Genome-wide association study identifies candidate loci associated with intraoperative remifentanyl requirements during laparoscopic-assisted colectomy. D. Nishizawa.
- 1952T** Alternative splicing of *ICAM3* in Crohn's disease. I. Arijis.
- 1955T** Markers of the adaptive immune response are associated with progressively worse chronic kidney disease status. D.C. Crawford.
- 1958T** *NUDT15* variants contribute to thiopurine-induced myelosuppression in European populations. M.D. Voskuil.
- 1961T** Dysregulated gene and miRNA expression in different stages of Crohn's disease. I. Cleyen.
- 1964T** An analysis of Crohn's disease genes in the French-Canadian population. B.E. Avila.
- 1967T** Mendelian randomization shows non-linear causality between vitamin D levels and kidney function. A. Teumer.
- 1970T** Fetal but not maternal *APOL1* genotype is associated with increased risk for preeclampsia among African-Americans. C.L. Simpson.
- 1973T** Genome-wide CNV analysis identifies *TGFBR3* as a candidate causal gene for endometriosis and infertility. E. Hatchwell.
- 1976T** Transcriptomic analysis of the ratio of serum aspartate transaminase to serum alanine transaminase (Ast/Alt ratio) using a genotype-by-diet interaction model identifies a number of potentially important genes for liver disease in the San Antonio Family Heart Study. V.P. Diego.
- 1979T** An integrative analysis of gene expression profiling and genome-wide DNA methylation datasets shows a different underlying molecular mechanism between Kashin-Beck disease and osteoarthritis. Y. Wen.
- 1982T** Identification of *IRF4*, *NOTCH4* and *RPS12* genes for non-syndromic sagittal craniosynostosis in a genome-wide association study using logistic regression. H. Sung.
- 1985T** Broad mutation spectrum of *FBN1* gene implicated in a cohort of idiopathic scoliosis and its related genotype-phenotype correlation study. M. Lin.
- 1988T** ‡ The genetic architecture of osteoarthritis: Insights from UK Biobank. E. Zeggini.
- 1991T** Association of TGF  $\beta$ 1 gene polymorphisms with primary knee osteoarthritis in Asian Indians. Q. Hasan.
- 1994T** Shared and subtype-specific genetic variation define the genetic susceptibility of juvenile idiopathic arthritis. Y. Li.
- 1997T** Polymorphisms of genes involved in extracellular matrix homeostasis may play a role in the risk to develop anterior cruciate ligament and medial meniscus tears. L. Casilla.
- 2000T** Mapping functional regulatory variants at Alzheimer's disease risk loci. M. Allen.
- 2003T** Whole-genome sequencing in non-Hispanic white familial late-onset Alzheimer's disease identifies rare variation in AD candidate genes. G.W. Beecham.

‡ Indicates Reviewers' Choice Abstract; "ES" Indicates Epstein Trainee Award Semifinalist; "EF" indicates Epstein Trainee Award Finalists

Photographing and recording posters are strictly prohibited if the author has displayed the no photography symbol. You agreed to adhere to this policy when you registered.

- 2006T** Genome-wide association study of brain amyloid deposition as measured by PiB-PET imaging and assessment of the genetic variance of amyloid deposition. F.Y. Demirci.
- 2009T** A whole exome study of Alzheimer's disease which is augmented by population data found the noble AD risk genes. J. Kim.
- 2012T ‡** Novel Alzheimer disease loci identified in subsets of whole exome sequencing data stratified by APOE genotype. Y. Ma.
- 2015T** Contribution to Alzheimer's disease risk of rare variants in *TREM2*, *SORL1* and *ABCA7* in 1,779 cases and 1,273 controls. G. Nicolas.
- 2018T** Targeted sequencing of deep-phenotyped individuals for Alzheimer's disease susceptibility prediction. J. Seo.
- 2021T** A new CAG repeat disease responsible for X linked cerebellar ataxia? L. Parodi.
- 2024T** Multiple sclerosis in Orkney: The contribution of common variants to excess prevalence. C.L.K. Barnes.
- 2027T** Assessment of genomic variations in multiple sclerosis patients identifies mutations in *ADAMTS14*, *IL22RA2*, *HNRNPA1* and *TNPO1* genes indicating the existence of molecular mimicry and cytokine/interferon receptor pathway disruption inducing autoimmunity. A.M. Veerappa.
- 2030T** A genome-wide screen to identify suppressors of neurodegeneration in Gaucher disease. S.U. McKinstry.
- 2033T** Defining the critical region for brain malformations in 6q27 microdeletions. M.D. Dias Hanna.
- 2036T** RNA-seq analysis after moderate blast exposure in peripheral blood samples. H. Kim.
- 2039T** Mutation identification for epilepsy in the U.S. Latino population using whole exome sequencing. C. Xu.
- 2042T** Polygenic analysis of persistent cisplatin-induced peripheral neuropathy implicates immune-mediated processes. O. El Charif.
- 2045T** Whole genome sequencing and rare variant analysis in essential tremor families. Z. Odgerel.
- 2048T** Genome-wide association study reveals candidate susceptibility loci for idiopathic hypersomnia. K. Tanida.
- 2051T** *Gba1* haploinsufficiency in a Parkinson mouse impacts longevity and symptom severity independent of SNCA aggregate. N. Tayebi.
- 2054T** Interplay of genetic risk at *SNCA* locus and dysbiosis of gut microbiome in Parkinson's disease. Z.D. Wallen.
- 2057T** ONDRISeg: Genetic diagnosis of neurodegenerative disease patients using targeted next-generation sequencing. A.A. Dilliott.
- 2060T** CGG interruptions alter protein properties and increase disease penetrance in *SCA8*. B.A. Perez.
- 2063T** Identification of candidate amyotrophic lateral sclerosis risk loci using pedigree based analyses of next-generation sequencing data. K.L. Russell.
- 2066T** No rare deleterious variants from *STK32B*, *PPARGC1A*, *CTNNA3* are associated with essential tremor. G. Houle.
- 2069T** Genetic analysis of SNCA gene polymorphisms in Parkinson's disease in an Iranian population. M. Rahimi.
- 2072T** The generation of iPSC-derived astrocytes from patients with Gaucher disease with and without Parkinsonism provide a model to study Parkinson pathogenesis. B. McMahan.
- 2075T** Identifying the genetic underpinnings of social withdrawal. N. Roth Mota.
- 2078T** Inherited mutations in Human Accelerated Regions (HARs) are associated abnormal social and cognitive behavior. R.N. Doan.
- 2081T ‡** Discovery of multifaceted genomic features as a promising approach to novel autism risk gene identification. Y. Ji.
- 2084T** Epigenetic dysregulation of *DYRK1A* may have a role in ASD development in a discordant monozygotic twin pair. C. Sjaarda.
- 2087T** Complete gene knockouts in autism spectrum disorder. T.W. Yu.
- 2090T** Genetic polymorphism and gene-environment interactions of dopamine receptor genes and nicotine dependence in the population of the Northwest Indian region. J. Kaur.
- 2093T** Minds, genes, and machines: Performance on online cognitive assessments is correlated with individual characteristics in 23andMe customers. O.V. Sazonova.
- 2096T** Abnormal expression of sonic hedgehog as a biomarker and therapeutic target for depression and suicide in bipolar disorder. M. Galdzicka.
- 2099T ‡** A genome-wide association study reveals a novel locus significantly associated with ADHD in African Americans and replicating in ADHD cases of European ancestry. B. Almoguera.
- 2102T** Schizophrenia and adult height show an inverse polygenic correlation within specific functional domains of the genome. A.P.S. Ori.
- 2105T** Integrating multi-omics data to boost the translation of GWAS to biology and therapeutics for schizophrenia. Q. Wang.
- 2108T ‡** Exome sequencing study of bipolar disorder in a genetically isolated population. L. Hou.
- 2111T** Identification of ADHD risk genes in extended pedigrees by combining linkage analysis and whole-exome sequencing. M. Klein.
- 2114T** Genome-wide associations with generalised anxiety disorder symptoms and self-reported anxiety disorder: An investigation of unique and shared genomic contributions. K.L. Purves.
- 2117T** Genome-wide association study of comorbid alcohol dependence and major depression. H. Zhou.
- 2120T** The regulatory landscape of genetic variants associated with psychiatric disorders and neurodegenerative diseases. A. Amalie-Wolf.
- 2123T** DNA banking and genetic analysis of adverse drug reactions in the New Zealand healthcare setting. M.A. Kennedy.

