



UNIVERSITY OF  
**GEORGIA**

# Accuracies of multi-breed genomic evaluation using joint estimation of SNP effects

Y. Steyn, D.A.L. Lourenco, B. Fragomeni & I. Misztal

# Introduction

- Multi-breed evaluations a common challenge
- Shared SNP model/effects
- Joint G-matrix simple
- At a cost
- Too many breeds
- Jersey & Holstein

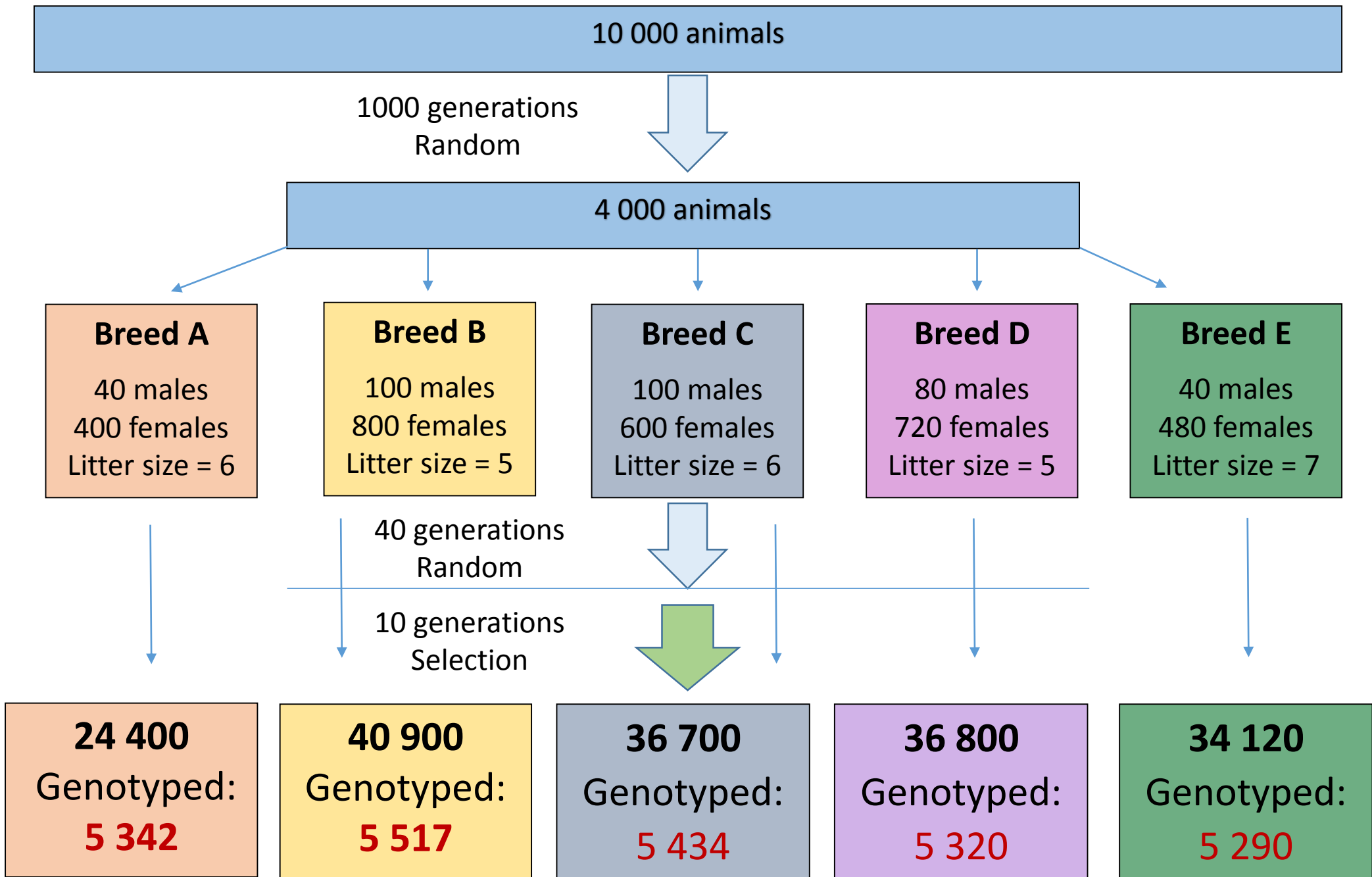
# Objective

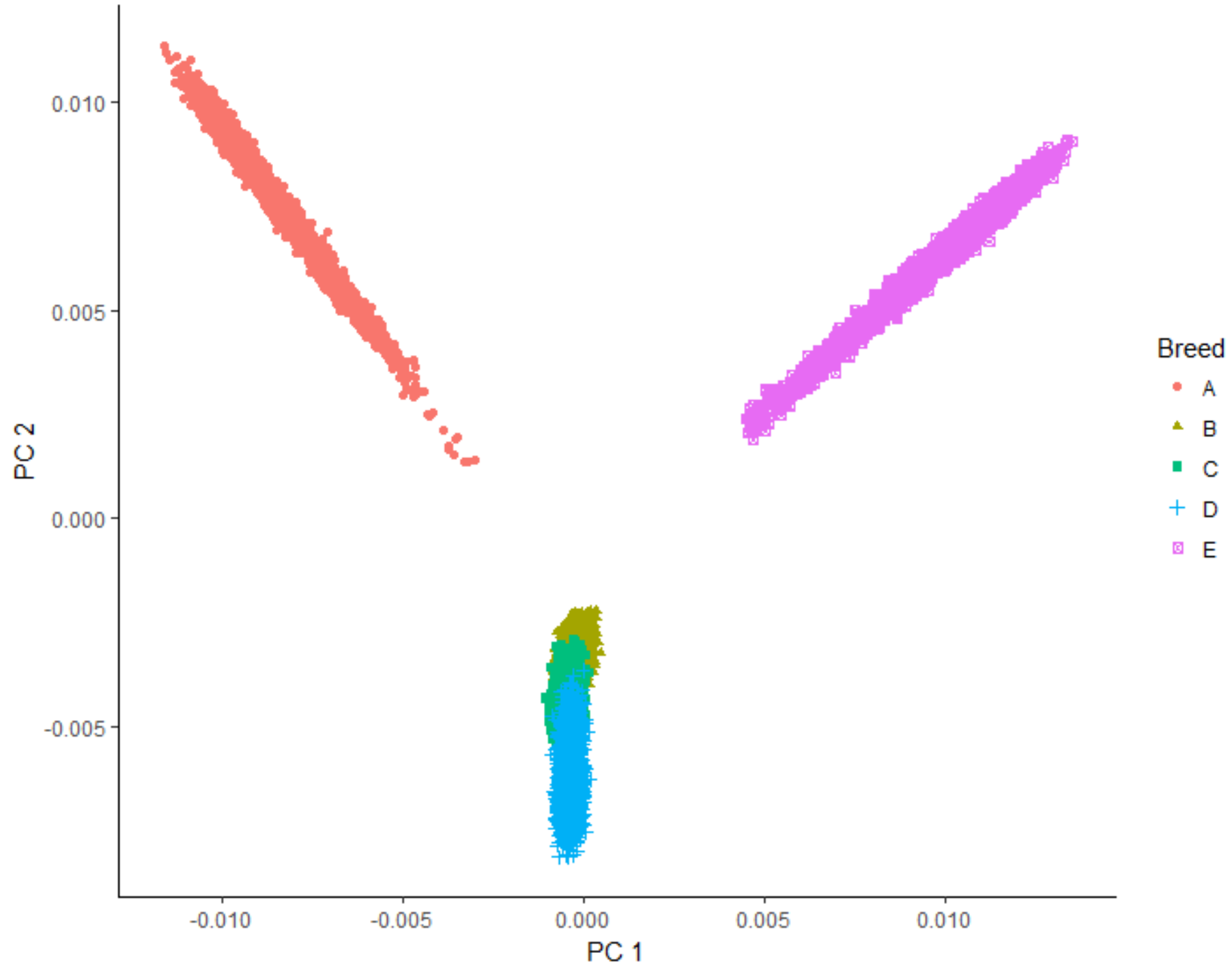
Investigate the accuracy of multi-breed evaluations (up to 5 breeds) by using different SNP densities and shared SNP effects

