Single and multi-breed ssGBLUP using preselected variants from whole-genome sequence data in pigs

Sungbong Jang[1], R. Ros-Freixedes[2,3], J. Hickey[3], C.Y. Chen[4], W.O. Herring[4], I. Misztal[1], D. Lourenco[1]

[1]University of Georgia, USA
[2]Universitat de Lleida, Spain
[3]University of Edinburgh, Scotland
[4]Genus PIC, USA

8/25/2022
OP18-3

Animal Breeding and Genetics Group
College of Agricultural & Environmental Sciences
UNIVERSITY OF GEORGIA

Motivation

- Genomic evaluation in farm animals is performed with SNP chip data
  - Number of SNP ≈ 50k

- Number of QTL
  - Cattle: 192k for 701 traits
  - Pig: 35k for 716 traits

https://www.animalgenome.org/cgi-bin/QTLdb/index

- Whole-genome
  - 20k ~ 25k genes
  - 30M ~ 40M SNP

- Can 50k SNP include all information about genes and QTL?

Motivation

- WGS data
  - All genomic information
  - Becoming cheaper

In Humans: $100 (UG 100)

www.ultimagenomics.com

- Should we use all SNP?
  - Genome has limited dimensionality
  - SNP within segments are likely inherited together due to strong LD
  - Redundant
  - Providing same information

Motivation

- Small to NO benefit with WGS in cattle

VanRaden et al., 2017
Fragomeni et al., 2019
Moghaddar et al., 2019
de Las Heras-Saldana et al., 2020
Lopez et al., 2021

- In pigs?
  - Only few studies

Zhang et al., 2018
Song et al., 2019

- Challenge
  - Small number of WGS pigs (< 300) and IWGS pigs (< 7k)
  - No to limited benefits were observed
  - Small effective population size (*Ne)* required large data to capture QTN

Jang et al., 2022

Objective

- Investigate the impact of using preselected variants from WGS for large-scale genomic predictions in single-breed and multi-breed scenarios

Data

- 3 terminal breeds
  - B1, B2, B3
  - MB (multi-breed)

- Traits
  - ADFI, ADG, BF
  - ADGX, BFX (recorded in crossbred animals)

Data

Breed	ADFI	ADG	BF	ADGX	BFX	Number of Animals in pedigree
B1	35k	0.36M	0.34M	150k	149k	1.13M
B2	40k	0.30M	0.30M	158k	156k	0.84M
B3	64k	0.94M	0.86M	299k	247k	3.14M
MB	140k	1.60M	1.50M	578k	525k	5.28M

Data

- Genotype
  - GGP-Porcine HD BeadChip (Chip1 – SBE)
  - Jointly imputed for MBE (Chip2 – MBE)
  - Chip2SB

