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

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Introduction

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

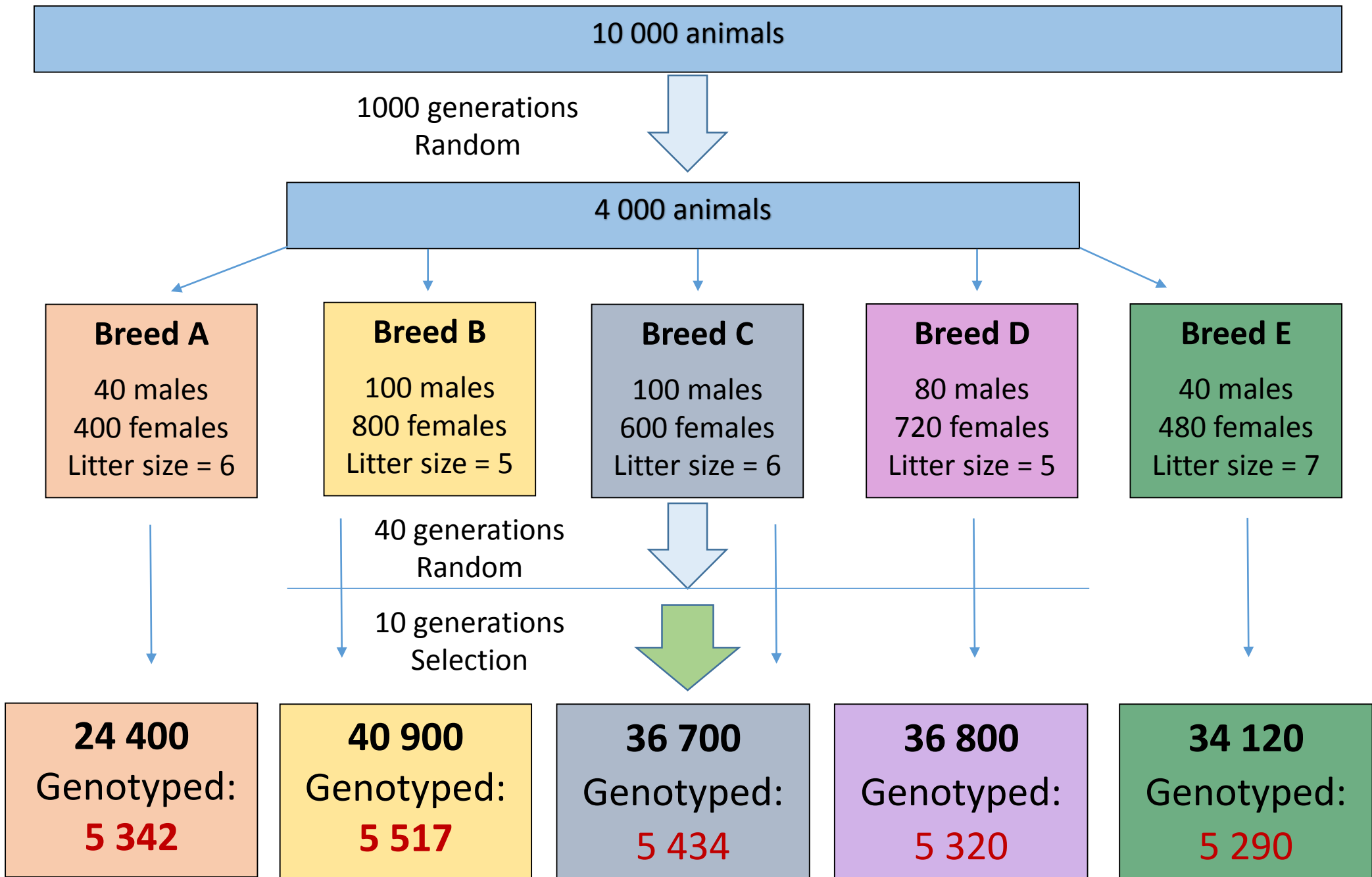
Objective

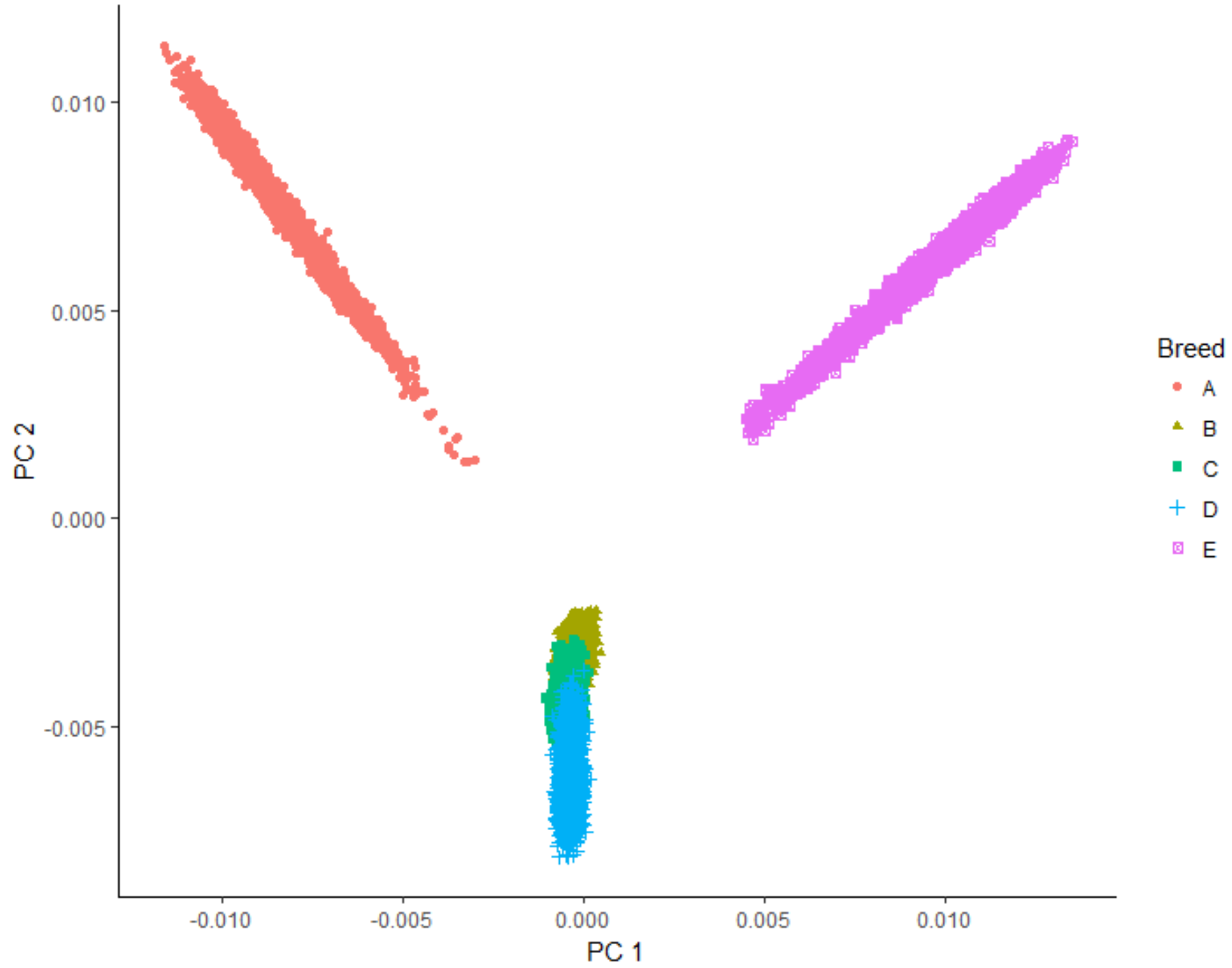