# Materials and Methods

## Simulation using QMSim16 (Sargolzaei & Shenkel, 2009)

- 5 Breeds
- Heritability = 0.30
- 18 chromosomes
- Specified chromosome length & markers per chromosome
- 400 potential QTL (gamma shape 0.4)
- Mutation rate =  $2.5 \times 10^{-5}$
- 40K SNPs

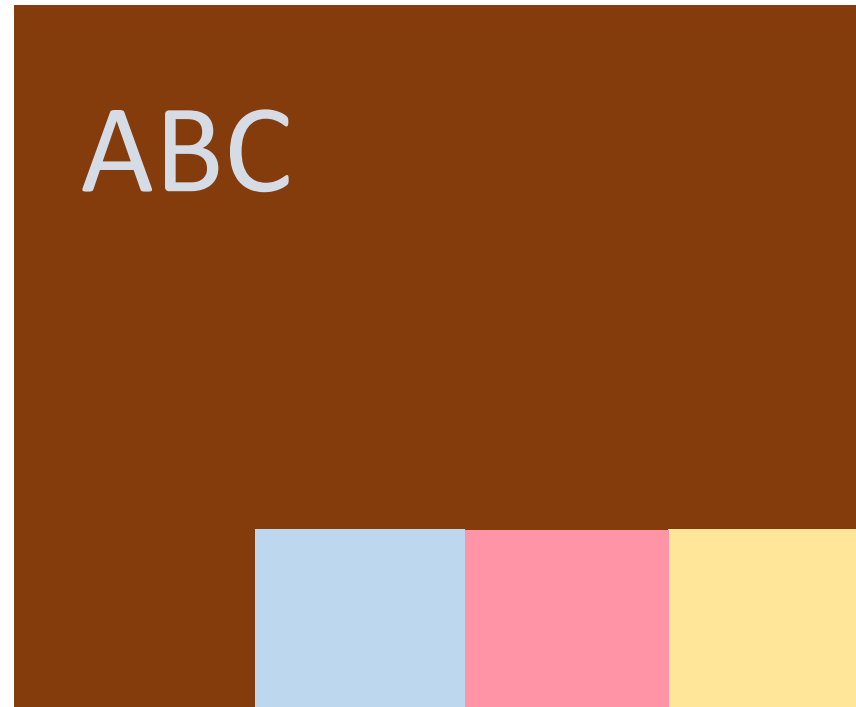
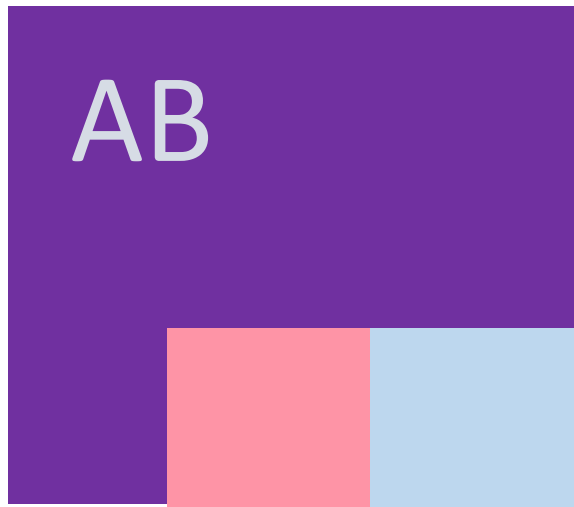
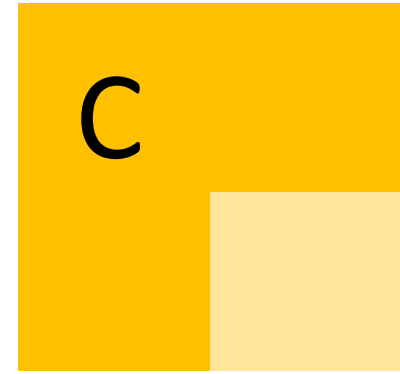
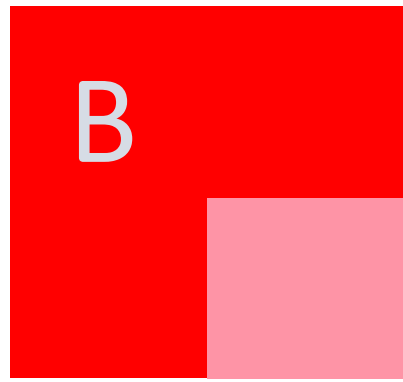




