Poster Session A: Sunday, October 12, 3:15pm-4:45pm		
Poster/Abstract #	**Abstract Title**	**Presenting Author**
2	*Impact of Reference Panel Choice for imputation on Genome-Wide Association Study Results for Type 2 Diabetes in Arab population*	Almeer, H
7	*A Framework for Transcriptome-Wide Association Studies in Breast Cancer in Diverse Study Populations*	Bhattacharya, A
10	*Genomic imprinting analyses reveal maternal effects to be a cause of genotypic variability in type 1 diabetes and rheumatoid arthritis*	Blunk, I
12	*Association of Polygenic Risk Scores for Body Mass Index and Systolic Blood Pressure in a Pediatric Cohort Requiring Surgery for Congenital Heart Defects*	Breeyear, J
14	*Next generation MB-MDR: taking the challenge to enhance replication and interpretation in epistasis studies for complex traits*	Camargo, A
17	*PCSK9 variants and type 2 diabetes risk in people of African Ancestry: a meta-analysis study N = 30 000*	Chikowore, T
19	*A principal component approach to polygenic risk scores to avoid over- and underfitting*	Coombes, B
21	*QTL Remapping of Murine Eye Weight Reveals Novel Candidate Genes for Ocular Growth*	Cordero, R
23	*Statistical Interaction and Mendelian Randomization: are they the same?*	de Andrade, M
26	*Epigenome-wide association study of Immunoglobulin E levels using high-resolution DNA methylation profiling*	Demenais, F
30	*Host Genome-Wide Association Study of Infant Susceptibility to Shigella-Associated Diarrhea*	Duchen, D
33	*Optimal Two-Phase Designs in Practice: Considerations and an Illustration*	Espin-Garcia, O
35	*Role of functional non coding variants in the germline DNA in the ovarian cancer predisposition*	Ezquina, S
38	*Applications of time scale to investigations in the immune system behavior.*	Fundator, M
41	*Whole-exome sequencing and protein interaction networks to prioritize candidate genes for susceptibility to melanoma*	Goldstein, A
46	*Discovery of pleiotropic variants associated with multiple sclerosis and migraine*	Horton, M
48	*GWAS of the postprandial triglyceride response yields common genetic variation in hepatic lipase (LIPC)*	Ibi, D
50	*A recall-by-genotype pilot study to assess the effects of common TMPRSS6 variants on oral iron absorption*	Jallow, M
53	*Genome-wide Analysis of Non-completion of Controlled Exercise Trials in Sedentary Adults*	Jiang, R
57	*Epigenetic loci for blood pressure are associated with hypertensive target organ damage in an older African American population*	Kho, M
60	*Four novel signals suggest possible genetic component to age-of-onset of idiopathic pulmonary fibrosis*	Kraven, L

65	*Can identity-by-descent sharing information complement population based imputation algorithms?*	Leutengger, A-L
67	*FamRVC program for family-based rare variant association tests for censored traits and its applications to age-at-onset of Alzheimer,Äôs disease*	Li, Y-J
69	*Independent Replication of Genetic Associations with Urinary Bladder Cancer Prognosis in the UK Biobank using Hospital Record Data*	Lipunova, N
73	*Comprehensive Analysis of Pulmonary Surfactant Metabolism Genes and Gene Expression Patterns Associated with Lung Cancer Risk*	Luyapan, J
75	*Analysis of Whole Exome Sequencing Data of Hereditary Lung Cancer Families Identifies Germline Copy Number Variations (CNVs) in Multiple Genes*	Mandal, D
77	*Genetic correlations and exploration of uterine fibroid clinical phenome in black and white women*	Mautz, B
81	*Germline mutations in the BRCA1 gene are associated with increased risk for additional cancers including female reproductive system cancers*	Middlebrooks, C
83	*Highly Aggregated Lung Cancer Families Show Significant Linkage to Chromosome 12q23.3 for Cancer Risk*	Musolf, A
86	*Prostate cancer risks for male BRCA1 and BRCA2 mutation carriers: prospective analysis of the EMBRACE study cohort*	Nyberg, T
88	*LDScore regression identifies novel associations between glioma and auto-immune conditions*	Ostrom, Q
90	*Orienting the causal relation between two traits*	Pan, W
92	*An adjusted survival tree model in search of genetic polymorphisms predictive for oxaliplatin treatment in colorectal cancer*	Park, H
94	*Integrating germline and somatic genetics to identify genes associated with lung cancer*	Pattee, J
96	*Interaction analyses of MUC5B risk allele status and the HLA region for idiopathic pulmonary fibrosis susceptibility*	Paynton, M
98	*A Novel Statistical Test Identifies Eight Loci Associated with Two Non-syndromic Orofacial Cleft Subgroups in GWAS of Multi-Ethnic Case-Parent Trios*	Ray, D
100	*Association analyses of handgrip strength leveraging longitudinal and sequence data from the Trans-Omics for Precision Medicine (TOPMed) Program*	Sarnowski, C
103	*Change in ancestry-related assortative mating in the United States: implications for genetic diseases*	Sebro, R
105	*Comparison of multiple phenotype association tests using summary statistics in genome-wide association studies*	Sitlani, C
108	*Multi-omic Analysis of Discordant and Concordant Sib-pairs with Inflammatory Bowel Disease*	Stiemke, A
110	*Polygenic risk scores and epistatic components for Alzheimer,Äôs disease prediction*	Sun, R
112	*MOPower: a web application and reporting tool for the simulation and power calculation of multi-omics study data.*	Syed, H
114	*Epigenetic aging of the placenta: sexually dimorphic influence on fetal growth and risk of low birth weight*	Tekola-Ayele, F