Session 1

Day of poster placing	Monday - Wednesday
Day of poster presentation	Monday

Poster number	Presenter	Title
1	Kenneth Aase	How accurate is genomic prediction across wild populations?
3	Leen Nanchira Abraham	Genetic and epigenetic variants underpinning within-species transcriptional polymorphism in a major fungal pathogen
5	Samir Alarmed	Unlocking barley root genetics using machine learning and drone-measured vegetation indexes
7	Hassan Aliloo	Multi-breed genome-wide association for birth weight in beef cattle
9	Oussama Antar	Development of an inter-specific MAGIC population combining Solanum lycopersicum var. cerasiforme and S. pimpinellifolium genomes for dissecting quantitative traits
11	Salvador Gezan	ASRgwas: An R package to perform complex Genome-Wide Association Studies (GWAS)
13	Bjarne Nielsen	Genetics of wheat cultivar mixtures
15	Young Jun Park	Genome-wide interaction study between PM10 and thyroid stimulating hormone among Koreans reveals functional polymorphisms
17	Gina Henderson	The genomic basis and evolution of immune trait variation in Soay sheep
19	Jan Willem Koten	Familywise heritability estimates of the brain
21	Rafaela Prado Graciano	Exploring the Application of Phenomic Selection in Corn Breeding
23	Julia Höglund	Characterisation and quantification of deleterious genetic variants in non-model organisms: from present to extinct species
25	Alexa Lupi	Mapping the Relative Accuracy of Cross-Ancestry Prediction
27	Daniel Tolhurst	Disentangling non-crossover and crossover genotype by environment interaction for selection
29	Sverre Ofstad	Nature meets schooling: Why boys fall behind in GPA despite equal genetic potential
31	Marianne Laurençon	Early vigor in rapeseed depends of the germplasm type and the genetic determinants were partly selected during growth habit selection.
33	Ida Hansson	Towards the optimal approach to assess indirect genetic effects in dairy cattle
35	Mila Tost	Identification of polygenic selection for drought stress in European beech populations
37	Seema Yadav	Genomic mate-allocation strategies exploiting additive and non-additive genetic effects to maximise total clonal performance in sugarcane
39	Morgane Roth	Using non-additive effects in genome-wide association studies and genomic predictions to improve biotic stress tolerance in peach
41	Xiao Feng	Dual-trait genomic analysis in highly stratified populations using genome-wide association summary statistics
43	Antonio Reverter	On the relationship between genomic kinship and opposing homozygotes in a selected population of Australian Angus cattle
45	Ekaterina Maksimova	Estimating the genetic basis of quantitative traits across populations
47	Sadoun Sarah Ben	Genomic predictions and Genome-wide association studies on DNA pools to characterize traditional maize landraces and identify genomic regions associated with agronomic traits and environmental adaptation
49	Juan Li	Genetic variation in a polygenic trait under stabilizing selection and population structure
51	Huicong Zhang	Updated CattleGTEx resource for dissecting complex traits in cattle
53	Anne Jansen	CrossOver: The potential of selection on crossovers in animal breeding
55	Dörte Wittenburg	A resource of bovine genetic maps and a use case of selection signatures
57	Christian Werner	Reviving the desired gains index: an optimal solution for parent selection in public plant breeding programs
59	Zhengcao Li	Expression and alternative splicing QTL mapping reveals novel loci and genes associated with downy mildew resistance in spinach
61	Prerna Goel	The interplay of temperature and laboratory adaptation: A case study using reduced genetic variation
63	Agnes Holstad	Comparing genetic and phenotypic variance matrices
65	Erin Smith	Random regression modelling of fibre diameter measured along the wool staple for use as a potential indicator of resilience in sheep.
67	Renzo Bonifazi	Within and across population genomic predictions incorporating functional genomic annotations
69	Luboš Vostrý	Inbreeding depression and purging inference considering the effects of autosomal and sex-specific inheritance on milk production in dairy cows
71	Valentin Hivert	Unveiling the challenges: the difficulty in making reliable inferences of between-population mean genetic differences from GWAS
73	Aimee Schulz	Across-species association mapping to identify the genetics of perenniality
75	Yuna Zhang	Polygenic adaptation to gradually changing environments
77	Qiongyu He	Effect of inbreeding on height in Brown Swiss cattle
79	Guoliang Li	One-dimensional association mapping scan for heterotic QTL leveraging whole-genome resequencing data
81	Erin Smith	Random regression modelling of fibre diameter measured along the wool staple for use as a potential indicator of resilience in sheep.
83	Song Xu	Assembly of a chromosome-scale and haplotype-resolved sugarcane reference genome
85	Zohar Meir	Understanding the formation of stem-cell niches in plants by massively parallel analysis of single-organisms
87	Merete Sarup Pernille	Assessing myBaits target capture sequencing methodology using short read sequencing for variants detection in oat genomics and breeding
89	Changyi Xiao	The genomic selection signatures of interacting environmental stressors
91	Sheng-Kai Hsu	The genetic basis of cold and drought adaptation in grasses
93	Enogieru Osatohanmwen Bright	Machine Learning Combined with Locus-Specific Degree of Dominance Transformation for Genomic Prediction in Hybrid Maize
95	Giovanny Eduardo Covarrubias-Pazaran	LME4BREEDING: Enabling Genetic Evaluation in the Era of Genomic Data.