# Materials and Methods

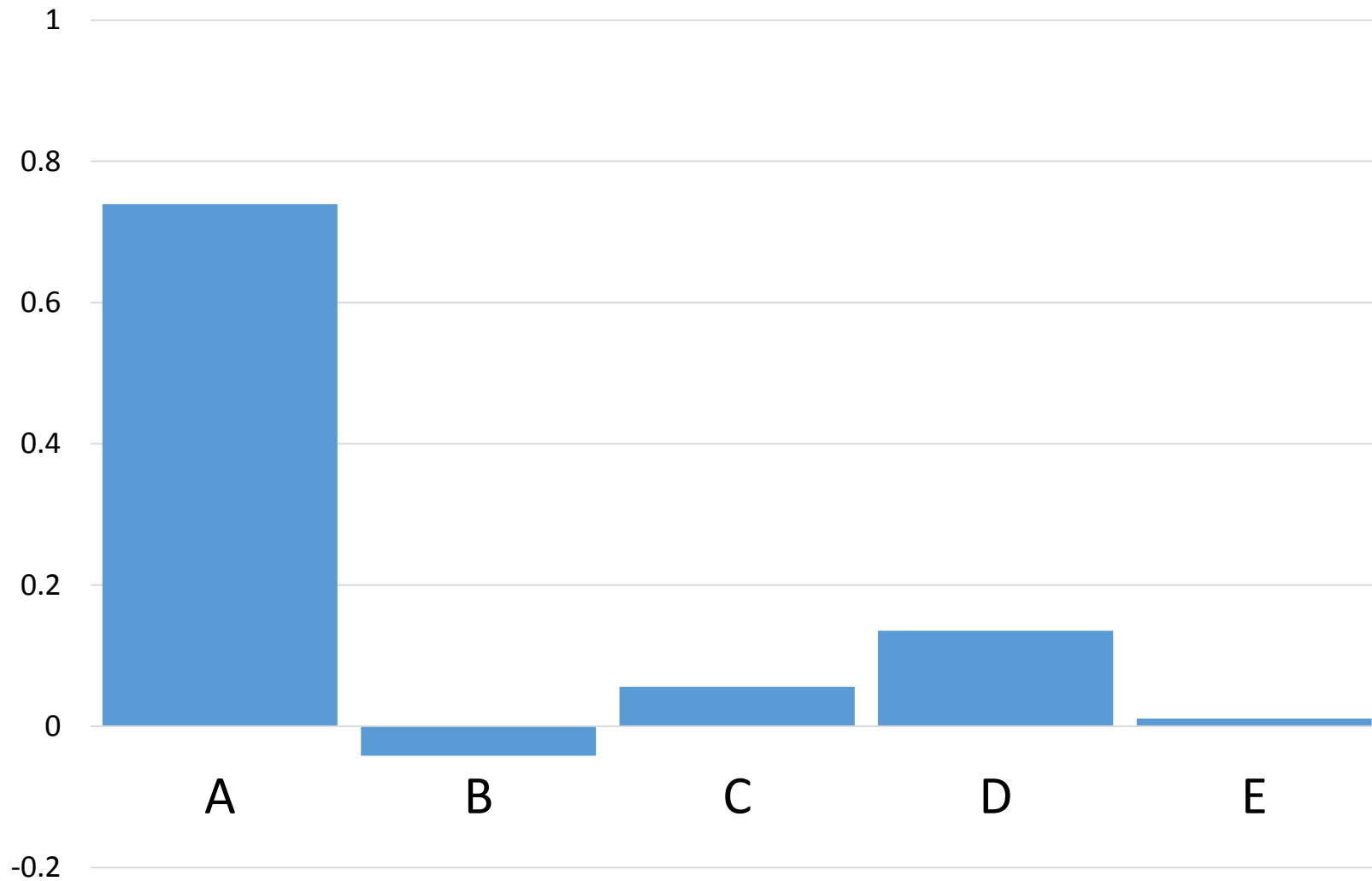
- Single-step GBLUP
- Validation on last generation
- $\text{Acc} = \text{cor}(\text{GEBV}, \text{TBV})$