‡ Indicates Reviewers' Choice Abstract; "ES" Indicates Epstein Trainee Award Semifinalist; "EF" indicates Epstein Trainee Award Finalists  
The author listed is the first/presenting author of the abstract. The letter following each poster number indicates the day that the author will present at their posters. W=Wednesday; T=Thursday; F=Friday.

- 2126T** Genetic and functional analysis of the *GRIN2C* gene as a candidate gene of schizophrenia. M. Cheng.
- 2129T** Genetics of cognitive function in schizophrenia and bipolar disorder. P.D. Harvey.
- 2132T** Sex-stratified analysis of obsessive-compulsive disorder reveals minor differences in genetic architecture. E.A. Khrantsova.
- 2135T** Large meta-analysis of Scandinavian exome sequencing studies of schizophrenia. F. Lescai.
- 2138T** Initial results from the meta-analysis of the whole-exomes of 20,000 schizophrenia cases and 45,000 controls. T. Singh.
- 2141T** The role of miRNAs in 22q11.2 deletion syndrome. A.K. Victor.
- 2144T** Genetics of attention deficit hyperactivity disorder dimensions. T. Zayats.
- 2147T** Rare human knockouts in consanguineous pedigrees aggregated with schizophrenia and bipolar disorder compared to matched healthy population controls. Q. He.
- 2150T** Antidepressant effectiveness study in major depressive disorder in STAR\*D patients. W. Guo.
- 2153T** Autism spectrum disorder in the Amish: Exome sequencing in a founder population unveils novel coding variants. C.G. Tise.
- 2156T** ‡ Using electronic health records for the identification of novel genes associated with adverse drug reactions. L. Milani.
- 2159T** Novel mutation in the *MT-ND4* gene at low heteroplasmy level likely associated with a mild phenotype: A case report. A. Gonzalez Garcia.
- 2162T** Cochlear nerve deficiency presenting as auditory neuropathy spectrum disorder. A. Pandya.
- 2165T** New risk loci for primary open-angle glaucoma. P. Gharahkhani.
- 2168T** Optimizing accurate classification of electronic health record case control status for age-related macular degeneration in the Million Veteran Program. S.K. Iyengar.
- 2171T** ‡ Forty novel genetic loci associated with intraocular pressure in a large multi-ethnic genome-wide association study. H. Choquet.
- 2174T** Loss of *ELOVL6*, a fatty acid elongase, rescues ER stress-induced apoptosis in model of retinitis pigmentosa. R.A.S. Palu.
- 2177T** *ANGPT1* association with adult-onset primary open angle glaucoma. J.N. Cooke Bailey.
- 2180T** Genome-wide gene expression profiling in the retina of common marmosets exposed to hyperopic or myopic defocus reveals large-scale sign-of-defocus-specific changes in gene expression, pathway switching, and strong left-right eye yoking. A. Tkatchenko.
- 2183T** Robinow, Ter Haar, Teebi or a new syndrome? Complex genotype with distinctive craniofacial features. F. Uysal.
- 2186T** ‡ Identification of 16q21 as a modifier locus for orofacial cleft phenotypes. E.J. Leslie.
- 2189T** Microdeletion of Xp22 encompassing *SHOX* and *ARSE*, showing incomplete penetrance and variable expressivity. B. Simpson.
- 2192T** Genotype-phenotype correlation in WAGR syndrome: Large deletion of chromosome 11p in a patient with classical and non-classical symptoms of the syndrome. P.N. Moretti.
- 2195T** ‡ Whole-exome analysis of late-onset Alzheimer's disease reveals novel candidate genes involved in cognitive function. C. Preuss.
- 2198T** Age-related changes in white blood cell gene expression associated with skeletal fragility. E. Quillen.
- 2201T** Identifying genetic variants associated with leukocyte telomere length in African Americans. A. Little.
- 2204T** Allele-specific expression in healthy centenarians. L.C. Tindale.
- 2207T** ‡ Telomere length across many human tissues. K. Demanelis.
- 2210T** Influence of guideline adherence and *ADRB2* SNPs in predicting exacerbation frequency in asthma patients. A. Santani.
- 2213T** Low frequency genetic variation in *TP53* is associated with final head circumference. B. St Pourcain.
- 2216T** The impact of *MUC5B* and *KLK4* genes on dental caries. T. Cavallari.
- 2219T** ‡ Performance of polygenic scores across ancestrally diverse populations. L. Duncan.
- 2222T** Adult height and risk of cardiometabolic disease. E. Marouli.
- 2225T** Ayurveda based deep phenotyping, a likely game changer for gene hunt in complex traits. B.K. Thelma.
- 2228T** Structural variation influencing complex traits and metabolic measurements. A. Sabo.
- 2231T** Whole exome sequencing reveals a novel candidate gene, *HSPA1L*, for spontaneous preterm birth. J.M. Huusko.
- 2234T** Connection of *RAB8A* and *MED16* with implications on 5'-deoxy-5-fluorouridine response. C.M. Murtagh.
- 2237T** Whole genome sequencing in severe chronic obstructive pulmonary disease. D. Prokopenko.
- 2240T** Fetal genome-wide meta-analysis of gestational age and preterm delivery. X. Liu.
- 2243T** GWAS reveals loci associated with velopharyngeal insufficiency. J. Roosenboom.
- 2246T** Pinpointing GWAS signals: Indels vs. SNPs. S.A. Gagliano.
- 2249T** Genetic typing of DC-SIGN in recurrent vulvovaginal candidiasis. N. Kalia.
- 2252T** Genome-wide association study of cranial vault shape reveals novel loci at 15q26.3 and 17q11.2. M. Lee.