- WGS and imputation
  - Imputation using AlphaPeel software
  - IWGS

Whalen et al., 2018
Ros-Freixedes et al., 2020

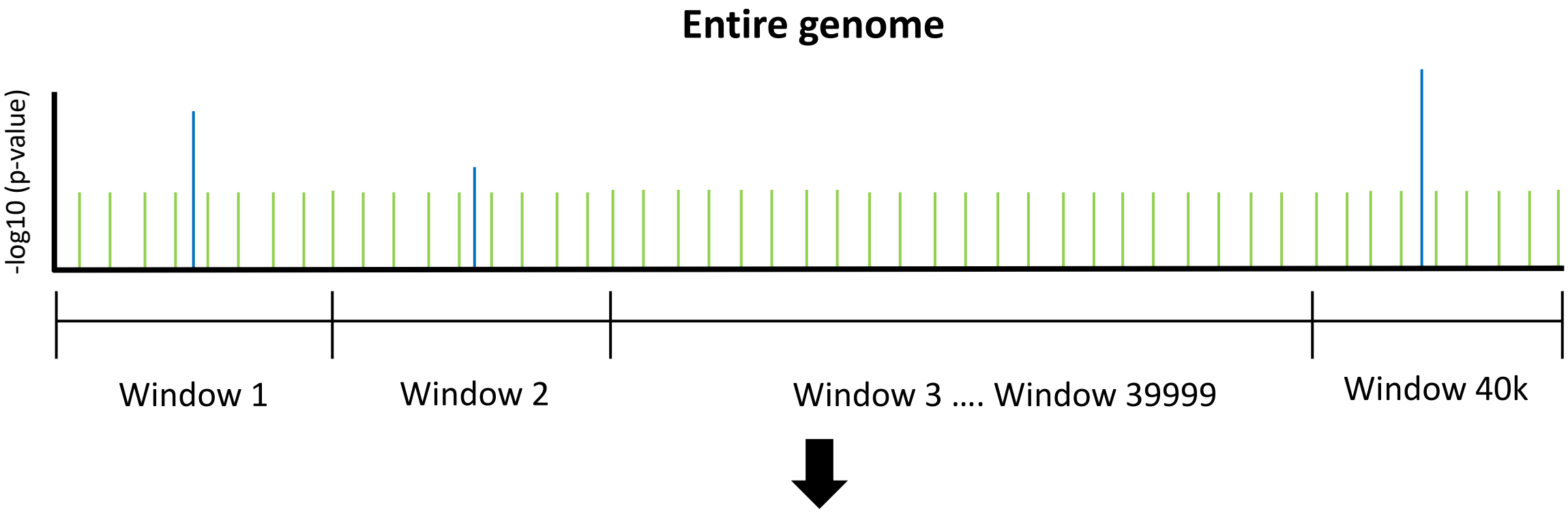
Data

Breed	N of genotyped individuals	N of SNP (Chip1)	N of sequenced individuals	N of imputed sequenced individuals
B1	60,467	35,786	731	60,474
B2	41,572	40,311	760	41,573
B3	104,644	43,032	1,856	104,661
MB	206,634	41,303	3,347	206,708

Data

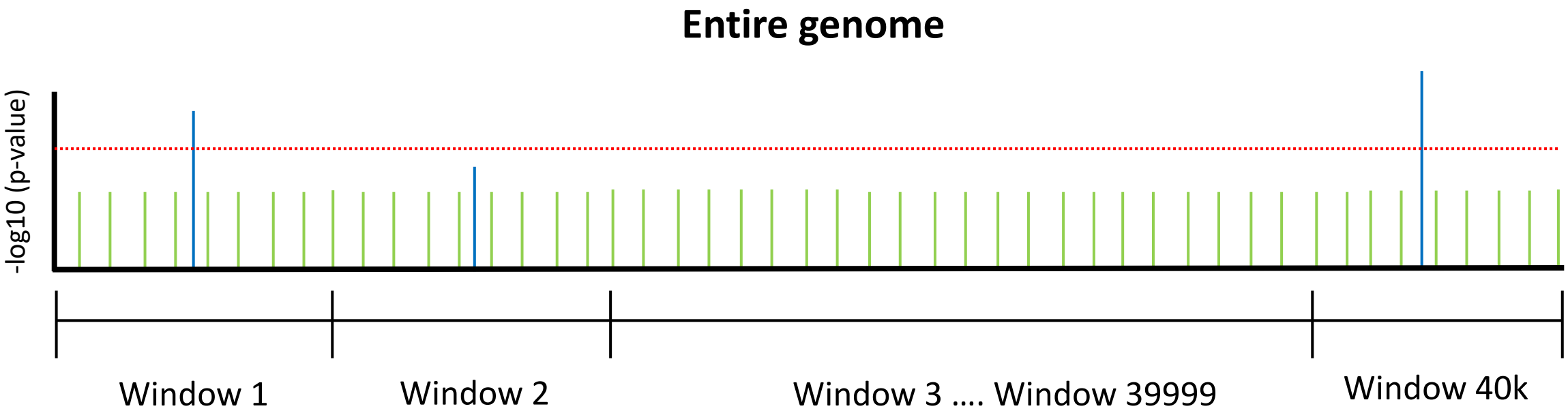
- Preselected genotype panels Ros-Freixedes et al., 2022
- GWAS: Fast-LMM software Lippert et al., 2011
  1. Top40k
     - SNP with lowest p-value in each 55-kb windows
  2. ChipPlusSign
     - Combining **TopSign** to regular SNP chip data
     - **TopSign**: Only significant ones