# Validation

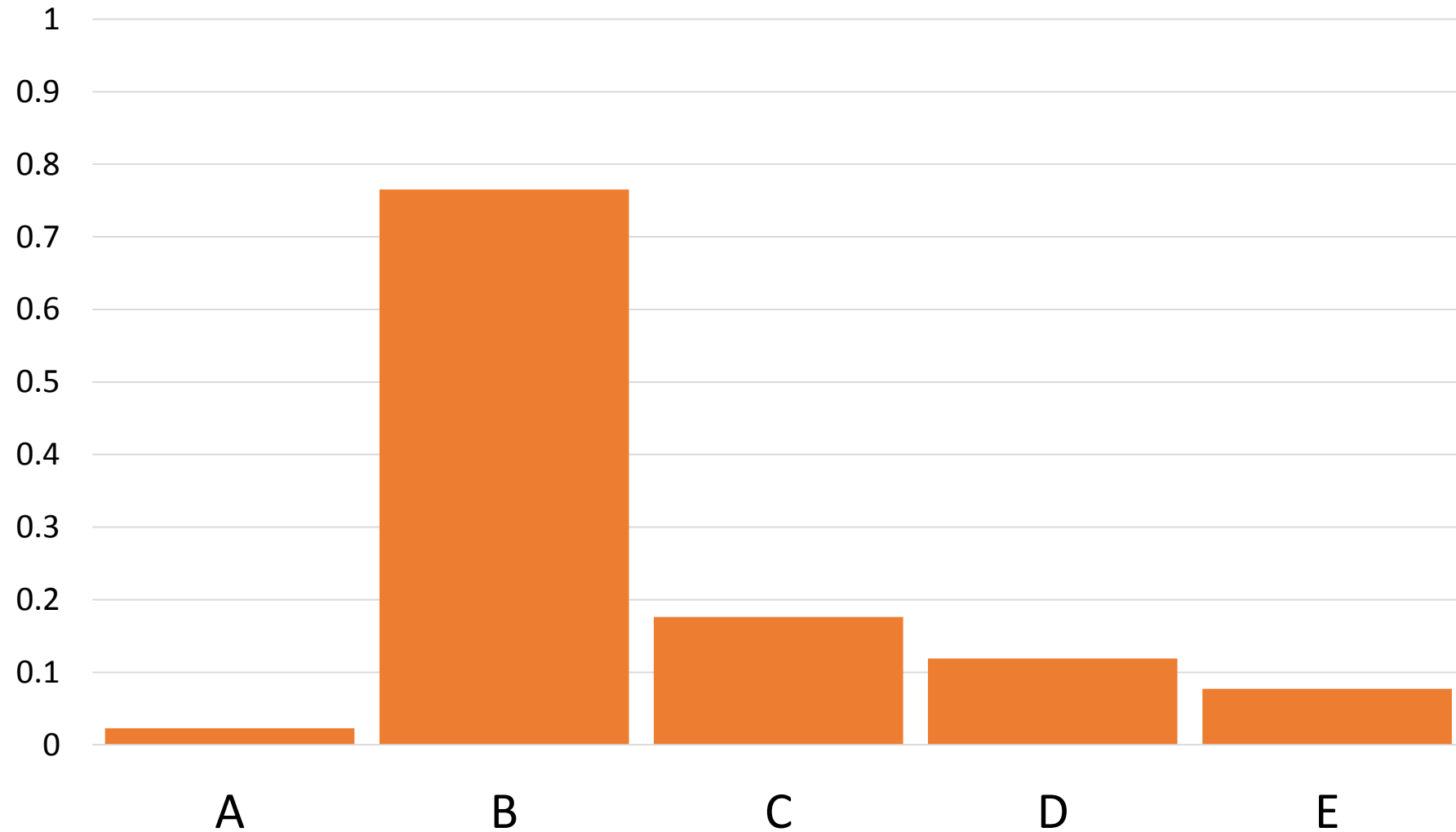




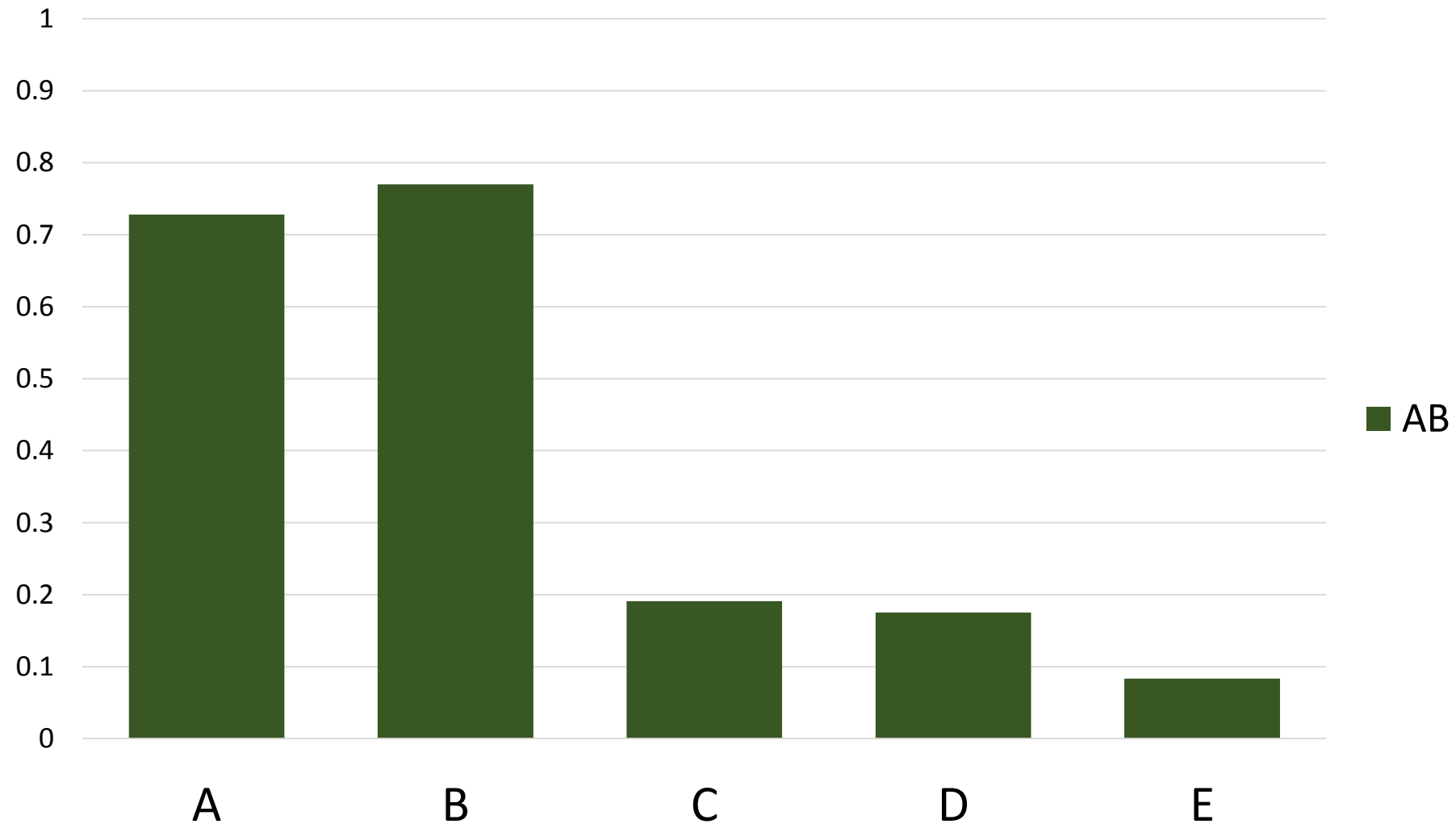
# Accuracy using phenotypes of Breed A- 40K