Investigate the accuracy of multi-breed evaluations (up to 5 breeds) by using different SNP densities and shared SNP effects

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 = 2.5×10^{-5}
- 40K SNPs

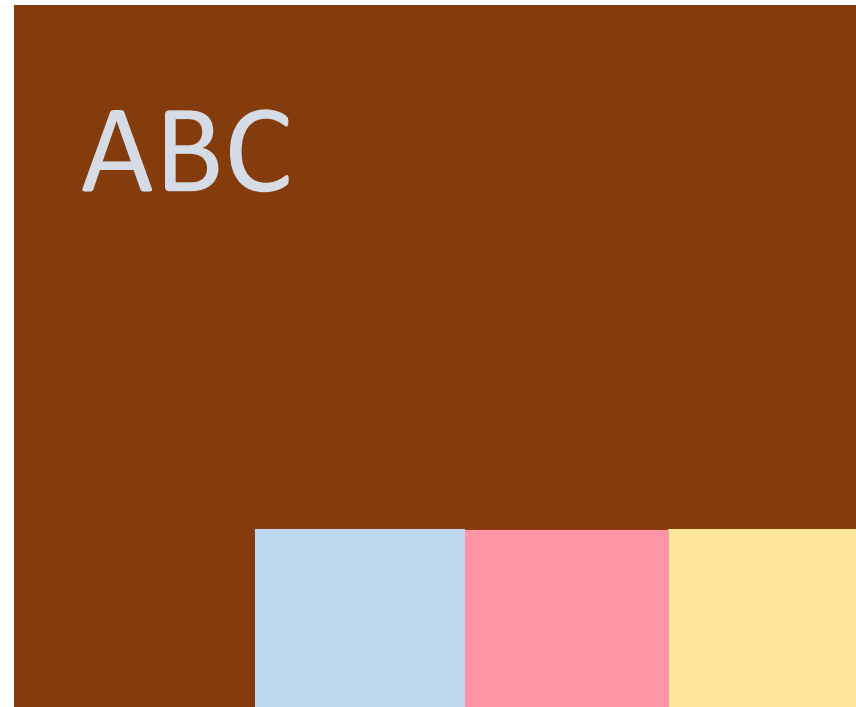
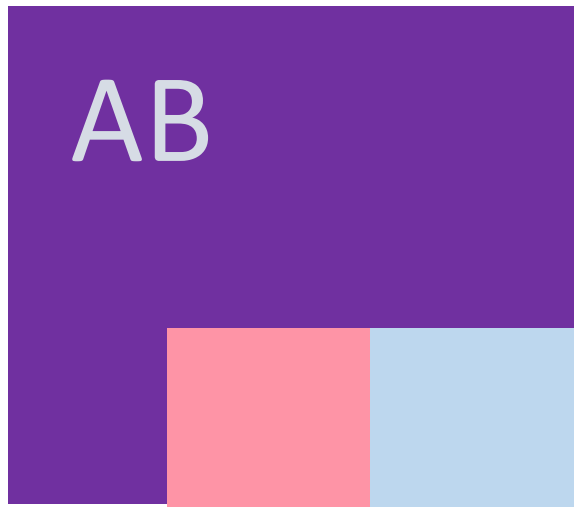