Session 2

Day of poster placing	Monday - Wednesday
Day of poster presentation	Tuesday

Poster number	Presenter	Title
2	Katie Louise Abson	Predicting adaptive potential from genomic data and its implications for conservation
4	Zachary Aldiss	Exploring genetic variation for root architecture in global and Australian barley
6	Davinia Perdomo	Quantitative Analysis of Genetic Dominance in the Pura Raza Española Horse
8	Yafei Guo	The genetic architecture of climate adaptation unveiled by 1,628 wheat genomes
10	Sara Duarri-Redondo	Back to the wild: disentangling shared selection between natural and experimentally evolved populations
12	Gábor Mészáros	Genomic regions influencing milking speed in Fleckvieh cattle
14	Andres Legarra	ABSOLUTE MEASURES OF GENETICS SIMILARITY OF POPULATIONS USING SNP MARKERS AND CONSIDERING COMPLEX PEDIGREES
16	Davorka Gulisija	The Evolutionary Basis of Sustained Rapid Phenotypic Evolution of Polygenic Traits
18	Natalia Soledad Forneris	Genomic prediction of individual inbreeding levels for the management of genetic diversity in populations with small effective size
20	Hector Marina	Understanding the optimal genotyping strategy to assess the indirect genetic effect in dairy cattle
22	Kahsa Tadel Gebre	No strong heterosis effects for milk production and calving interval of crosses of local Ethiopian and international dairy breeds kept under on-farm conditions
24	Chin-San Liu	A Pilot Study: Postprandial Insulin|IGF1 Spectrum in SCA3
26	Laura Morales	Genome-wide association study on wood quality traits in two Norway spruce populations
28	Claudia Ramirez-Lanzas	Phenotypic patterns of polygenic adaptation in large and small populations of Drosophila
30	Houcheng Li	Understanding cell-type specific genetic regulation of gene expression in cattle
32	Bertrand Servin	Sex differences in recombination rates are associated with hotspot usage in sheep
34	Richard Hillis	Mapping immune cell gene networks with single cell data for human and animal health
36	Jack Windig	Quantitative genetic approaches for the management of highly inbred dog populations with multiple genetic diseases
38	Sang Le	GENOME-WIDE ASSOCIATION STUDY AND ITS IMPACT ON THE ACCURACY OF GENOMIC PREDICTION FOR LIVE BODY WEIGHTS IN AUSTRALIAN MERINO SHEEP
40	Nantapong Kamprasert	Effect of Using Preselected Markers from Imputed Whole-Genome Sequence in Genomic Prediction in Angus cattle
42	Ulises Bercovich	Measuring linkage disequilibrium and improvement of pruning and clumping in structured populations.
44	Isidore Houaga	The potential of spatial modelling for quantitative genetic analysis of Tanzanian smallholder crossbred dairy cattle
46	Vidyadheesh Kelkar	Identifying the importance of non-additive effects with experimental evolution study.