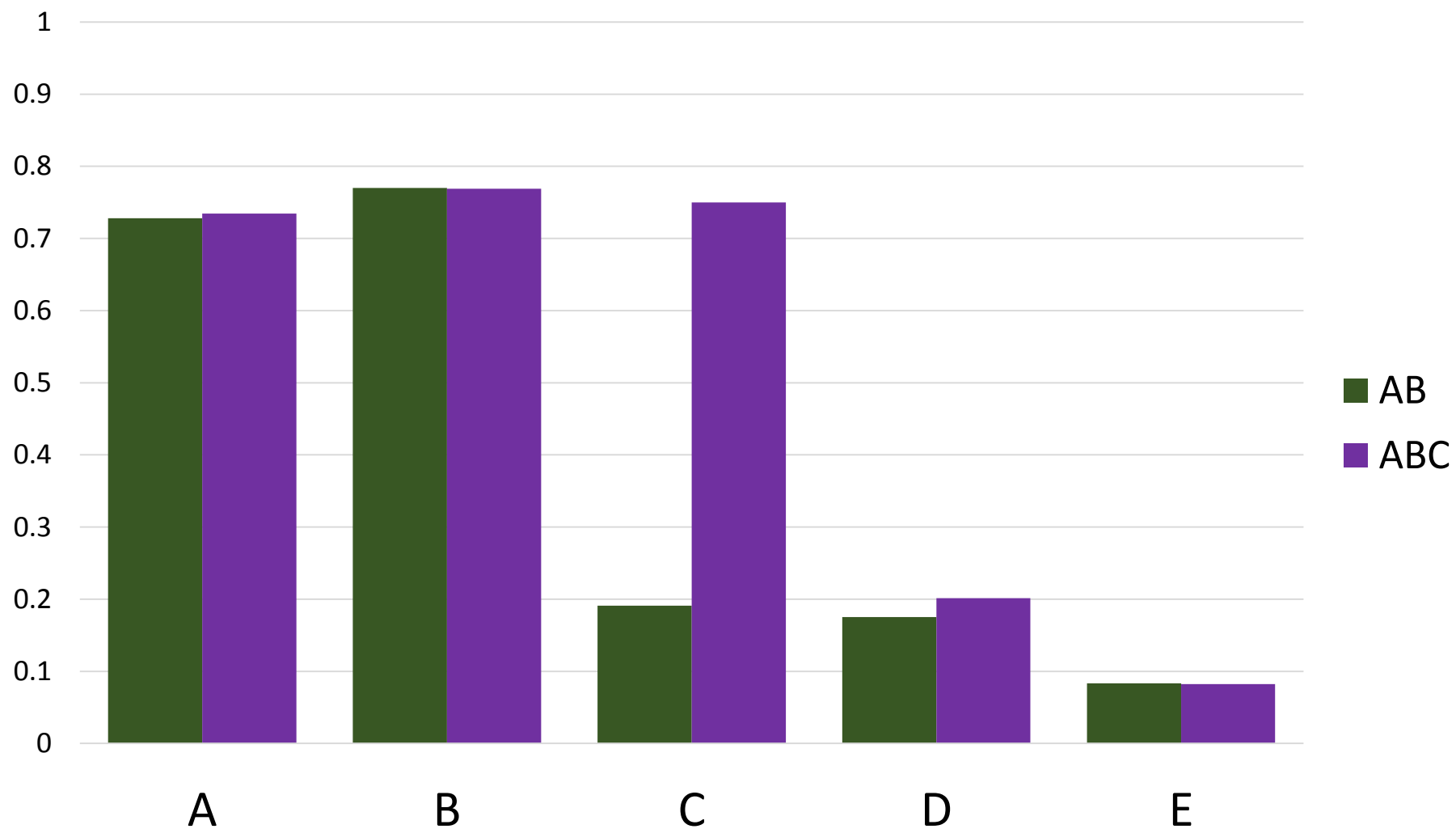
# Accuracy using phenotypes of Breed B- 40K