- **Top40k**



Extracting only 40k SNPs: Similar number as regular chip data (~40k)

- **ChipPlusSign**



Extracting only significant ones + SNP chip data

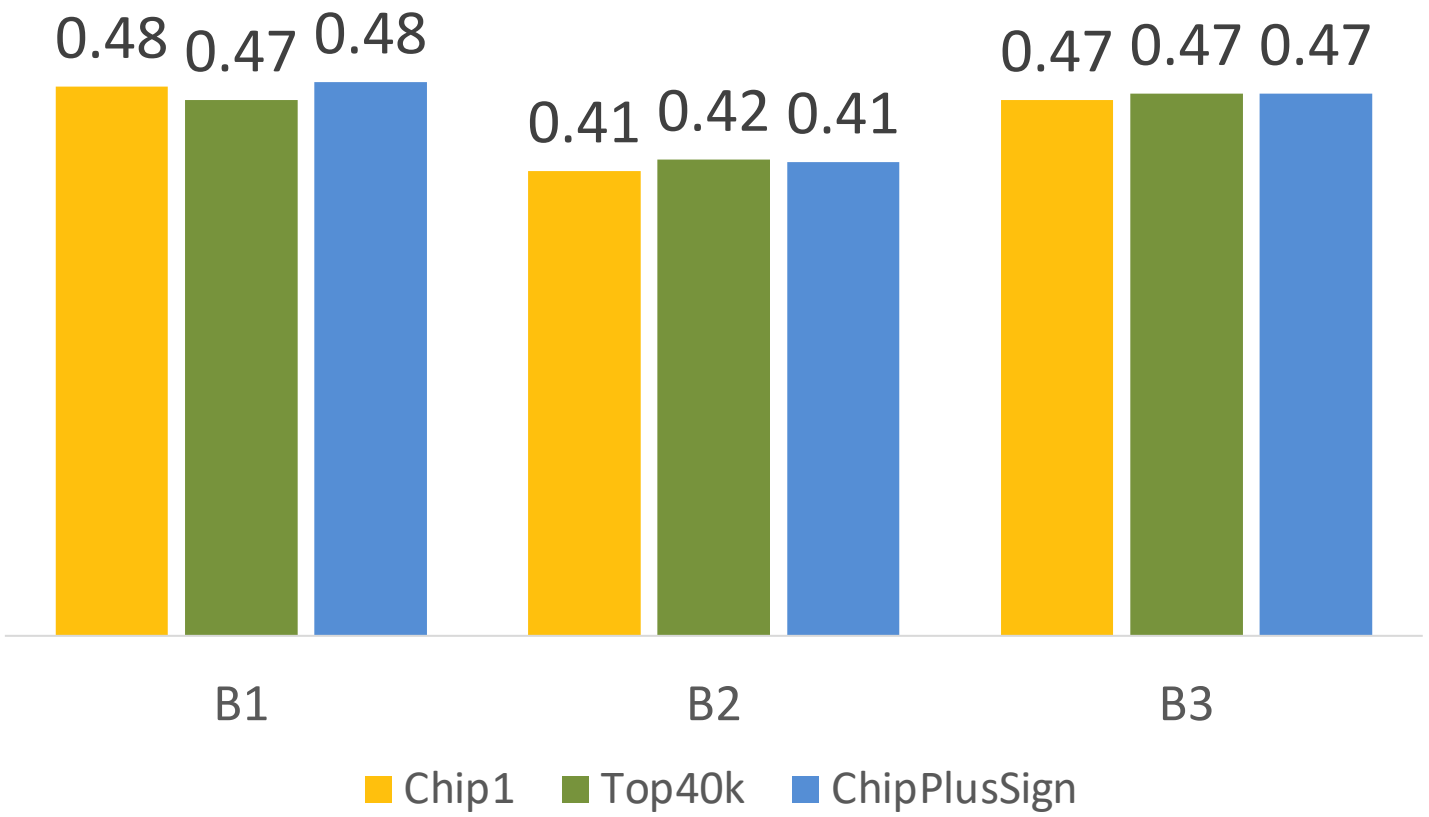
Genomic prediction

- ssGBLUP with APY
- UPG

- Validation
  - Prediction accuracy = cor(DEBV, GEBV)