48	Javier Fernández-Gonzalez	The Role of Sparse Designs and Advanced Modeling in Improving Genomic Selection for Plant Breeding
50	Lacalle Evangelina López de Maturana	Multimodal machine learning-based integration of genomics, radiomics and pathomics prognostic scores improves pancreatic ductal adenocarcinoma clinical-based patient stratification
52	Ino Curik	Modelling the influence of mitochondrial inheritance on quantitative traits: pleiotropic effects of haplotypes on milk production in dairy cows
54	Yue Yao	Estimating the genomic landscape of human complex traits using summary association statistics
56	Lucas Ayres	A single-locus quantitative genetic model to include DNA methylation information
58	Xiaochun Sun	Integrated GS: Prescriptive Breeding to Guide Transgenic Platform Transition
60	Yunlong Liu	Massively parallel reporter assays enable the identification of genes associated with complex traits
62	Marijuan Ariadna Villanueva	MOC-BayesW: Multi-Omics penalized Bayesian regression for time-to-event phenotypes
64	Sang Le	Selection signature analyses identify genomic footprints in Lao native goats
66	Caelinn James	Integrating deep phenotyping and whole-genome sequencing to decipher genetic basis of feed efficiency in dairy cattle
68	Joanna Szyda	Toward a biological interpretation of the effect of probiotic supplementation expressed by the microbiome composition of the fish gut microbiome
70	Azadeh Hassanpour	Optimizing breeding program designs through evolutionary algorithm
72	Po-Ya Wu	Optimal implementation of genomic selection in potato breeding programs
74	Masoud Shirali	Northern Ireland Farm Animal Biobank (N.I.FAB): The Foundation for Precision Animal Breeding in Sustainable Production
76	Zulma Vitezica	Predicting hidden individual inbreeding depression load from Mendelian decomposition of inbreeding in dairy sheep
78	Zhiliang Zhang	Identifying the full disease-resistance gene repertoire using pooled HiFi sequencing
80	Wentao Jiang	Characterization of genetic regulatory variants associated with energy balance in Holstein dairy cows via RNA-Seq
82	Youngjune Bhak	Genetic relationship between number of morbidities and life expectancy.
84	Huiming Liu	Evaluating Methods for Tracing Breed Origin Alleles in Crossbred Dairy Cattle
86	Kiat Edwin Ong Jun	Utilizing machine learning in genomic selection of Holstein dairy cattle's gross feed efficiency
88	Siraj El Masri	Genetic and adaptive architecture of body size variation under truncating selection in Drosophila
90	Nicholas Santantonio	Lessons learned from modernizing a breeding program with high-dimensional genomics and high-throughput phenotyping
92	Filip Thor	Contrastive Learning for Dimensionality Reduction of SNP Genotype Data
94	Cornelius Nel	Additive and dominance genetic variance are significant predictors of early survival in artificially reared ostriches