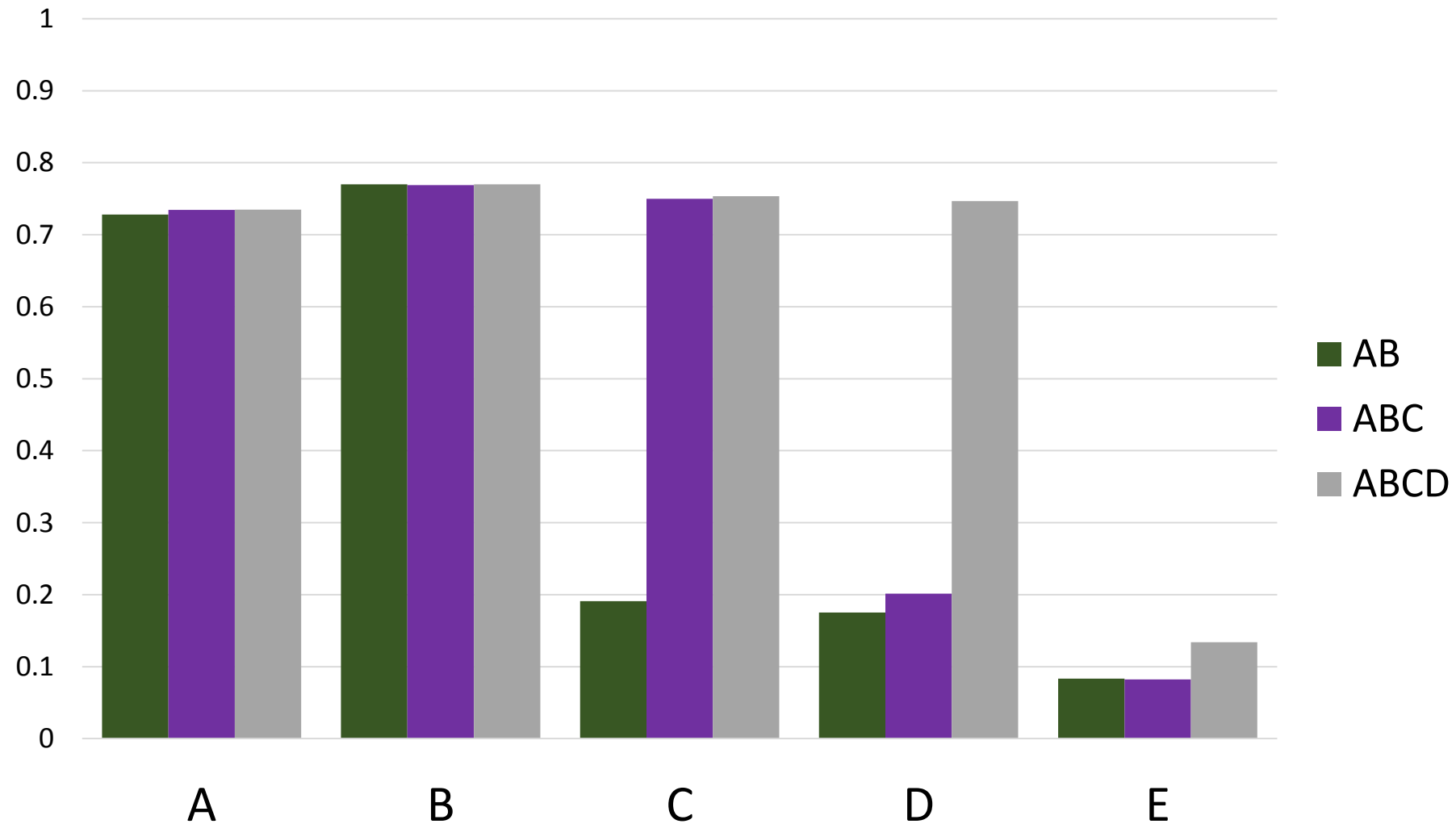
# Accuracy using phenotypes of AB - 40K



# Accuracy using phenotypes of ABC - 40K

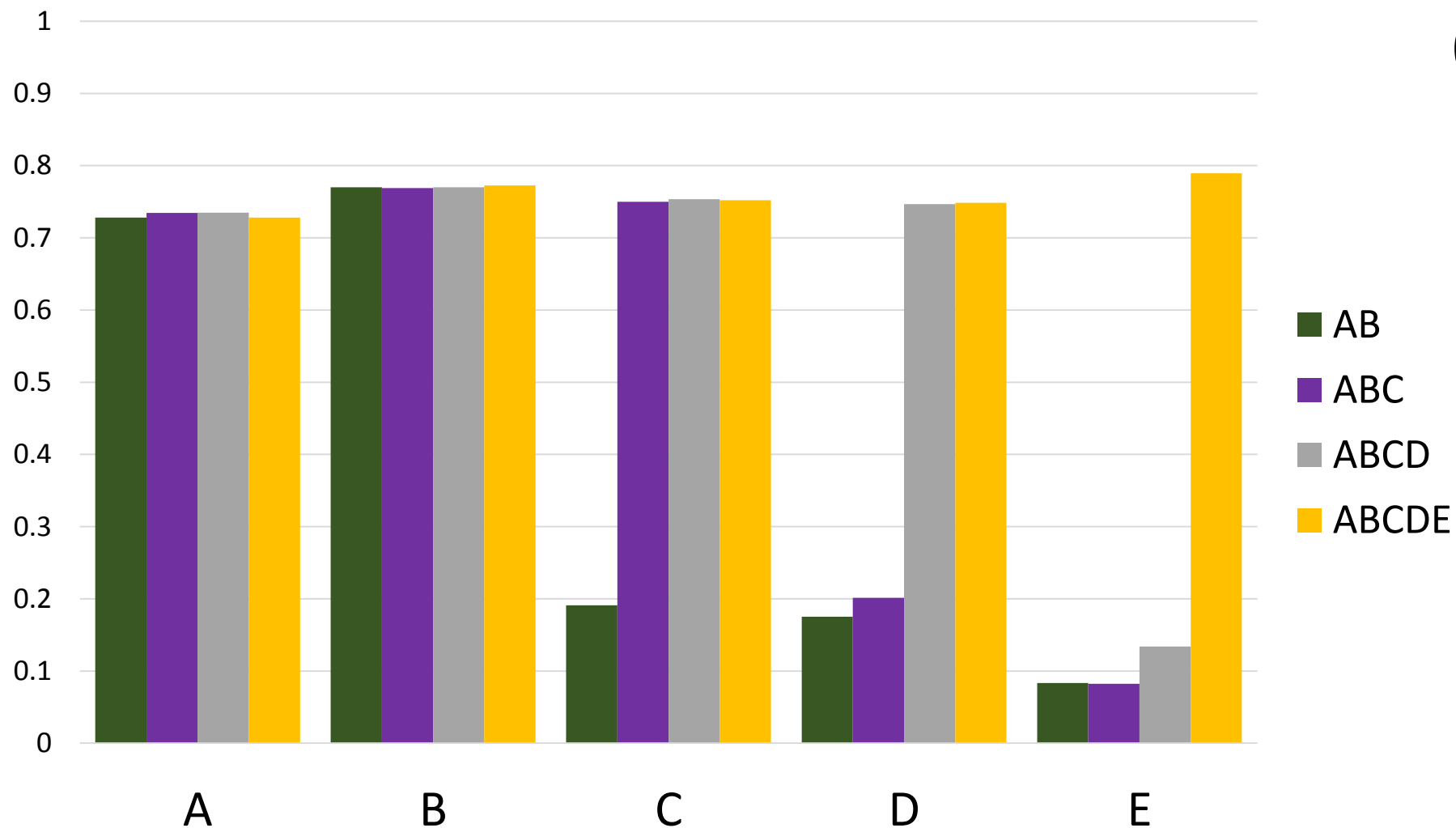


# Accuracy using phenotypes of ABCD - 40K



# Accuracy using phenotypes of ABCDE- 40K

**Average loss:  
0.004**



# Accuracy

$$M_e = 4N_eL$$

Daetwyler *et al.* (2010)

