Poster Numbers & Titles

| 1 | The regulatory landscape of genetic variants associated with psychiatric disorders and neurodegenerative diseases A Amlie-Wolf, L Qu, EE Mlynarski, CD Brown, GD Schellenberg, LS Wang |
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| 2 | Applying Next-Generation Sequencing to the Genetics and Ecology of Rhodnius pallescens, A Vector of Chagas Disease $FBermudez$ |
| 3 | More precise metagenomics classifications using unique k-mer counts FP Breitwieser, SL Salzberg |
| 4 | Widespread hyper RNA editing sites in bovine genome $W\mathit{Cai}, \mathit{SZhang}, \mathit{JSong}$ |
| 5 | BrainSeq Phase II: schizophrenia-associated expression differences between the hippocampus and the dorsolateral prefrontal cortex L Collado-Torres, EE Burke, A Peterson, JH Shin, SA Semick, BrainSeq Consortium, R Tao, A Deep-Soboslay, TM Hyde, JE Kleinman, DR Weinberger, AE Jaffe |
| 6 | Detection of de novo copy number deletions from targeted sequencing of trios JFu, E Leslie, A Scott, J Murray, M Marazita, T Beaty, R Scharpf, I Ruczinski |
| 7 | Evaluating the contribution of cell-type specific alternative splicing to variation in lipid levels K Gawronski, W Bone, E Pashos, Y Park, X Wang, W Yang, D Rader, K Musunuru, B Voight, C Brown |
| 8 | Violence Exposure, Stress Biomarkers and Gender Differences in Buccal Telomere Length among African American Young Adults $L Jackson, F Saadatmand$ |
| 9 | Assembling the building blocks for a unified splicing code $A\ Jha, M\ Gazzara, Y\ Barash$ |
| 10 | Integration of Transcriptomic Data Identifies Global and Cell-Specific Asthma-Related Gene Expression Signatures M. Kan, M. Shumyatcher, BE Himes |
| 11 | Identifying the genetic and environmental determinants of gene expression variation in Africans DE Kelly, R Ma, NG Crawford, Y Ren, RA Rawlings-Goss, GR Grant, M Yeager, S Chanock, A Ranciaro, S Thompson, JB Hirbo, W Beggs, TB Nyambo, SA Omar, DO Meskel, G Belay, CD Brown, H Li, SA Tishkoff |
| 12 | Genomics of Addiction T Koschitzky, L Almasy, COGA Collaborators |
| 13 | HiPPIE2: Identifying the transcription factors mediating enhancer–target gene regulation in the human genome YC Hwang, PP Kuksa, A Amlie-Wolf, BD Gregory, LS Wang |
| 14 | Evaluation of PrediXcan capabilities to predict gene expression levels and prioritize variant-based associations using datasets with varied population background $BLi,SVerma,YVeturi,AVerma,YBradford,DHaas,MRitchie$ |
| 15 | QC Software for Analysis of Sequence Data in Family-based Studies $QLi, JBailey\text{-}Wilson$ |

| 16 | Analysis of differential abundance of taxa in microbiome studies using an off-set based linear regression $HLin, SPeddada$ |
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| 17 | Transcriptome-Guided Imaging Genetic Analysis via a Novel Sparse CCA Algorithm K Liu, X Yao, J Yan, K Nho, SL Risacher, AJ Saykin, JH Moore, L Shen |
| 18 | Determining and inducing gene expression patterns underlying cell identity IA Mellis, H Edelstein, R Truitt, PP Shah, W Yang, R Jain, A Raj |
| 19 | Genetic Discrimination between LADA and Type 1 Diabetes within the MHC R Mishra, JP Bradfield, DL Cousminer, A Chesi, KM Hodge, H Hakonarson, D Mauricio, NC Schloot, KB Yderstræde, B Voight, S Schwartz, BO Boehm, RDG Leslie, SFA Grant |
| 20 | Nonparametric Survival Analysis with Delayed Treatment Effect $KNam, NC$ Henderson, D Feng |
| 21 | MAJIQ-HET robustly detects changes in RNA splicing between large heterogeneous sample groups SS Norton, J Vaquero-Garcia, Y Barash |
| 22 | Life History of Metastatic Breast Cancer Reveals Promising Therapeutic Targets MR Paul, T Pan, D Pant, N Shih, Y Chen, LA Lee, A Solomon, D Lieberman, JJD Morrissette, D Soucier-Ernst, W Stavropoulos, KN Maxwell, C Clark, GK Belka, M Feldman, A DeMichele, LA Chodosh |
| 23 | DNA methylation changes in Alzheimer's disease across multiple brain regions implicate ANKRD30B S Semick, R Bharadwaj, L Collado-Torres, R Tao, JH Shin, A Deep-Soboslay, J Weiss, D Weinberger, T Hyde, J Kleinman, A Jaffe, V Mattay |
| 24 | Bivariate GWAS scan identifies six novel loci associated with lipid levels and coronary artery disease $KSiewert, BVoight$ |
| 25 | Carpe D.I.E.M: A Data Integration Expectation Map of Multi- Omics Data In Complex Disease Disparities T Tate Hudson, C Williams-DeVane |
| 26 | Calculating Overall Biological Process Dysfunction Related to Autism Risk Genes Identifies Clinically-Meaningful Genetic Information OJ Veatch, DR Mazzotti, JS Sutcliffe, RS Schultz, T Abel, B Tunc, SG Assouline, E Brodkin, JJ Michaelson, TK Nickl-Jockschat, ZE Warren, BA Malow, AI Pack |
| 27 | Multiplexed in situ analysis of the human pancreas using imaging mass cytometry $YJWang, DTraum, JSchug, KKaestner$ |
| 28 | Bulk Tissue Gene Expression Deconvolution Using Single Cell RNA-seq Data $X Wang, MLi, NZhang$ |
| 29 | Identifying Tissue-Specific Functional Interaction Modules: An Amygdala Imaging Genetic Studye X Yao, K Liu, J Yan, K Nho, S Risacher, C Greene, J Moore, A Saykin, L Shen |
| 30 | Generalized Integration Model for Improved Statistical Inference by Leveraging External Summary Data H Zhang, L Deng, M Schiffman, J Qin, K Yu |