Session 3

Day of poster placing	Wednesday - Friday
Day of poster presentation	Thursday

Poster number	Presenter	Title
1	Masri Siraj El	Genetic and adaptive architecture of body size variation under truncating selection in Drosophila
3	Michalina Jakimowicz	Influence of Effective Microorganism Supplementation on the Water and on Gut Microbiome of Common Carp
5	Olivia Katz	Investigating the potential for selecting pigs on recombination rate
7	Zefreh Masoud Ghaderi	Validation and selection on resilience indicators derived from longitudinal performance measurements
9	Jakub Bajzik	Genome-wide analysis of multi-ancestry summary statistics using vector approximate message passing
11	Xiaotong Wang	T-COJO: A trans-ancestry conditional and joint analysis approach
13	Ana-Marija Križanac	A large meta-analysis of health traits in hundreds of thousands of German Holstein cows
15	Kira Villiers	Testing theories of genetic variation in complex traits using machine learning techniques
17	Christina Rochus	Genomic estimation of dominance variance and inbreeding depression in a local sheep breed
19	Xiqiong Wang	Exploiting the Multi-omics data to decipher function genes of the egg quality traits in chickens
21	Ines Rebollo	Heterogeneous genetic covariances in genomewide prediction in maize
23	Arne Bielke	Genomic Diversity, Ancestry and Inbreeding in New Zealand Feral Kaimanawa Horses
25	Elise Tourrette	Joint distribution of adaptive and quantitative effects of QTLs affecting a complex trait under selection
27	David Hobby	Integrating Dynamic Mode Decomposition with Genomic Prediction to predict plant development
29	Ettore Riccucci	Integration of genetic information from eQTL mapping for gene regulatory network reconstruction
31	Nhu Tran	The contribution of molecular variation to genetic variance components and plant fitness in Arabidopsis lyrata populations
33	Lillith Zijmers	What determines levels of adaptive genetic diversity?
35	Adrián Gaite	Molecular dissection of genetic gisk partitioning strategies to explore inflammatory bowel disease (IBD) patient heterogeneity
37	Gonzalo Casorzo	Integrating multi-omics and interpretable artificial intelligence models for flavor-assisted selection in blueberry
39	Carl Nettelblad	Imputato: fast and accurate reference-based imputation of diploids and autopolyploids based on separate haploid models
41	Himani Sachdeva	Pleiotropy and selection on multiple traits: connections with GWAS
43	Xiaoning Zhu	Deciphering the genetic mechanisms of complex traits in chicken AIL populations using multi-omics data
45	Abdulraheem Musa	Optimizing Multi-Trait Improvements through Strategic Parental Selection in Genomic Breeding
47	Jingyang Tong	Advancing genetic improvement and stability of stripe rust resistance in Australia and Ethiopia with the Vavilov wheat collection and haplotype-based selections
49	Clément Bienvenu	Exploring the effects of the training set properties on Phenomic selection's performance: a case study on a large sorghum BCNAM population
51	Ines Berro	Genomic Prediction for Grain and Panicle Architecture Image-based Phenotyping
53	Krzysztof Kotlarz	Rank aggregation-based feature selection for comprehensive multi-breed cattle classification
55	Ingrid David	Compsim, a Shiny app to build and compare similarity matrices
57	Joia Zhang	Leveraging a Transformer-Based Large Language Model on QSAR Molecular Datasets
59	Alejandro Domínguez-Rondón	Evaluating Genomic and Biocontrol Strategies for Managing Septoria Tritici Blotch in Wheat
61	Vasilis Raptis	Dissecting the genetic and proteomic risk factors for delirium
63	Yong Jiang	A comprehensive overview and benchmarking analysis of fast algorithms for genome-wide association studies
65	Tzayhri Osorio Gallardo	Genetic analysis of laying hen movement based on computer vision data
67	Lovepreet Singh	Comparison of imputation methods for projection of markers from low density to high density for genomic selection in soybean (Glycine max)
69	Evans Cheruiyot	Age-related changes in methylome networks are associated with key biological process driving human aging
71	Andreas Hoppe	Wrap it all up - Recent advances in Varroa resistance breeding for honeybees in the BeeBreed.eu family
73	Loic Thibaut	Saturated GWAS yields new functional annotation of the human genome
75	Lipeng Kang	Traversing the genome constraint: the role of regulatory plasticity in wheat adaptation
77	Jiayu Dong	Population genomics unravels the evolution of mutation burden in bread wheat and its relatives
79	Xiangyu Guo	Can metabolomic-genomic prediction improve accuracy of predicted breeding values in pigs?
81	Lea Hoerdemann	Multivariate basis of drought resistance strategies
83	Azad Seyedeh Assal Tabatabaei	Discovery of Gene Dysregulated in OCD Patients Using Machine Learning
85	Tom Rohmer	Copula multi-trait animal model to improve the genetic selection
87	Juan Menor de Gaspar	Empirical Insights into Training Set Optimization for AAFC's Wheat Breeding Program
89	Gregor Wettstein	Identifying recessive resistances against powdery and downy mildew in the domesticated grapevine
91	Selma Aydemir	Correlation of PI3K p85|p110 alpha and Glucose Transport Proteins in Gestational Diabetic Placentas
93	Chao-Qiang Lai	Machine Learning Predictions of Obesity: Analysis of Gene–Diet Interactions Using Genome and Epigenome Data
95	Gabriela Mafra Fortuna	Estimating haplotype and mutation effects in the context of genome sequence via ancestral recombination graphs