Independent chromosome  
segments

Chromosome length (Morgan)  
**18**

Effective population size

Generally corresponds  
to Eigenvalues  
explaining 98% variation  
Pocrnic *et al.* 2017

$$1/2\Delta F$$

Average = **41**

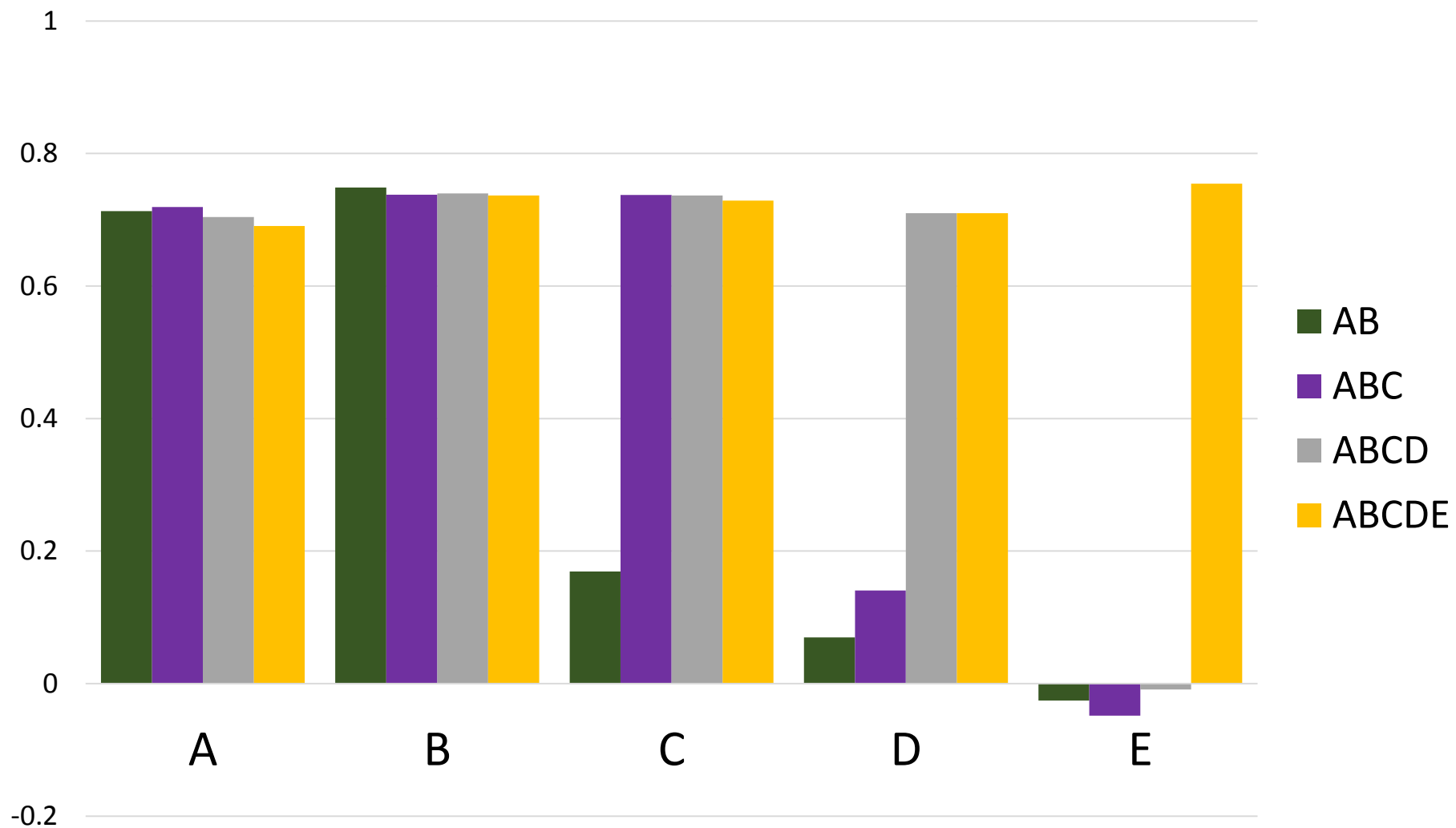
# Eigenvalues

<b>Animal</b>	<b>Ne</b>	<b>Eigen</b>
Angus	113	10.6K
Holstein	149	14K
Pig	48	4.1K
Study	41	<b>1.8K</b>



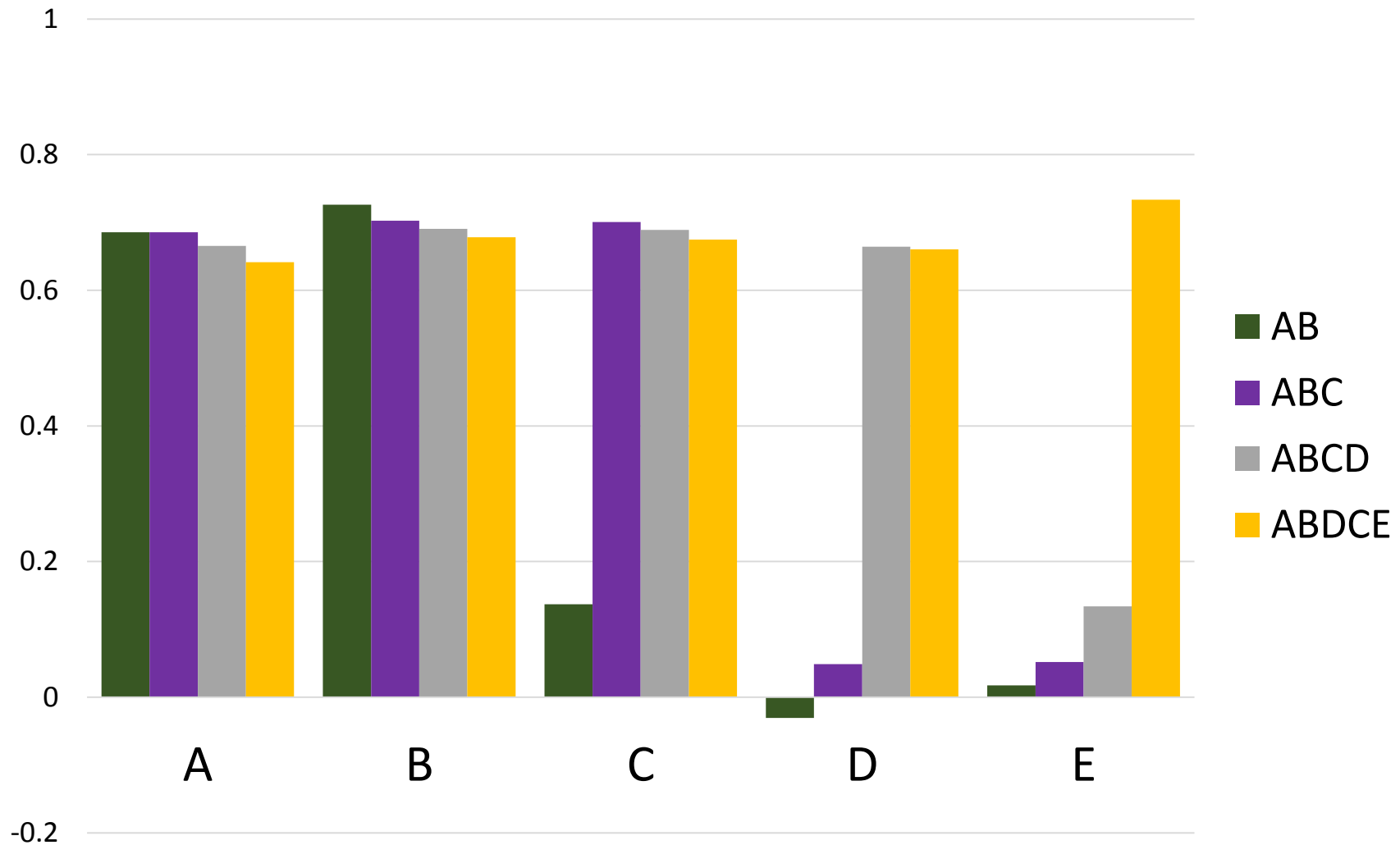
# Accuracy using phenotypes of ABCDE - 10K