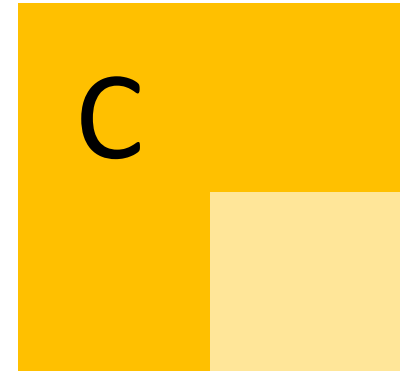
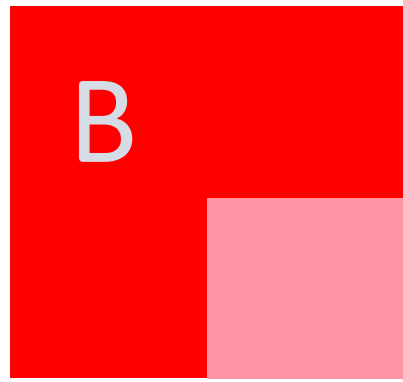




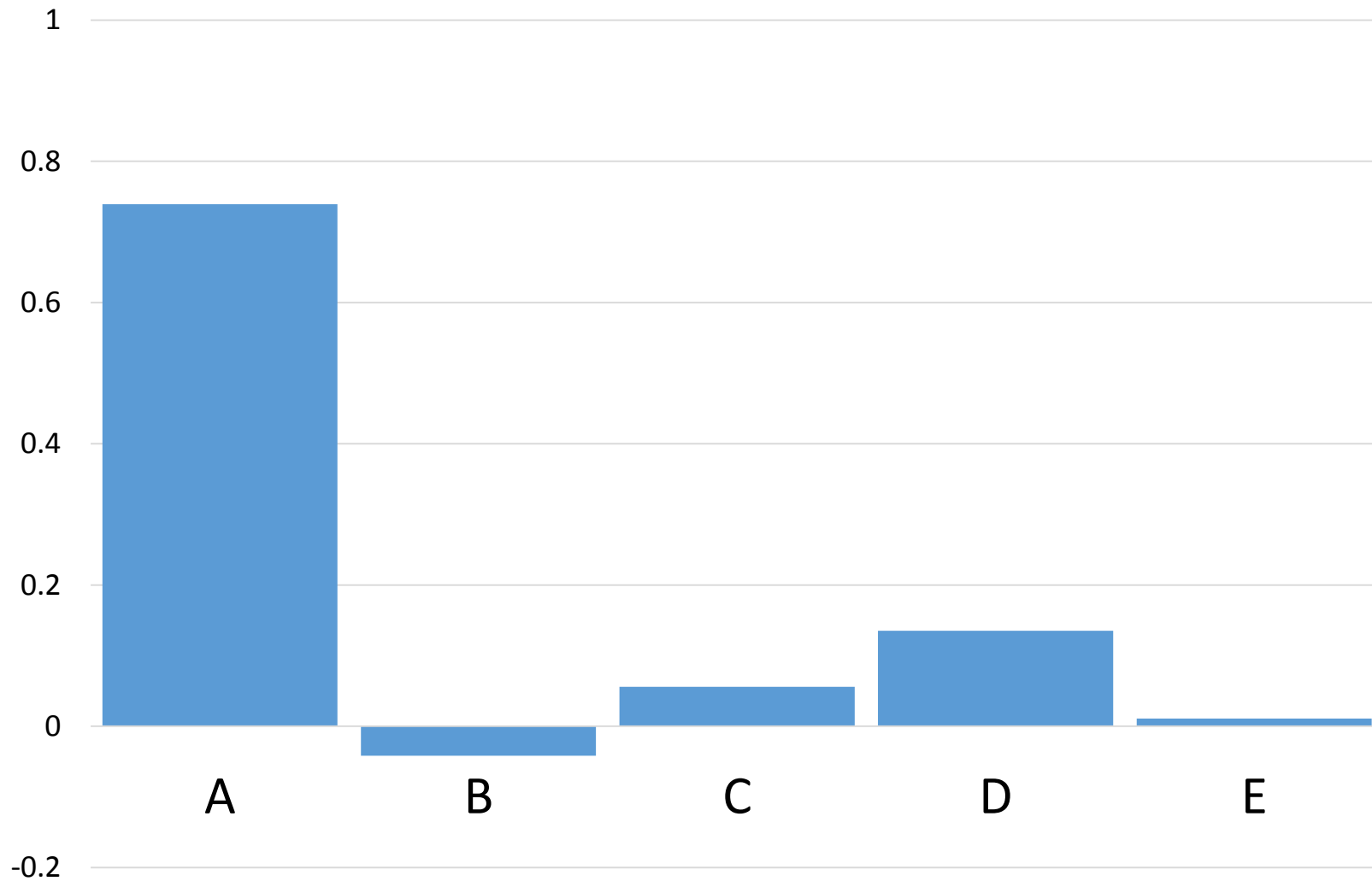
Materials and Methods