Session 4

Day of poster placing   Wednesday - Friday

Day of poster presentation Friday

Poster number	Presenter	Title
2	James Cheverud	Genetic Mapping of Depot-specific QTLs for Obesity in Mice
4	Conghao Zhong	Exploiting multitissue molQTLs to decipher the molecular mechanisms of age-dependent genetic architectures for body weight changes in chickens
6	Maria del Rosario Garcia Gil	Landscape breeding
8	Leonel Stazione	Genetic basis of reproductive traits associated to thermal adaptation at heat environments using Drosophila melanogaster as a study model.
10	Bjarke Poulsen	Estimation of covariance matrices with completely missing information for one component
12	Thinh Tuan Chu	Model of genotypic effects accounting for multiple allelic QTL and different ploidy levels
14	Natasha Johansen	Prediction of non-neutral variants with temporal allele frequency information to improve genomic prediction models
16	Hannes Becher	Breeding simulations with efficient haplotype tracking – putting ARGs into AlphaSimR
18	Bernadett Hegedűs	Indirect genetic models including early life social effects for ear damage in pigs
20	Tom Rohmer	Copula multi-trait animal model to improve the genetic selection
22	Claudia Kasper	Parent-of-Origin Effects in Birth Weight in Large White Piglets: Disentangling Genomic Imprinting and Maternal Effects
24	Philippe Barre	Genomic selection in perennial forage species: the example of alfalfa
26	Christel Marie-Etancelin	Similarity matrix from microbiota data: impact of methods on 1-week stability
28	Alice Etourneau	Genomic landscape and genetic determinism of recombination in the domestic goat
30	Wei-Yun Lai	Evolutionary mining of cold tolerance alleles in maize for future farming sustainability
32	Julio Isidro Sánchez	There is no Solutions, only trade offs.
34	Guilherme Da Silva Pereira	Tree sequences efficiently store autotetraploid haplotype information from a multi-parental breeding population of potato
36	Fatima Shokor	GBLUP and Deep Learning Integration: A Novel Approach to Evaluating Nonlinearly Related Genetic Traits
38	Di Zhu	RNAseq profiling and molecular QTLs mapping for reproductive-related tissues across various egg-laying stages in chickens.
40	Ang Li	Benchmark and improvement of genetic cell type mapping
42	Camous Moslemi	Exploring techniques for variant effect prediction
44	Prerna Goel	The interplay of temperature and laboratory adaptation: A case study using reduced genetic variation
46	Can Yuan	Evaluation of heritability partitioning approaches in livestock populations
48	Sarunas Dzinkevivcius	Exploring the Relationship between Host Genome, Rumen Microbiome, and Methane Emission Production
50	Steffimol Rose Chacko Kaitholil	Unveiling the genetic landscape of sheep methane production: Insights from RNA-Sequencing and Network analysis.
52	Junya Watanabe	New mathematical tools for analyzing genetic constraints with G matrix
54	Ellen Risemberg	Genetic mapping and mediation analysis reveals immune phenotypes underlying genetic susceptibility to severe coronavirus disease in mice
56	Kengo Sakurai	Crossing Strategy Considering Multiple Traits Based on the Ability of Future Inbred Lines in Plant Breeding Programs
58	Johann Sölkner	Heritabilities and genetic correlations of feed intake patterns and their day-to-day variation in station tested growing pigs
60	Charlotte Brault	Leveraging environmental covariables in historical wheat disease trials to enhance genomic prediction accuracy
62	Will Valdar	Categorizing gene-by-treatment effects in molecular count phenotypes using Bayesian model selection
64	Silvia Shen	Investigating the heritability of atopic dermatitis
66	Hilde Schneemann	Hybrid fitness and the quantitative genetics of autopolyploids: A fitness landscape perspective
68	Tal Dahan-Meir	Adaptive seed-size variation in Arabidopsis thaliana
70	Madison Caballero	Identification of moderate effect size genes in autism spectrum disorder through a novel gene pairing approach
72	Claudia Kasper	Genetic parameters for genetic variance uniformity in Swiss pigs' birth weight
74	Fei Lu	Population genomics unravels the Holocene history of bread wheat and its relatives
76	Ting Li	Genetic atlas of human membrane protein complexes.
78	Bruno Perez	Dynamic inclusion of functional genome annotations to improve accuracy of genomic prediction in pigs
80	Cathrine Kiel Skovbjerg	Multi-population GWAS greatly Enhance Power of QTL Detection in a Small Population
82	Xiaowei Mao	The evolutionary landscape of complex traits in East Asia using ancient DNA
84	Zineb El Ghazzal	Genetic determinants of vegetative growth traits of lucerne used as living mulch for cereal production
86	Yuying Li	Consistent estimation of local heritability and genetic covariance using high-definition likelihood
88	David López Carbonell	Exploring Imprinting Phenomena: AlphaSimR's New Functionalities
90	Jon BANČIČ	A transition two-part breeding strategy shows advantage under multiple-trait selection and different genotype by environment interaction levels
92	Norman Munyengwa	Increased accuracy of genomic predictions for fruit quality traits and tree vigour in mango (Mangifera indica. L) using preselected variants from genome-wide association studies (GWAS) with whole-genome sequence (WGS) data.
94	Nan Zhang	XWAS using multi-generational data from crossbred Bos indicus-Bos taurus cattle