**2255T** Translating pharmacogenetics: An electronic phenotyping algorithm and survey study of diverse BioMe biobank patients treated with ACE inhibitors. H. Naik.

**2258T** Designing of an efficient genotyping chip for discovery and pan-disease screening in the VA's Million Veteran Program. S. Pyarajan.

**2261T** Novel genes and mutations in patients affected by recurrent pregnancy loss. P. Quintero-Ronderos.

**2264T** Association study of placebo-treated patients from 35 clinical trials suggests genetic contribution to the placebo response. A. Wuster.

**2267T** ‡ A broad survey of the relationship between autozygosity and fitness-related and sociodemographic traits in the UK Biobank. E.C. Johnson.

**2270T** New insights into the genetic architecture of complex human traits from Bayesian mixture model analyses in a large dataset. J. Sidorenko.

**2273T** Utilizing protein quantitative trait loci to identify functional candidates from genome-wide association studies. S. Sivertson.

**2276T** The Macaque Genotype and Phenotype (mGAP) database: a novel resource to support genetic disease model development and translational research in nonhuman primates. B. Ferguson.

**2279T** ‡ Drug target genes associated with clinical phenotypes in the genetically isolated population of Finland are more likely to succeed in pharmaceutical development. R. March.

---

## Evolution and Population Genetics

---

**2282T** Isolated population from Runta, Boyacá: Findings related to founder effect of the nonsense variant of the HGSNAT gene. L.J. Torres.

**2285T** New favored haplotype alleles in human adaptation to high altitude in Andes. T. Stobdan.

**2288T** *GCH1* plays a role in high altitude adaptation of Tibetans. Y. He.

**2291T** Evolutionary rate and the human transcriptome: Function, mechanism, and disease genes. P. Evans.

**2294T** Dietary adaptation of *FADS* genes varied geographically in Indian populations. D. Wang.

**2297T** *HLA-G* and *HLA-A* extended haplotypes in a Brazilian population sample: The close relationship between *HLA-G* promoters and *HLA-A* coding alleles. E.C. Castelli.

**2300T** One step for study of transposable element-associated structural variations (TASVs) using de novo assembled Korean genome. S. Mun.

**2303T** Relationships between the regulation of gene expression, mutational burden, and recombination in a large population cohort. H. Edgington.

**2306T** Evolutionary patterns of long non-coding RNAs with coding capacity of oligopeptides. W. Lin.

**2309T** MixFit: Methodology for computing ancestry-related genetic scores at the individual level and its application to the Estonian and Finnish population studies. T. Haller.

**2312T** Association of *VASP* polymorphisms and infectious disease burden in global populations and identification of candidate resistance haplotypes in sub-Saharan Africa. M. Phun.

**2315T** Recent changes in contemporary effective population size from identical by descent segments. A. Urniykyte.

**2318T** Standardized visualization of demographic history. Y. Zhou.

**2321T** Archaic-genome-agnostic detection of introgressed segments. S.R. Browning.

**2324T** Tracing the origin of ancient polynesian human genomes across the Pacific. P. Salazar-Fernandez.

**2327T** Inference of allele-frequency trajectory histories from present genomes. Y. Field.

**2330T** Distribution of common and rare variants in an underrepresented population in public genomic databases and the possible impact in precision medicine. C.S. Rocha.

**2333T** Patterns of shared signatures of recent positive selection across human populations. K.E. Johnson.

**2336T** ‡ Adaptive eQTLs in human populations. M. Quiver.

**2339T** The composition and intensity of *de novo* mutations in the Lithuanian exome. L. Pranckėnienė.

**2342T** Inverse correlation between mutational and selective forces in human coding regions with distance from gene ends leads to opposite patterns of synonymous and non-synonymous variant prevalence. Y. Waldman.

**2345T** NHGRI Sample Repository for Human Genetic Research: Cell lines and DNA from the 1000 Genomes and HapMap collections. E.M. Kelly.

**2348T** *HLA-A* extended promoter and coding variability in a Brazilian population sample by using massively parallel sequencing. T.H.A. Lima.