**Average loss:  
0.03**

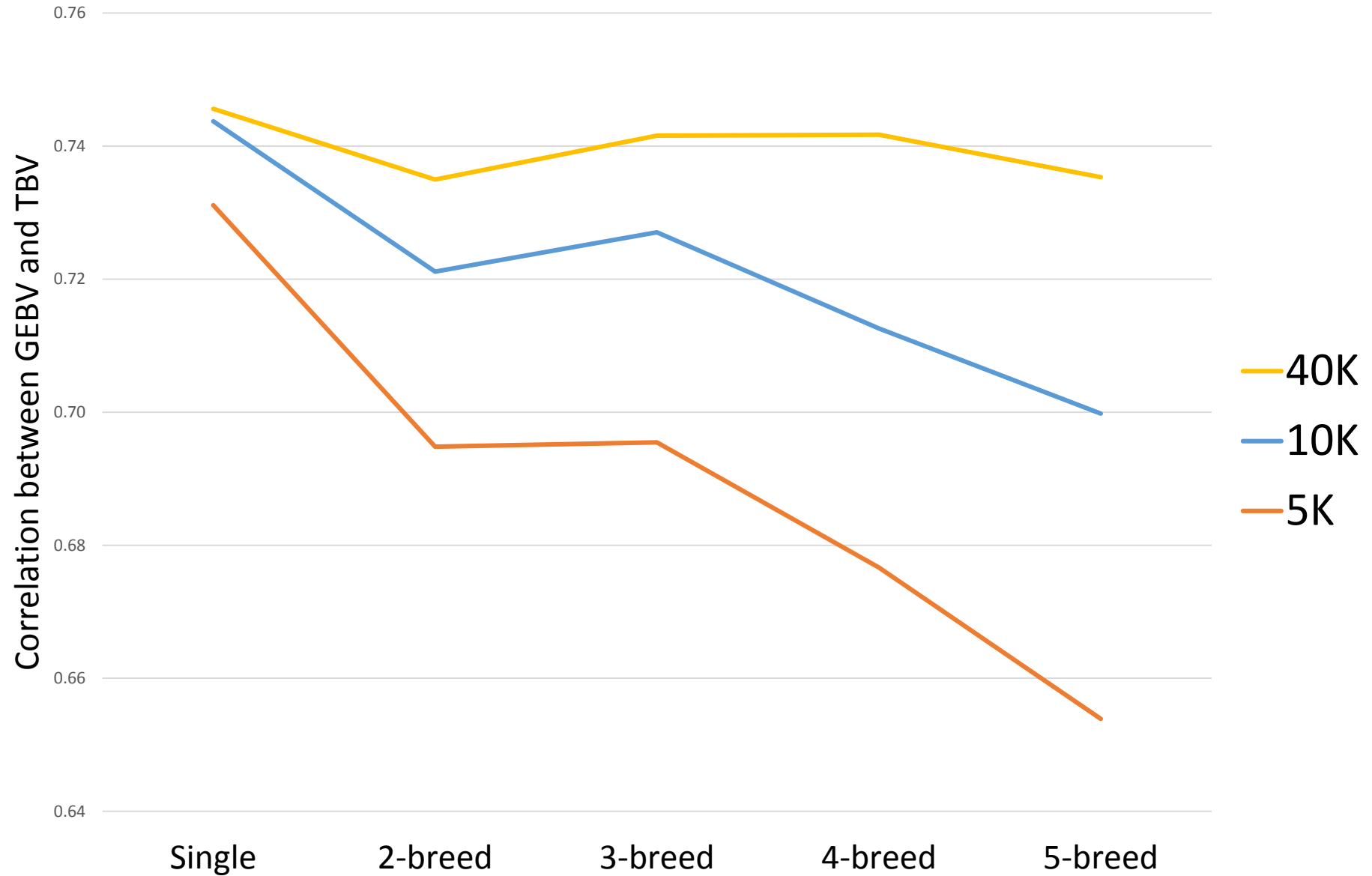


# Accuracy using phenotypes of ABCDE- 5K

**Average loss:  
0.07**



# Breed A GEBV accuracy



# Conclusion

- The accuracy of prediction decreases with the inclusion of more breeds in the same evaluation
- Extent of loss depends on SNP density
- Future:
  - Limit the loss
  - Other species
  - Crossbreeds
  - Real data

Thank you



**UNIVERSITY OF**  
**GEORGIA**