Agarwal, Divyansh
Borrowing information from publicly available data to denoise new single-cell transcriptomics data improves pattern discovery 40

Alasoo, Kaur
Genetic effects on gene expression across tissues, cell types and biological contexts 41

Alsulaiman, Reem Presenters: Alsulaiman, Reem; Shahbeck, Noora
Variable clinical presentations of 30 patients with dihydrolipomide dehydrogenase (DLD) deficiency due to homozygous c.685G>T mutation 42

Alsulaiman, Reem Presenters: Alsulaiman, Reem; Shahbeck, Noora
Clinical exome sequencing in 508 Middle Eastern families with Mendelian diseases provides a high diagnostic yield and discovery of novel genes 43

Altenhofen, Delsi
Nbg15 locus from C3H protects NZO mice from diabetes 44

Aypek, Hande
Does P3H2 (Prolyl3-Hydroxylase 2) modulate the glomerular basement membrane? 45

Azim, M. Kamran
Inflammatory gene expression profile of blood leukocytes in type II diabetes 46

Baeza-Centurion, Pablo
Combinatorial genetics reveals a scaling law for the effects of mutations on splicing 47

Bankier, Sean
Causal inference approaches for the reconstruction of cortisol responsive gene networks 48

Barbitoff, Yury
A phenome-wide search for pleiotropic loci highlights key genes and molecular pathways for human complex traits 49

Bergstedt, Jacob
Factors driving DNA methylation variation in human blood 50

Billon, Victor
Detection of neuronal mosaicism of model organisms using single-cell whole genome sequencing 51

Blein-Nicolas, Mélisande Presenter: de Vienne, Dominique
GWAS for protein expression under normal and water deficit conditions in maize leaves 52

Bonder, Marc Jan
Genetic regulation across 1,300 human induced pluripotent stem cell lines 53

Boruah, Nabamita
Involvement of epigenetic changes in raw areca nut induced carcinogenesis 54

Bosio, Mattia
The contribution of alternative splicing in individual variation and disease 55

Broekema, Roeland
Fine-mapping causal SNPs in autoimmune diseases using SuRE-SNP 56

Brümmer, Anneke
Bias of putative codons in lincRNAs: A mechanism to prevent translation? 57

Bujassoum, Salha Presenters: Alsulaiman, Reem; Bujassoum, Salha
Lynch syndrome in two families with classical hereditary breast and ovarian cancer syndrome phenotype: A new perspective of Lynch syndrome 58

Busby, Bede P.
The impact of the genetic background on gene deletion phenotypes in Saccharomyces cerevisiae 59

Campos-Martin, Rafael
R-TIGER: A robust HMM-based model for genotyping-by-sequencing and recombination breakpoint identification 60

Carugo, Alessandro
Dissection of clonal heterogeneity unmasks pre-existing chemoresistance and functional vulnerabilities in pancreatic cancer 61

Chapal, Michal
Resolving noise-control conflict by gene duplication 62

Chen, Kuan-Ju
Dysregulation of A-to-I RNA editing sites in lung adenocarcinoma 63

Clauw, Pieter
Studying complex trait architecture of temperature adaptation in Arabidopsis thaliana 64

Cohn, Ofir
Studying influenza virus infection in a genetically diverse population 65

De Zan, Erica
FACS-based genomic screen identifies a Ragulator-FLCN compensatory mechanism for mTORC1 activation 66

Dederichs, Tsai-sang
Single-cell genomic and transcriptomic parallel sequencing method validation with human cell lines 67

Demars, Julie
Both oligogenic determinism and epistatic interactions account for the molecular architecture of coat colour variability 68

Fakhri, Omid
Genomic recombination between infectious laryngotracheitis vaccine strains occurs under a broad range of infection conditions in vitro and in ovo 69

Frenkel, Nelly
Chromatin modification effects on DNA replication 70

Girardi, Enrico
The genetic interaction landscape of human membrane transporters 71

Gnanapragasam, Niranjani
Genetic diversity study of the Indian river buffaloes using mitochondrial genomic variations 72

Grézal, Gábor
Widespread regulatory rewiring upon antibiotic resistance mutations shapes cross-resistance 73

Gui, Yujuan
Phenotypic differences of dopaminergic circuitries of mouse strains are associated with extensive regulatory variation in the midbrain 74

Herrera-Rivero, Marisol
Homozygosity mapping identifies further genomic regions associated with cardiac phenotypes in a SCN5A-mutation founder population 75

Hordyjewska-Kowalczyk, Ewa
Analysis of variants associated with clubfoot 76

Huang, Jia-Hsin
Identification of novel genetic regulators linked to the biological traits 77

Jiang, Peijia
ERAP1 and ERAP2 susceptibility alleles in HLA-stratified classical Hodgkin lymphoma patients 78

Kaulich, Manuel
Single and combinatorial CRISPR gene perturbations with 3Cs gRNAs 79