**2351T** ‡ Substantial fraction of genes under recessive selection illuminates a missing component of human variation in population genetics and model organism studies of human disease. D.J. Balick.

**2354T** ‡ Extremely rare variants reveal patterns of germline mutation rate heterogeneity in humans. S. Zöllner.

**2357T** Genetic origins of Easter Island and remote Oceania. A. Ioannidis.

**2360T** The genetic substructure of the Japanese population: Results from the Japan Multi-Institutional Collaborative Cohort Study. M. Nakatochi.

**2363T** Signatures of multiple-mergers coalescence in genomic diversity data. D.P. Rice.

---

‡ Indicates Reviewers' Choice Abstract; "ES" Indicates Epstein Trainee Award Semifinalist; "EF" indicates Epstein Trainee Award Finalists

The author listed is the first/presenting author of the abstract. The letter following each poster number indicates the day that the author will present at their posters. W=Wednesday; T=Thursday; F=Friday.

2366T The Irish DNA Atlas: Revealing fine scale population structure and history within Ireland. E.H. Gilbert.

2369T FastNGSadmix: Admixture proportions and principal component analysis of a single low-depth sequencing sample. E. Jørsboe.

---

## Molecular and Cytogenetic Diagnostics

---

2372T Mutational spectrum in *BRCA1* and *BRCA2* genes in Colombia. I. Briceno.

2375T Novel acute myeloid leukemia amplicon panel for uniform detection of all target genes, including *CEBPA*. C. Clear.

2378T Differential expression of kallikreins as prognostic markers in recurrent prostate cancer. E. Guzel.

2381T TaqMan dPCR liquid biopsy assays targeting the TERT promoter region. M. Laig.

2384T Clinical and molecular findings correlation in patients with hereditary cancer syndromes: Experience of a Colombian reference laboratory. T. Pineda.

2387T Hereditary cancer risk testing within a Colombian cohort reveals high incidence of Lynch syndrome. J.A. Rugeles.

2390T Towards prediction of platinum treatment response in ovarian cancer using machine learning approaches. A. Vladimirova.

2393T Frequent detection of chromothripsis in acute myeloid leukemia with complex karyotype and marker chromosomes. J. Lee.

2396T Identification of cancer-associated copy number variations through integrated genomic analysis. M. Luo.

2399T A plasma cell myeloma case with an abnormal clone showing a t(8;22)(q24.1;q11.2) within the context of a hyperdiploid complex karyotype. C.A. Tirado.

2402T Implementation of a multi-gene panel in selected Greek breast and ovarian cancer patients reveals loss-of-function mutations in multiple genes. F. Fostira.

2405T Current laboratory practices in *BRCA1* and *BRCA2* testing: Results from an international survey of 86 laboratories. A. Toland.

2408T Hereditary cancer risk testing of 11,570 individuals with a multi-gene panel. J. Ji.

2411T ‡ Mate-pair sequencing provides advanced molecular characterization of genomic rearrangements in B-Chronic Lymphocytic Leukemia (CLL) and non-Hodgkins lymphoma. S.S. Smoley.

2414T The prevalence of mosaicism in common cancer susceptibility genes from 232,328 individuals undergoing sequential testing. T. Slavin.

2417T Applying synthetic long reads to a custom Lynch Syndrome NGS panel to overcome pseudogene interference in *PMS2*, detect structural variations, and enable allelic phasing. C. Kao.

2420T Diagnostic yield and mutation spectrum of multigene panel testing for hypertrophic cardiomyopathy. L. Qin.

2423T ‡ Involvement of mtDNA variants in patients with cardiac manifestation. H. Cui.

2426T Molecular review of Polish patients with Smith-Lemli-Opitz syndrome. P. Halat.

2429T Concurrent determination of *ABO Rhd* blood types and the HIV-1 resistance marker *CCR5* deletion via rapid multiplex PCR and capillary electrophoresis-based genotyping. E. Schreiber.

2432T Xq22.1 contiguous deletion syndrome as a diagnostic challenge: Detection of a 17 kb deletion ends 30-year diagnostic odyssey. G. Raca.

2435T Analysis of germ line predisposition in Chinese children with bone marrow failure. N. Dai-jing.

2438T Novel approach using NGS assay for detection of mutations of the *CYP21A2* gene. G. Bennett.

2441T Mutations in the *DHX37* gene identified by whole-exome sequencing (WES) are a novel cause of the embryonic testicular regression syndrome (ETRS). T.E. da Silva.

2444T Pathogenic variants and variants of uncertain significance in autosomal dominant polycystic kidney disease (ADPKD) causative genes are commonly found in early-onset PKD patients: 2.5-year experience in a CAP/CLIA diagnostic laboratory. W. Chen.

2447T Novel pathogenic variants in craniosynostosis genes identified by NGS. E. König.

2450T Mendelian disorders of cornification in Iran: Spectrum of clinical and genetic characteristics in a cohort of 189 consanguineous families including a new entity of ichthyosis follicularis with profound bilateral deafness and leukonychia totalis. L. Youssefian.

2453T Incidentaloma in neurogenetics: Pathogenic variant in *NSD1* in a patient with spinocerebellar ataxia. H.M. Velasco.

2456T Further investigation of variants discovered in an early onset dementia cohort: Additional family member sequencing. S.A. Bucks.

2459T Novel myopathic phenotype due to a newly detected stop-loss mutation in *MYH7* gene. K. Sumegi.

2462T Combining repeat expansion testing with phenotype based NGS panels provides significant diagnostic benefit. H.A. Marton.

2465T Clinical application of whole exome sequencing in patients with uncertain neurological disorders. Y. Lee.

2468T Detection rate of chromosomal microarray in individuals with ADD/ADHD. A.L. Baxter.

2471T Parental variant study is informative for variant classification in significant number of neurodevelopment genes. E.C. Weltmer.

2474T Analysis of total RNA in the cerebrospinal fluid environment. S.L. Farrugia.

2477T An inherited distal 16p11.2 deletion demonstrates association with rhizomelic shortening, variable expressivity, and incomplete penetrance for psychiatric illness: A case report. E. Morris.