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

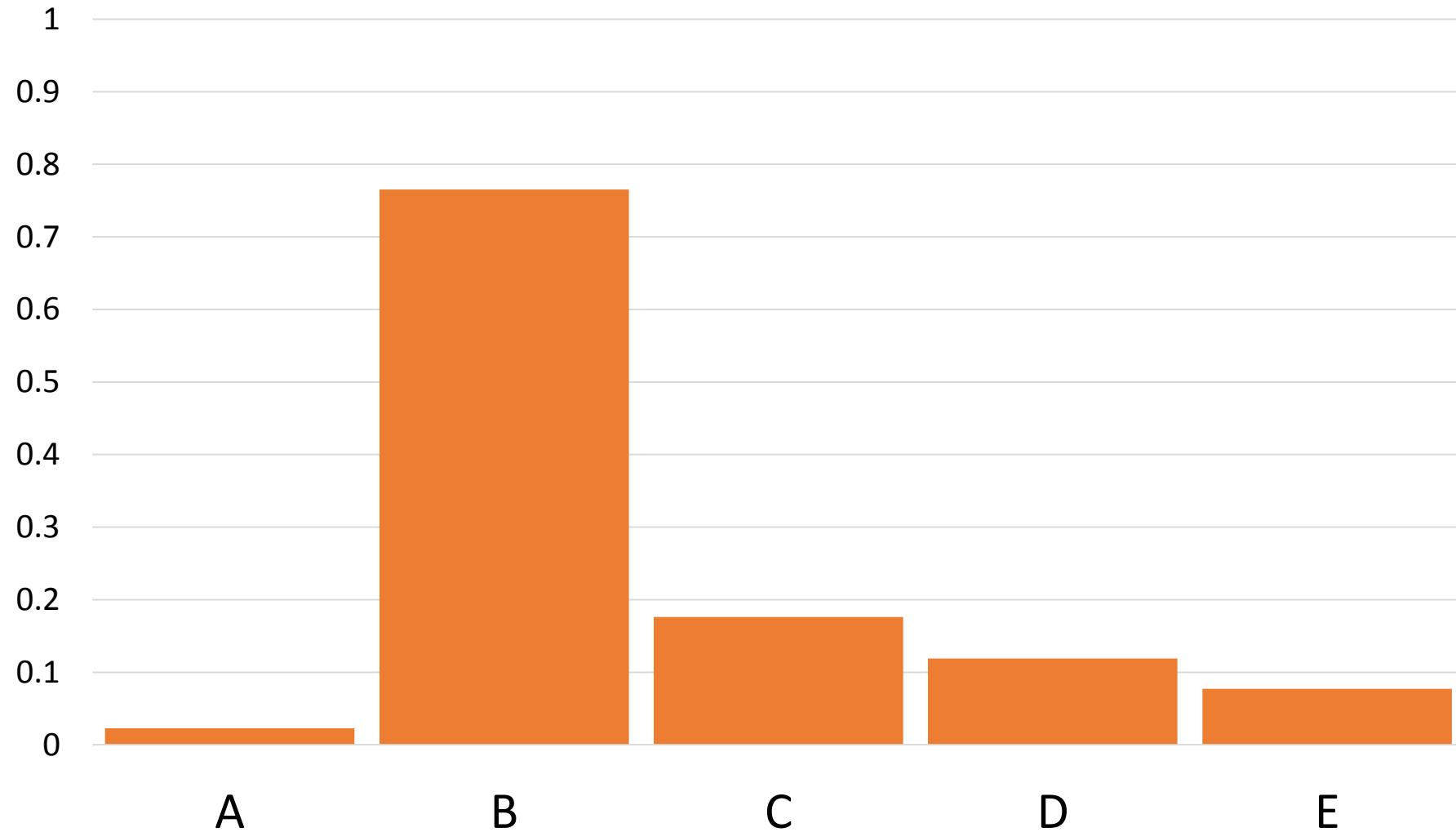
Validation



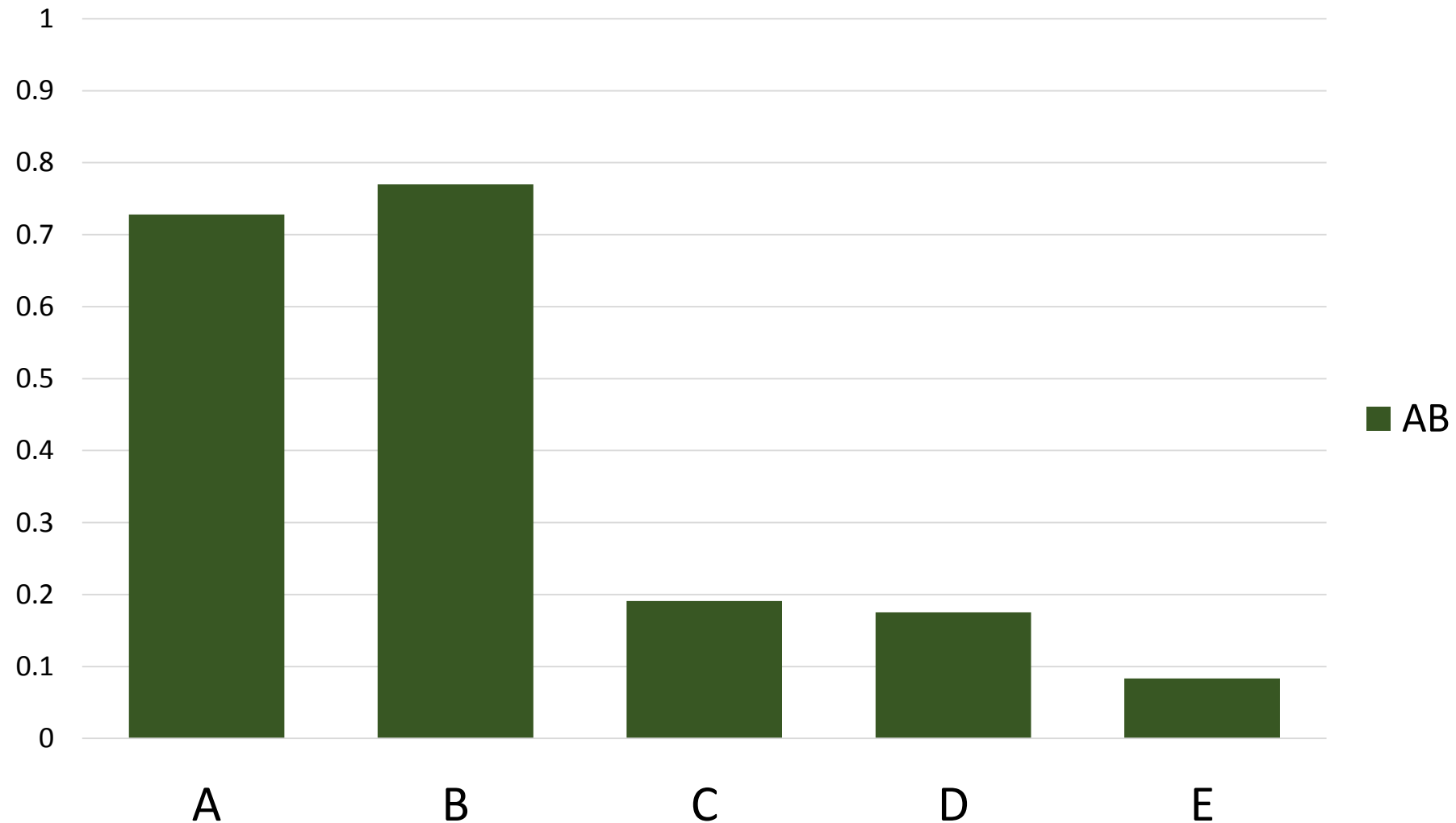