Kogelman, Lisette J. A.
Association of efficacy of migraine-specific drugs with genetic load of migraine 80

Krivtsova, Olga
Functional effects of germline variant rs56391007 in MET in hepatocellular carcinoma 81

Lee, Wei Shern
Genetic and cellular characterisation of brain malformation using patient-derived brain tissues 82

Linder, Robert
Dissecting complex traits using an outcrossed 18-way multi-parent population of budding yeast 83

Lundberg, Mischa
Dissecting the genetic architecture of chronic pain using CTG-VL – Complex-Traits Genetics Virtual Lab 84

Majic, Paco
Enhancers facilitate the birth of de novo genes and their functional integration into regulatory networks 85

Melé, Marta Presenters: Melé, Marta; Garcia-Perez, Raquel
The anatomy of the human transcriptome in health and disease 86

Mighell, Taylor
An integrated deep mutational scanning approach to defining the PTEN genotype-phenotype map 87

Min, Josine
Genomic and phenomic insights from an atlas of genetic effects on DNA methylation 88

Mortlock, Sally Presenters: Mortlock, Sally; Montgomery, Grant W.
Identifying associations between tissue specific genetic regulatory mechanisms and risk of female reproductive diseases using multi-omic data 89

Nicoletti, Chiara
Identification of pathogenic SNPs for muscle-driven cardiovascular disorders 90

Odrzywolski, Adrian
Genomics structural variations analysis in family with Gollop-Wolfgang Syndrome 91

Ovezmyradov, Guvanch
Mining protein interactome of the candidate tumor suppressor protein CTCF 92

Petrizzelli, Marianyela Presenter: de Vienne, Dominique
Integration of proteomic data into constraint-based models reveals the molecular bases of yeast life-history trade-offs 93

Pott, Janne
Genome-wide meta-analysis identifies novel loci of plaque burden in carotid artery 94

Prabh, Neel
Exploring the omnigenic model 95

Pradhananga, Sailendra
Enhancer variants in coronary artery disease using allele specific promoter-enhancer interaction 96

Rainbow, Daniel
Analysis of IL2RA traits associated with autoimmune disease 97

Ramirez-Corona, Bryan
Cis and trans effects equally contribute to differences in the immune response of distinct lines of Drosophila melanogaster 98

Schaarschmidt, Stephanie
De novo transcriptome reconstruction for different rice (Oryza sativa) subspecies using PacBio sequencing 99

Sen, Shurjo
Genomics2020: An overview of the ongoing NHGRI strategic planning process 100

Sengupta, Melanie
Genetic modifiers of Alzheimer's disease 101

Shaymardanov, Abusaid
Interplay of cis and trans factors shape species-specific evolution of gene regulation and expression in primate brain 102

Shibata, Hiroki Presenter: Oda-Ueda, Naoko
Habu snake (Protobothrops flavoviridis) genome study: Genomic architecture implicated in the multiplication and accelerated evolution of venom protein genes 103

Shunkwiler, Lauren
CRISPR/Cas9-generated rat model of 16q12.1 variant effects confirms Tox3 is an ER+ breast cancer susceptibility gene and critically involved in lipid metabolism and neurodevelopment 104

Sin, Celine
ROADdt: Regulation network remodeling along disease development trajectories 105

Szappanos, Balázs
The evolution of the yeast metabolome 106

Taskiran, Ibrahim Ihsan
Deep learning on single-cell ATAC-seq data to decipher enhancer logic 107

Teixeira, Samantha K.
Selection of inflammation-induced candidate genes underlying obesity-related traits using an integrated epigenomic approach 108

Thiesen, Hans-Juergen
Nearly haploid HAP 1 cell models provide an entry to study the coevolution of KRAB-TRIM28 interactions with SETDB1 from fish to human 109

Toropainen, Anu
Role of CAD-associated genetic variation in the regulation of cell type specific enhancer activity 110

Vulliard, Loan
Understanding chemical-genetic Interactions: Morphological screen of combined perturbations 111

Wislowska-Stanek, Aleksandra
Changes in histone tri-methylation (H3K9) after chronic restraint stress and amphetamine administration in subcortical mesolimbic areas in low- and high-anxiety rats 112

Wohlers, Inken
An Egyptian genome reference indicates variation of molecular impact and disease relevance 113

Xavier, Joana M.
Mapping cis-regulatory variants pinpoints target genes of breast cancer risk loci 114

Zamudio, Alicia
Phase-separated transcriptional condensates enriched in disease-associated variation 115

Zaorska, Katarzyna
Unmethylated SOCS3 promoter region and chosen single nucleotide polymorphisms can predict steroid unresponsiveness in Polish children with nephrotic syndrome 116

Zayed, Hatem
Influence of mutations in protein-protein interaction of BRCA1-BARD1 complex: A computational approach 117