---

‡ Indicates Reviewers' Choice Abstract; "ES" Indicates Epstein Trainee Award Semifinalist; "EF" indicates Epstein Trainee Award Finalists

Photographing and recording posters are strictly prohibited if the author has displayed the no photography symbol. You agreed to adhere to this policy when you registered.

- 2480T** A framework to identify contributing genes in patients with Phelan-McDermid syndrome. A.C. Tabet.
- 2483T ‡** Whole genome sequencing of neurodevelopmental disorders in Japanese. C. Abe-Hatano.
- 2486T** Using parental report questionnaires to identify developmental delay in a 22q11.2 deletion specialty clinic. K. Coleman.
- 2489T** StarSeq, an innovative method based on NGS for accurate detection of punctual mutations and copy number variants in children with intellectual disability and obesity. A. Bonnefond.
- 2492T** MIDAS Project status report: Trio whole exome sequencing in patients with intellectual disability. Y. Dinçer.
- 2495T ‡** Reanalysis of whole exome and genome data leads to new diagnoses in children with intellectual disability and developmental delay. C.R. Finnilla.
- 2498T** Genetic evaluation of patients with intellectual disability (ID) using chromosomal microarray and next-generation sequencing at the "ID clinic". K. Takano.
- 2501T** Recurrent telomere captures as the mechanism producing uniquely complex 1p UPD mosaicism. P.L. Pearson.
- 2504T** Development of a unified *DMPK* and *CNBP* PCR workflow for determining repeat expansions relevant to myotonic dystrophies. J. Wisotsky.
- 2507T** Wide range of maternal heteroplasmy for inherited pathogenic mtATP6 variants. J. Thompson.
- 2510T** Mitochondrial genome sequencing in phenotype-based panels and exome sequencing increases test sensitivity. M.A. Reott.
- 2513T** Exome sequencing leads to the identification of two novel MYO15A mutations in a German family with autosomal recessive non-syndromic hearing loss. R. Birkenhager.
- 2516T** Kagami Ogata Syndrome caused by a 14q32 microdeletion that did not encompass MEG3 DMR. W.T. Keng.
- 2519T ‡** Constitutive supernumerary marker chromosomes are the chromothripsis remnant of the supernumerary chromosome present in trisomic embryos. N. Kurtas.
- 2522T** Breakpoint mapping in five Brazilian cases of distal 5p deletion: Influence of copy number variable regions and haploinsufficiency to clinical phenotype. S.N. Chehimi.
- 2525T** Familial interstitial deletion 1(q43q44) due to maternal complex balanced insertional translocation (IT) and inversion in 3p. Y. Hadid.
- 2528T** Concurrent exome and copy number variation (CNV) analyses enable more precise diagnoses and shorten diagnostic testing time in patients with pediatric disorders. A.V. Dharmadhikari.
- 2531T** Diversity of *JAG1* mutations in Japanese patients with Alagille syndrome. T. Togawa.
- 2534T ‡** Application of next generation sequencing in NICU experiences from a 1239-patient pilot study. W. Zhou.
- 2537T** Whole *ROR2* gene deletion uncovering a pathogenic mutation in a patient with autosomal recessive Robinow syndrome. B.M. Ferreira.
- 2540T ‡** AMELIE accelerates Mendelian patient diagnosis directly from the primary literature. J. Birgmeier.
- 2543T** The first Japanese patient of Mandibular hypoplasia, deafness, progeroid features, and lipodystrophy syndrome (MDPL) diagnosed via *POLD1* mutation detection. I. Imoto.
- 2546T** Clinical validation of whole-genome sequencing assay for constitutional disorders. A. Abhyankar.
- 2549T** Human ring chromosome atlas: A web-based registry and a comprehensive review of ring chromosome cases in the Chinese population. Q. Hu.
- 2552T** A unique case of male/female chimerism in buccal specimen due to a bone marrow transplant. H. Risheg.
- 2555T** Clinical whole genome sequencing in a pediatric hospital. C. Saunders.
- 2558T** Gene-specific criteria for PTEN variant curation. J. Mester.
- 2561T** Going beyond the ACMG recommendations for reporting secondary findings: From decision-making to follow-up. N.T. Strande.
- 2564T** Workshop in genomic medicine for paediatric specialists. A.D. Gilbert.
- 2567T ‡** Correctly building, evaluating and using clinical grade pathogenicity classifiers for variant of unknown significance. G. Bejerano.
- 2570T** Identifying single fetal trophoblastic cells in the maternal circulation: A modified NGS genotyping method. X. Zhuo.
- 2573T** Long read capture sequencing for clinical applications. K.C. Worley.
- 2576T ‡** Copy number variant discrepancy resolution using the ClinGen dosage sensitivity map. E.R. Riggs.
- 2579T** Diagnostic digital PCR copy number assay for NKX2-1 related disorders. K.M. Robbins.
- 2582T** Structural variant detection with optical mapping and microfluidic partitioning: A t(9;13) case report. D. Baldrige.
- 2585T** No consistent phenotype in patients with copy number variants of the SHOX downstream regulatory domain. A. Wray.
- 2588T** High throughput linked-read sequencing for improved variant detection. A. Fehr.
- 2591T ‡** Towards automated variant pathogenicity assessment: A Bayesian classification framework. L.G. Biesecker.
- 2594T** Clinically significant small indels detected by whole genome sequencing: A proof of concept case series. C.M. Brown.
- 2597T** Challenges and solutions for FFPE DNA quantitation. K. Plasman.

**2600T** WGS is an imperfect but valuable tool for predicting the risk of genetic disease in children. M.S. Meyn.

---

## Cardiovascular Phenotypes

---

**2603T** Analysis of 181 selected genes associated with dilated cardiomyopathy by next-generation sequencing. K. Al Harbi.

**2606T** Novel heterozygous mutations of *KCNQ1* gene in a Jervell and Lange-Nielsen syndrome patient with gastric neuroendocrine tumor. K. Choi.