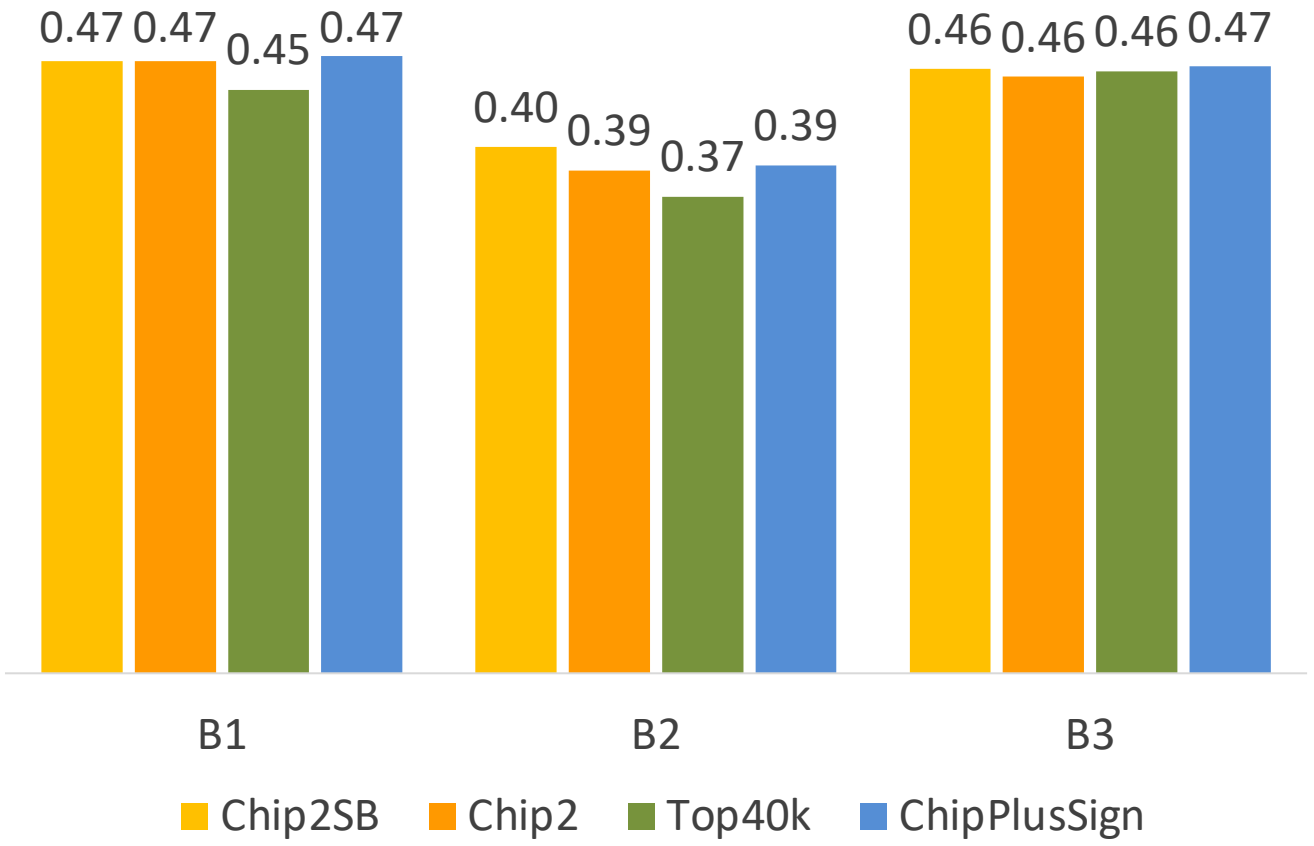
- Test sets
  - Entire litters from the last generation (youngest genotyped pigs)

