# Poster Numbers and Titles

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| 1 | Transcriptomic analysis of coding genes and non-coding RNAs in grain-fed and grass-fed Angus cattle muscle tissue<br>*Y Bai, JA Carrillo, Y He, Y Li, J Song* |
| 2 | mtDNA G4 Sequences Associate with Variants and Polymerase Stalling<br>*T Butler, K Estep, J Sommers, R Maul, A Moore, S Bandinelli, L Ferrucci, D Schlessinger, J Ding, R Brosh Jr.* |
| 3 | Regulation of Janus kinase 2 by an inflammatory bowel disease causal noncoding SNP<br>*C Cardinale, M March, X Lin, Y Liu, L Spruce, Z Wei, S Seeholzer, S Grant, H Hakonarson* |
| 4 | A novel locus identified in chromosome 14 of mouse modulates lens weight<br>*J Cordero, R Williams, L Lu, C Simpson* |
| 5 | QTL Remapping of Murine Eye Weight Reveals Novel Candidate Genes for Ocular Growth<br>*R Cordero, R Williams, L Lu , C Simpson* |
| 6 | Genome-wide cell-free DNA fragmentation in patients with cancer<br>*S Cristiano, A Leal, J Phallen, J Fiksel, R Scharpf, V Velculescu* |
| 7 | Facilitating Analysis of Publicly Available ChIP-Seq Data for Integrative Studies<br>*A Diwadkar, M Kan, BE Himes* |
| 8 | Deconvolution of Transcriptional Networks Identifies TCF4 as a Master Regulator in Schizophrenia<br>*A Doostparast Torshizi, C Armoskus, H Zhang, MP Forrest, S Zhang, T Souaiaia, OV Evgrafov, JA Knowles, J Duan, K Wang* |
| 9 | Incorporating single-cell RNA-seq data to infer allele-specific expression<br>*J Fan, R Xiao, M Li* |
| 10 | Enabling Precision Mitochondrial Medicine through Novel Integration, Visualization, and Complex Analytics of Clinical and Research Data<br>*I George-Sankoh, L MacMullen, D Taylor, B Devkota, R Ganetzky, MJ Falk* |
| 11 | Ancestry Clustering and Classification Using an Autoencoder<br>*S Gilhool, P Sleiman, H Hakonarson* |
| 12 | The association between African ancestry and telomere length across the African diaspora: evidence from the CAAPA study<br>*K Iyer, M Taub, M Daya, S Chavan, K Barnes, T Beaty, R Mathias* |
| 13 | Airway Smooth Muscle-Specific Transcriptomic Signatures of Glucocorticoid Exposure<br>*M Kan, C Koziol-White, M Shumyatcher, M Johnson, W Jester, RA Panettieri, BE Himes* |
| 14 | Genomic integrity of human induced pluripotent stem cells across nine studies in the NHLBI NextGen Program<br>*K Kanchan, K Iyer, LR Yanek, MA Taub, C Malley, K Baldwin, L C Becker, U Broeckel, L Cheng, C Cowan, M D'Antonio, KA Frazer, I Carcamo-Orive, JW Knowles, T Quertermous, G Mostoslavsky, G Murphy, M Rabinovitch, DJ Rader, MH Steinberg, E Topol1, W Yang, CE Jaquish, I Ruczinski, RA Mathias* |
| 15 | Mediation analysis of alcohol use disorder and alcohol consumption reveals both shared and unique genetic architecture<br>*RL Kember, RV Smith, M Vujkovik, H Zhou, AC Justice, J Gelernter, HR Kranzler* |
| 16 | Generalized Meta-Analysis for Combining Disparate Information Across Studies: Inference on Multiple Regression Models<br>*P Kundu, N Chatterjee* |
| 17 | Integrative analysis of untranslated regions in human messenger RNAs uncovers G-quadruplexes as constrained regulatory features<br>*D Lee, L Ghanem, Y Barash* |
| 18 | Joint Between-Sample Normalization and Differential Expression Detection through L0 Regularized Linear Regression<br>*K Liu, L Shen, H Jiang* |
| 19 | Detection of DNA base modifications by deep recurrent neural network on Oxford Nanopore sequencing data<br>*Q Liu, L Fang, G Yu, D Wang, CL Xiao, K Wang* |
| 20 | Investigating the Genetic Architecture of Psychiatric Disorders and their Medical Comorbidity<br>*AK Merikangas, RL Kember, K Ruparel, ME Calkins, RC Gur, RE Gur, L Almasy* |
| 21 | Defining regulatory variants for SLE susceptibility using an integrative post-GWAS functional genomic framework<br>*J Molineros, L Loooger, C Sun, S Nath* |
| 22 | WhatsGNU: a tool for identifying proteomic novelty<br>*AM Moustafa, PJ Planet* |
| 23 | Identifying SNP Associations in Under-Powered Whole-Genome Sequencing Association Studies Using eQTLs<br>*JS Ngwa, LR Yanek, K Kammers, MA Taub, RB Scharpf, N Faraday, LC Becker, DM Becker, RA Mathias, I Ruczinski* |
| 24 | Comparison of ARIMA, neural networks and hybrid models: Renal failure forecasting in Gaza<br>*S Safi* |
| 25 | Predicting Congenital Heart Defect risk from maternal SNPs<br>*B Stear, D Hammond, D Taylor* |
| 26 | Modeling metabolic variation with single-cell expression data<br>*Y Zhang, DM Taylor* |
| 27 | Genetic analysis of neuroblastoma in African American children<br>*A Testori, Z Vaksman, S Diskin, J Maris, M Devoto* |
| 28 | A multi-ethnic genome-wide association study (GWAS) identifies eleven new loci associated with neuroblastoma<br>*Z Vaksman, X Chang, G Lopez, A Modi, H Hakonarson, M Devoto, JM Maris, SJ Diskin* |
| 29 | Characterization of Genetic and Phenotypic Heterogeneity of Obstructive Sleep Apnea across Multiple United States Clinics<br>*OJ Veatch, CR Bauer, DR Mazzotti, BT Keenan, JD Robishaw, K Bagai, BA Malow, AI Pack, SA Pendergrass* |
| 30 | Signatures in the myeloma transcriptome<br>*RG Waller, MJ Madsen, J Gardner, D Sborov, NJ Camp* |
| 31 | Recovery of genetic heterogeneity for single-cell DNA sequencing<br>*C Wu, NR Zhang* |
| 32 | Exploring the Genetic Architecture of Autism Spectrum Disorder without Intellectual Disability<br>*J Zhang, A Ghorai, SC Taylor, LS Perez, HC Dow, BN Gehringer, ZL Griffiths, RL Kember, L Almasy, DJ Rader, ES Brodkin, M Bucan* |
| 33 | Phen2Gene: Rapid Phenotype Driven Gene Prioritization for Rare Diseases Using Human Phenotype Ontology Terms<br>*M Zhao, L Fang, Y Chen, C Liu , G Lyon, C Weng, K Wang* |
| 34 | cTP-net: Prediction of surface protein abundance from single cell transcriptomes by deep neural networks<br>*Z Zhou, C Ye, NR Zhang* |