**2609T** Cardiologic findings in 101 patients with Williams Syndrome. R.S. Honjo.

**2612T** Genetic testing in arrhythmogenic cardiomyopathy: New insights into the disease determinants and new doubts. E. Lazzarini.

**2615T** ‡ High incidence of *SCN5A* c.5350 G>A (p.Glu1784Lys) heterozygotes and prolonged QT intervals in a large biobank cohort. M.L.B. Schwartz.

**2618T** Novel *CACNA1C* variant associated with Long QT syndrome in a multigenerational family. V. Novelli.

**2621T** *HIVEP2* as a cause hypoplastic left heart syndrome: A report of a rare condition in an 18 month old boy. H. Holway.

**2624T** Mutation spectrum of the *KCNQ1*, *KCNH2*, and *SCN5A* genes for the long QT syndrome in Korea. M. Kim.

**2627T** Novel *PIEZO1* mutations in patients with autosomal recessive hereditary lymphedema. L. Lai.

**2630T** Thoracic aortic disease outcomes in 987 cases with pathogenic variants in *ACTA2*, *PRKG1*, *TGFBR1*, *TGFBR2* and *SMAD3* ascertained by the Montalcino Aortic Consortium. D. Milewicz.

**2633T** Genetic architecture of pulmonary arterial hypertension with congenital heart disease. N. Zhu.

**2636T** Genome-wide association study of cardiotoxicity and cardiac gene expression in NCCTG N9831 (Alliance) Adjuvant Trastuzumab Trial. D.J. Serie.

**2639T** ‡ Identifying and characterizing causal genes in GWAS-identified loci for heart rate variability using high-throughput, image-based screens in zebrafish larvae. B. von der Heyde.

**2642T** ‡ Genome-wide association study of congenital heart disease in the UK Biobank. A. Córdova-Palomera.

**2645T** The search for coronary heart disease biomarkers: A large scale reanalysis of gene expression data. B. Cunha.

**2648T** Arrhythmia and night vision blindness: Chicken and egg? Or could be chicken or egg? A. Faucon.

**2651T** ‡ Genome wide association study identifies nine novel loci for subclinical atherosclerosis traits and highlights genetic correlation with clinical cardiovascular disease. N. Franceschini.

**2654T** Elucidating the molecular causes of severe hypercholesterolemia in Finland. N. Junna.

**2657T** Novel compound homozygous mutations in genes involved in mitochondrial function associated with sudden death with cardiac fibrosis in infancy. K. Mittal.

**2660T** Evaluating the role of genetic variants on blood cell count variability in the Jackson Heart Study. J.R. Shaw.

**2663T** Genetics and outcome of noncompaction cardiomyopathy: A Dutch multicenter study. J. van Waning.

**2666T** African ancestry genome- and transcriptome-wide association study of blood pressure detects nine novel loci in a large cohort from the Million Veteran Program. J.N. Hellwege.

**2669T** Mendelian randomization to identify causal risk factors for atrial fibrillation. L. Weng.

**2672T** Large-scale validation of zebrafish larvae as a model system for genetic screens in dyslipidaemia, atherosclerosis and coronary artery disease. M. Bandaru.

**2675T** Genome-wide association study of susceptibility to rheumatic heart disease in South Asians: Preliminary results. K. Auckland.

**2678T** A genome-wide association study identifies novel genetic signatures associated with thiazide diuretics adverse metabolic events. M.H. Shahin.

**2681T** ‡ A novel LDL-lowering missense variant in *B4GALT1* identifies novel biological connection between protein glycosylation and cardiovascular risk factors in human. M. Montasser.

**2684T** Utilization of drugs with evidence for pharmacogenomic testing following percutaneous coronary intervention. N. El Rouby.

**2687T** Functional fine-mapping of coronary artery disease risk variants. B. Liu.

**2690T** Implementing genome-based predictive and preventive medicine: The GeneRISK follow-up study. E. Widen.

**2693T** Putative loss-of-function (pLOF) genetic variants in arrhythmogenic cardiomyopathy-associated genes: Prevalence and EHR-based phenotype in 50,000 biobank participants. C.M. Haggerty.

**2696T** The role of Kringle IV 2 copy number variation and SNPs on Lp(a) levels and cardio-metabolic risk. S.E. Ruotsalainen.

**2699T** Large-scale genomic study of >26,000 MyCode participants uncovers novel loci for hemostasis. J. Backman.

**2702T** StructLMM: Resolving genetic effects due to environmental sample substructure. R. Moore.

**2705T** Multi-ancestry genome-wide study incorporating gene-smoking interactions identifies 139 genome-wide significant loci for systolic and diastolic blood pressure. Y.J. Sung.

**2708T** Genome-wide association study of mitochondrial DNA copy number: The Cohorts for Heart & Aging Research in Genetic Epidemiology (CHARGE). R.J. Longchamps.

**2711T** Association of genetic risk score with childhood obesity-related traits: The Santiago Longitudinal Cohort Study (SLCS). G. Chittoor.

---

‡ Indicates Reviewers' Choice Abstract; "ES" Indicates Epstein Trainee Award Semifinalist; "EF" indicates Epstein Trainee Award Finalists

Photographing and recording posters are strictly prohibited if the author has displayed the no photography symbol. You agreed to adhere to this policy when you registered.

**2714T** Low frequency and rare variants of *RBFox1* are associated with blood pressure. K.Y. He.

**2717T** Partitioning genome-wide summary statistics improves polygenic risk prediction. S. Chun.

**2720T** Control of ethnically-stratified vascular risk factors in modeling of intracerebral hemorrhage. S. Marini.

**2723T** Heterogeneity in coronary artery disease GWAS results is associated with pan-tissue eQTL count. K.W. Johnson.

**2726T** Integrated analysis using RNA-Seq and ChIP-Seq data to understand the regulation of cardiogenesis. M. Toufiq.

**2729T** Data mining “normal” chromosome microarrays for gene discovery. N. Walton.

**2732T** ‡ High-throughput discovery of deleterious cardiac sodium channel variants. A. Glazer.

**2735T** ‡ The iPSCORE resource: 222 iPSC lines enabling functional characterization of genetic variation across a variety of cell types. E.N. Smith.