Single-breed evaluation



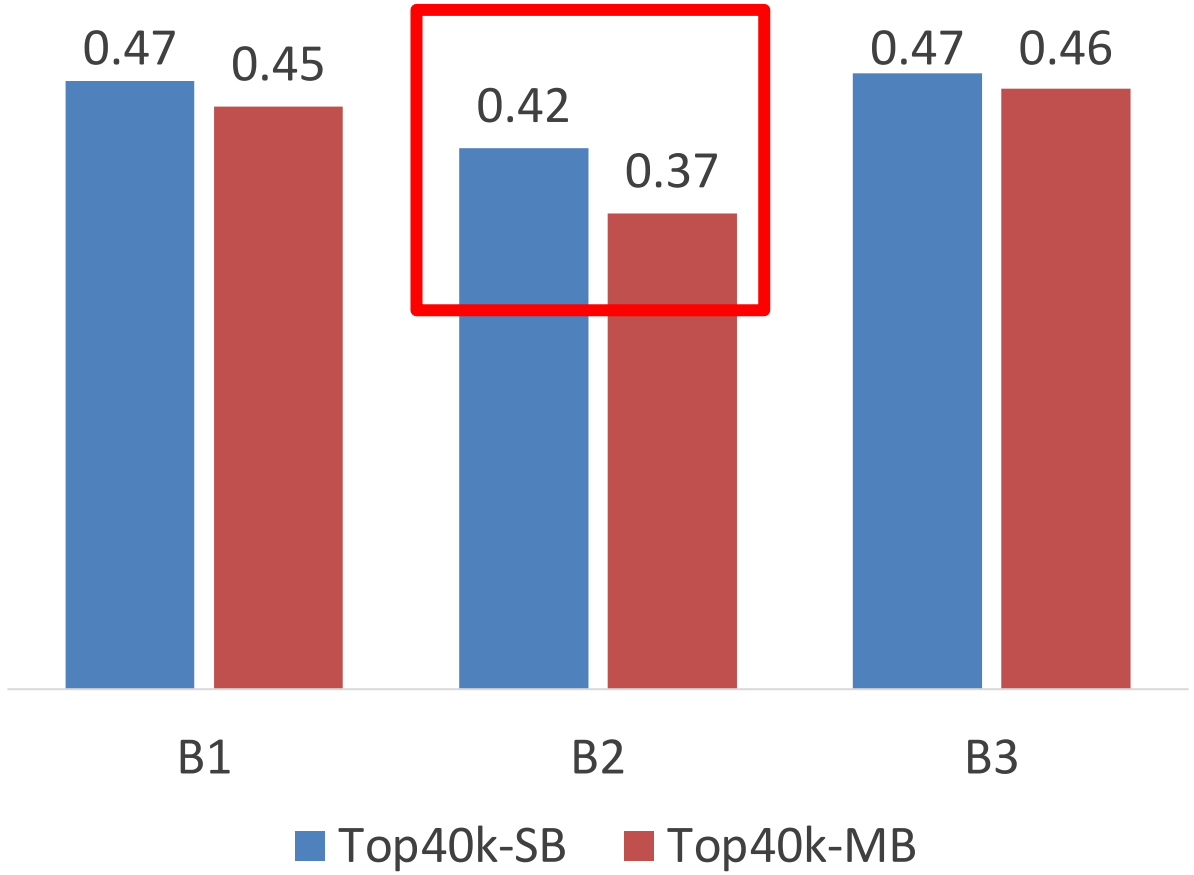
- Average acc
- Maximum gain
  - Compared to Chip1
  - ~0.03: Top40k
  - ~0.01: ChipPlusSign

Multi-breed evaluation



- Average acc
- No benefit in MBE
  - Chip2SB vs Chip2
- Maximum gain
  - ~0.01: Top40k
  - ~0.01: ChipPlusSign

Top40k (SB GWAS vs MB GWAS)



