Poster Session B: Monday, October 13, 10:00am-11:30am		
Poster/Abstract #	**Abstract Title**	**Presenting Author**
4	*Recurrency approaches using Random Forests to identify genetic risk factors while controlling family-wise false positive rates*	Bailey-Wilson, J
8	*Novel association of G-Quadruplex SNPs in schizophrenia candidate genes with cognition and tardive dyskinesia in a schizophrenia cohort*	Bhattacharyya, U
9	*Integrative omics approach identifies association between dementia risk and non-coding variants also associated with gene expression in brain*	Blue, E
11	*Covariate Adjusted Permutation for Millions of Samples*	Bohlender, R
13	*IMHOTEP - composite score integrating popular tools for predicting the functional consequences of non-synonymous sequence variants*	Caliebe, A
16	*Interrogation of the transcriptomic and exonic profiles in participants with hypertriglyceridemia and normal weight vs low triglycerides and obese*	Chen, H-H
20	*A novel locus identified in chromosome 14 of mouse modulates lens weight*	Cordero, J
22	*Developing a Genetic Risk Index for Peanut Allergy*	Daley, D
25	*Identification of selective sweeps through deep learning in whole genome sequenced malaria parasites*	Deelder, W
29	*Epigenome-wide association study of change in blood metabolite levels from young- to middle adulthood in the Northern Finland Birth Cohort 1966*	Draisma, H
31	*Improving efficiency in epistasis detection with a gene-based analysis using functional filters*	Duroux, D
34	*Using external controls to account for mating asymmetry in maternal genetic association*	Ewusie, J
37	*Case-only design to investigate interactions between genetic factors and tobacco smoke in patients with aggressive periodontitis*	Freitag-Wolf, S
40	*Association Mapping Of Multivariate Phenotypes In The Presence Of Missing Data*	Ghosh, S
42	*Circulating sex hormone levels and DNA methylation in blood ‚Äì an analysis of repeated samples from men*	Harbs, J
45	*Leveraging genetic ancestry for new insights into complex traits in admixed populations*	Horimoto, A
47	*Causal Inference for Highly Pleiotropic Biomarkers using Mendelian Randomisation and Bayesian Networks*	Howey, R
49	*Best practices to integrate transcriptome data with GWAS studies to understand the biology of complex traits*	Im, HK
51	*Cohort study of serum Bisphenol A, polygenetic risk score, and thyroid cancer in Korea*	Jee, SH
54	*Genome-wide association study in multiplex consanguineous Pakistani pedigrees with schizophrenia and bipolar disorder*	John, J
59	*Entanglement Mapping: A Model-Free Approach to Detecting Interactions Among Predictive Features.*	Kiser, D
61	*Comparison of Imputation Quality for an Arab Population Using Different References, GWAS Panels, and Methods*	Kunji, K

66	*QC Measurements of Exome Chip Sequence Data in a Family-based Study*	Li, Q
68	*Fast and powerful method for eQTL and fine-mapping integrating total and allele-specific expression*	Liang, Y
72	*Whole-genome bisulfite sequencing in systemic sclerosis provides novel targets to understand disease pathogenesis*	Lu, T
74	*Network-based Identification of Key Master Regulators for Immunologic Constant of Rejection in Cancer*	Mall, R
76	*Efficient Estimation of Hidden Ancestry Structure Using Summary Genotype Frequency Data*	Matesi, G
78	*A Bayesian model to estimate microbiome network changes with respect to a covariate profile*	McGregor, K
82	*Genetic association testing with multivariate outcomes: methods comparison with application to cognition and eye disease*	Montazeri, Z
84	*MetaSubtract: an R-package to analytically produce leave-one-out meta-analysis summary statistics*	Nolte, I
87	*Risk prediction for colorectal cancer based on extended family history and body mass index*	Ochs-Balcom, H
89	*A flexible copula-based approach for the analysis of secondary phenotypes in ascertained samples*	Oualkacha, K
91	*Genome-wide association study of the cerebrospinal fluid metabolome*	Panyard, D
93	*Polygenic Risk Scores Accounting for LD: Estimation and Model Selection Based on GWAS Summary Statistics*	Pattee, J
95	*Modeling Heterogeneity of Complex Traits using Mixture Models and Secondary Phenotypes*	Paul, S
97	*Uterine Leiomyomata Polygenic Risk Score (PRS) Confers Novel Relationships in the Clinical Phenome*	Piekos, J
99	*Imputation of missing genotypes and estimation of relatedness between subjects without genetic data across pedigrees*	Saad, M
102	*Testing for multiple shared variants in two traits with summary genetic association data*	Schoenbuchner, S
104	*Smoothed moving landmark analysis for the age-dependent effects of DNA methylation on the risk of coronary heart disease*	Shi, B
107	*Accounting for covariates in tiled regression analysis of complex traits*	Sorant, A
109	*A novel method to estimate the distribution of ancestral DNA sequence*	Sun, J
111	*Multi-ancestry genome-wide meta-analysis accounting for gene-education interactions in up to 227,850 individuals identifies several novel lipid loci*	Sung, Y
113	*Comparison of pathway guided random forests approaches for the integration of biological knowledge and omics data*	Szymczak, S
115	*SNP-based epistasis detection - a lost cause?*	Van Steen, K
117	*Gene-based rare variant association tests for ancestry-matched case-control data*	Wang, C