**2738T** Chromosome 22q11 microdeletion: Modifiers of the cardiovascular phenotype identified by whole exome sequencing. G. Repetto.

**2741T** The effects of missense mutations causing PRKAG2 cardiomyopathy on expression levels of selected genes involved in AMPK pathway. E. Komurcu-Bayrak.

**2744T** Epigenetic modulation in the pathogenesis and treatment of inherited aortic aneurysm conditions. B.E. Kang.

**2747T** Epigenetic regulation of PAR-4-mediated platelet activation: Understanding the mechanistic links between smoking and cardiovascular disease. N. Timpson.

**2750T** ‡ Enhancer signature of dilated cardiomyopathy. D. Hemerich.

**2753T** Functional analysis of  $\beta$ -globin locus control region hypersensitive site 2-associated proteins and noncoding RNA. A. Gurumurthy.

**2756T** Fibulin-4a inhibits vascular and enhances cardiac cell fate by inhibiting transforming growth factor beta signaling. Z. Urban.

**2759T** Homozygous *EEF1A2* mutation causes dilated cardiomyopathy, failure to thrive, global developmental delay, epilepsy and early death. P.B. Agrawal.

---

## Statistical Genetics and Genetic Epidemiology

---

**2762T** Contribution of AMD risk variants to the genetic architecture of choroidal thickness in the Amish. N. Restrepo.

**2765T** Preliminary evidence suggests that a 6.7 kb deletion polymorphism in *LILRA3* is associated with Type 1 Diabetes. C. Maroteau.

**2768T** Pleiotropic associations of adiposity-related genetic risk scores. Z. Fairhurst-Hunter.

**2771T** Gender-, genotype- and ethnic-specific effects of sugar-sweetened beverages on serum uric acid concentrations. X. Zhang.

**2774T** Diagnostic of a worldwide cohort of Gaucher patients: Glucosylsphingosine levels in blood reflects the severity of GBA mutations. A. Rolfs.

**2777T** Gene-level differential methylation analysis. H. Xu.

**2780T** Socioeconomic deprivation amplifies genetic susceptibility to obesity and its comorbidities. K.A. Kentistou.

**2783T** Principal component-based prediction of complex traits by using support vector machine approach. X. Li.

**2786T** Genome-wide association analysis in the UK Household Longitudinal Study offers insights into the genetic architecture of health-related biomarkers. K. Kuchenbaecker.

**2789T** Targeted sequencing of 109 genes in the eMERGEseq panel uncovers novel variants and genes influencing triglyceride levels. X. Fan.

**2792T** Do blood lipid levels influence bone mineral density? Findings from a Mendelian randomization study. J. Zheng.

**2795T** Genome-wide haplotype-based association study reveals novel non-HLA susceptibility loci for primary biliary cirrhosis in Japanese cohorts. C. Im.

**2798T** *HLA-DQ* variants interact with pregnancy to modify risk of multiple sclerosis among women of European ancestry. C. Adams.

**2801T** Variance component selection with microbiome taxonomic data. J. Zhou.

**2804T** Association study of *R3HDM1* variants with aspirin exacerbated respiratory disease and FEV1 decline after aspirin provocation. J. Kim.

**2807T** Trans-ethnic Bayesian meta-analysis detects novel replication evidence for multiple loci for inflammatory bowel disease in African Americans. R.Y. Cordero.

**2810T** Gene-based pathway analysis for osteoporosis: Insights from genomic-wide association. K.J. Su.

**2813T** Alzheimer's Disease Sequencing Project: Case-control analyses of over 10,000 whole exomes. J.C. Bis.

**2816T** Cell free single stranded DNA concentration in CSF as biomarker to diagnose Alzheimer's disease status. J.D. Gonzalez Murcia.

**2819T** Complex disease prediction: A framework to integrate SNP and imaging data. B. Zhao.

**2822T** Investigating the underlying genetic basis of the co-occurrence of epilepsy and psychiatric disorders. H.O. Heyne.

**2825T** Gene-gene interaction tests for genetic-imaging data analysis. W. Peng.

**2828T** Rare coding mutations in Alzheimer Disease. D. Patel.

---

‡ Indicates Reviewers' Choice Abstract; “ES” Indicates Epstein Trainee Award Semifinalist; “EF” indicates Epstein Trainee Award Finalists

The author listed is the first/presenting author of the abstract. The letter following each poster number indicates the day that the author will present at their posters. W=Wednesday; T=Thursday; F=Friday.