- Average acc
- Top40k-SB > Top40k-MB
- More decrease in B1 and B2

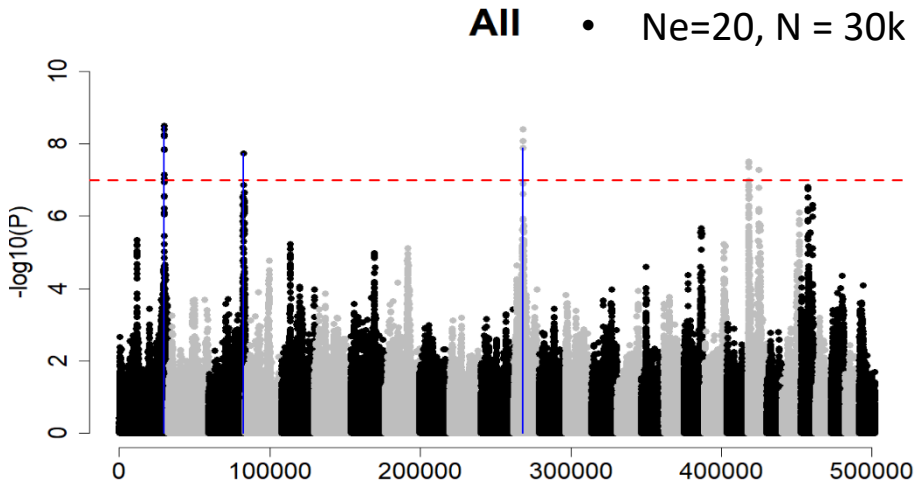
Why limited to no benefits with WGS?

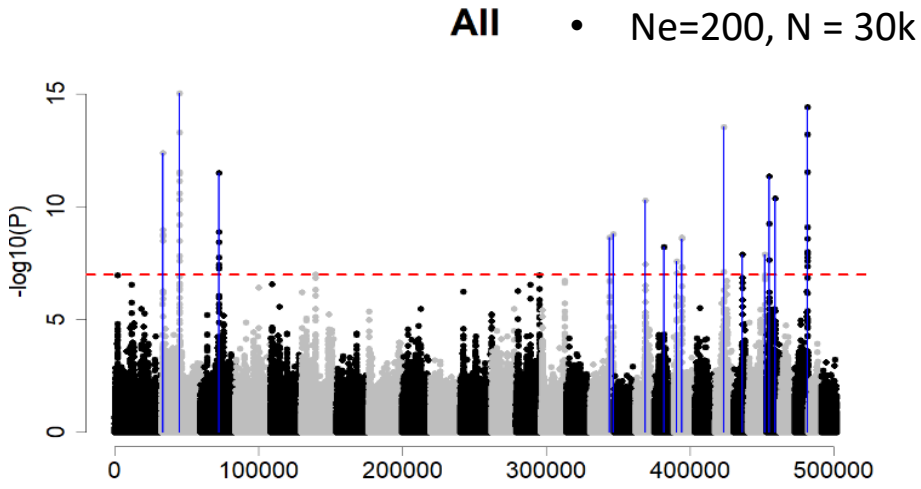
- Perfect prediction (acc≈1) is feasible Fragomeni et al., 2017
  - Real QTN
  - True effect as weight
  - Position in the genome

- *Ne*
  - Pigs and chickens have small Ne
  - Strong LD
  - Difficulty to pinpoint only causative variants

Why limited to no benefits with WGS?

- GWAS resolution
  - QTN
  - Relationships
  - Noise (small sample size, imputation, etc)





Jang et al., 2022

Why limited to no benefits with WGS?

- Genomic prediction with preselected variants + SNP chip — Jang et al., 2022
  - Limited gain in small *Ne* (~2%)
  - Larger gain in large *Ne* (~9%), still limited

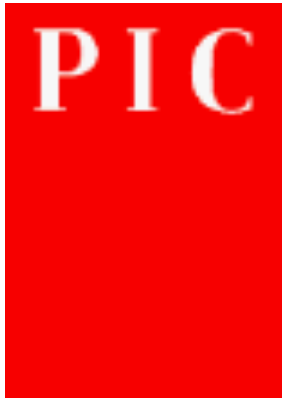
- Amount of information
  - Animals have a lot of information, high acc of GEBV
  - GEBV can be back-solved to SNP effects
  - $\hat{a} = \mathbf{DZ'G^{-1}}\hat{u}$
  - $pval_i = 2(1 - \Phi(\left|\frac{\hat{a}_i}{sd(\hat{a}_i)}\right|)$

Conclusions

1. Preselected genotype panels from WGS improved the prediction accuracy depending on the breed, trait, size of the genotyped population, and genotype panels, but limited

2. Multi-breed scenario did not benefit but showed similar accuracy to the single-breed scenario

Acknowledgments



Thank you! Questions?

jsbng@uga.edu