- 2831T ‡** Multivariate genome-wide association study for volumes of structural MRI regions of interest measures via a genetic correlation network modular analysis. J. Liang.
- 2834T** Severity modifiers in autism spectrum disorder: WGS perspective. S.P. Smieszek.
- 2837T** Testing the moderation of quantitative gene by environment interactions in unrelated but dependent individuals. R. Tahmasbi.
- 2840T** Genome-wide association study of dental treatment-related fear and anxiety nominates novel genes. J.R. Shaffer.
- 2843T** Allelic heterogeneity across psychotic disorders and related phenotypes. T. Polushina.
- 2846T** Genetic validation of bipolar disorder identified by automated phenotyping using electronic health records. C. Chen.
- 2849T** Whole genome sequencing in families with bipolar 1 disorder implicates cysteine transport process and synaptic neurotransmission pathway. A. Parrado.
- 2852T** Joint analysis of rare and common variants with the adaptive combination of Bayes factors method. W. Lin.
- 2855T ‡** Integrating eQTL data with GWAS summary statistics identifies novel genes and pathways associated with schizophrenia. C. Wu.
- 2858T** Global developmental delay: Genetic causes in a group of Mexican patients. M.L. Arenas-Sordo.
- 2861T** Targeted sequence analysis of human mitochondrial DNA using an IDT xGen® Lockdown® probe panel. R. Lopez.
- 2864T** Individualized glaucoma risk evaluation using the genomic profile. X. Gao.
- 2867T** Genetic risk score is associated with vertical cup-disc ratio and improves prediction of primary open angle glaucoma in Latinos. D.R. Nannini.
- 2870T** Tracing the dark matter: Prevalence of copy number variants across Mendelian disorders. R. Truty.
- 2873T** Genetic factors that modulate the relationship between education and Alzheimer's disease. R.A. Bhatta.
- 2876T** Gene by environment interaction in human longevity as observed in Danish birth cohorts from 1905 to 1915. Q. Tan.
- 2879T** Old before our time: Biological ageing in an ethnically diverse cohort of preschool children. K.N. Ly.
- 2882T** Robust inference of population structure from next-generation sequencing data with systematic differences in sequencing. Y.J. Hu.
- 2885T** Some novel methods of detecting gene-drug interactions. M. Rao.
- 2888T** High frequency of the MEFV c.1437C>G, p.F479L allele among Druze FMF patients. V. Adir.
- 2891T** To ERV is human: A phenotype-wide scan linking polymorphic human endogenous retrovirus-K insertions to tissue-specific gene expression and complex diseases. A.D. Wallace.
- 2894T** Genetic analyses for antiepileptic drug-induced cutaneous adverse reaction in a HK population. J. Ding.
- 2897T** The usage of local ancestry to Inform eQTL mapping in African Americans. Y. Zhong.
- 2900T ‡** Iranome: A human genome variation database of eight major ethnic groups that live in Iran and neighboring countries in the Middle East. M.R. Akbari.
- 2903T** Data-driven genetic encoding (DAGE) allows flexible identification of novel main effects and SNP-SNP interactions. M.A. Hall.
- 2906T** Assessing pleiotropy and mediation in loci associated with chronic obstructive pulmonary disease. M.M. Parker.
- 2909T** Large-scale inference in population cohorts. M.A. Rivas.
- 2912T ‡** Leveraging whole genome sequence data to improve imputation and increase power in GWAS of diverse populations. C. Quick.
- 2915T** Genome-wide association study identifies novel susceptibility loci for tanning ability in Japanese population: From ToMMo cohort study. K. Shido.
- 2918T** Genome-wide analysis of age-related macular degeneration progression. Q. Yan.
- 2921T** Genome-to-genome analysis: Correcting for population stratification in joint association analysis of host and pathogen genomes (G2G) reduces false positive and negative results. O. Naret.
- 2924T** Exploring genetic associations using self-reported phenotypes in genes for good. A. Pandit.
- 2927T** Summary statistic GWAS joint analyses across 50+ traits. H. Aschard.
- 2930T** Assessing the causal impact of smoking and drinking on human health outcomes: Using 239 novel genetic associations for smoking and drinking addictions and a robust ensemble method for causal inference. F. Chen.
- 2933T** Genome-wide association study identifies novel genetic loci in the Major Histocompatibility Complex (MHC) associated with reduction in *Clostridium difficile* Infection (CDI) recurrence in patients treated with bezlotoxumab. J. Shen.
- 2936T** Comparison of PC-based and LME-based population structure adjustment using GWAS and WES markers. Y. Chen.
- 2939T** Potentially causal rare variants identified using whole genome sequencing of distant relatives from multiplex families with oral clefts. F. Begum.
- 2942T** A fast algorithm for Bayesian multi-locus model in genome-wide association studies. W. Duan.
- 2945T** Bayesian methods for genetic associations and causal inference yield potential biological insight for genetics of gene regulation. B. Jo.
- 2948T** Modeling functional enrichment improves polygenic prediction accuracy in UK Biobank and 23andMe data sets. C. Marquez-Luna.

- 2951T ‡** Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types. H.K. Finucane.
- 2954T ‡** Local genetic correlation gives insights into the shared genetic architecture of complex traits. H. Shi.
- 2957T** A large-scale genome-wide enrichment analysis identifies new trait-associated genes, pathways and tissues across 31 human phenotypes. X. Zhu.
- 2960T** Reverse regression enables disease only case-control association studies for burden tests. J. Tom.
- 2963T** Imputation of exome array variants to the Haplotype Reference Consortium (HRC). S. Bomotti.
- 2966T** Leveraging polygenic functional enrichment to improve GWAS power. G. Kichaev.
- 2969T** Sequential fine-mapping from summary statistics in meta-analyses of genome-wide association studies. C. Benner.
- 2972T** Incorporating multiple functional annotations to infer trait-relevant tissues in genome-wide association studies. X. Hao.
- 2975T** A hierarchical clustering method for joint analysis of multiple phenotypes. X. Liang.
- 2978T** Estimating higher-order heritability components in GWAS data from 133,515 individuals. S.R. McCurdy.
- 2981T** Estimating effect-size distributions using summary level statistics from genomewide association studies and projecting trajectories of future discoveries for 32 complex traits. Y. Zhang.
- 2984T** GWAS genes whose expression is implicated by Mendelian randomization are highly connected in tissue-specific regulatory circuits. E. Porcu.
- 2987T** A highly adaptive microbiome-based survival analysis method. H. Koh.
- 2990T** PheCLC: A novel statistical method for phenome-wide association studies. H. Zhu.
- 2993T** A novel approach for parsing distribution of polygenic risk. L. Almasy.
- 2996T** HiREPRO: Evaluating Hi-C data REProducibility via Regression. C. Crowley.
- 2999T** A test for Hardy-Weinberg equilibrium in structured populations. W. Hao.
- 3002T** Estimating the contribution of gene-environment interactions to phenotypic variance. V. Laville.
- 3005T** Modeling ancestry-dependent phenotypic variance increases power in multi-ethnic association studies and enables detection of variance effects. S. Musharoff.
- 3008T** We didn't see this in GWAS: Understanding and fixing unfamiliar problems in association analyses, when pooling whole genome sequence data from multiple studies. K. Rice.
- 3011T** GWAS meta-analysis allowing for sample overlap estimated using summary statistics. S. Sengupta.
- 3014T** Estimating the proportions of additive, dominant and recessive genetic effects. H. Wu.
- 3017T** Robustly doubling the sample size: A unifying regression framework for allele-based association test. L. Zhang.
- 3020T** A Bayesian framework for transcriptome-wide association studies. J.D. Rosen.