Accuracy using phenotypes of Breed A- 40K



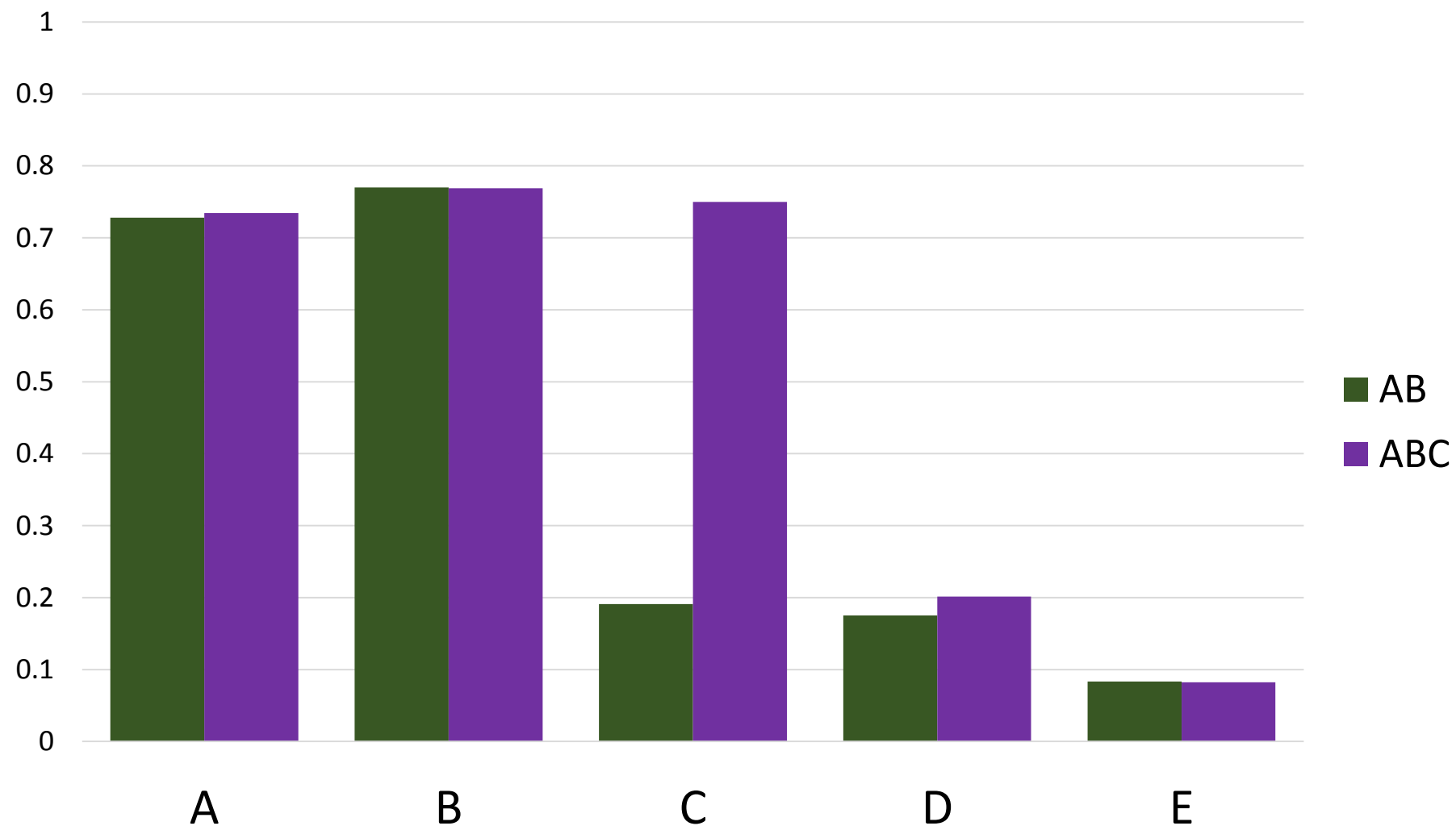
Accuracy using phenotypes of Breed B- 40K



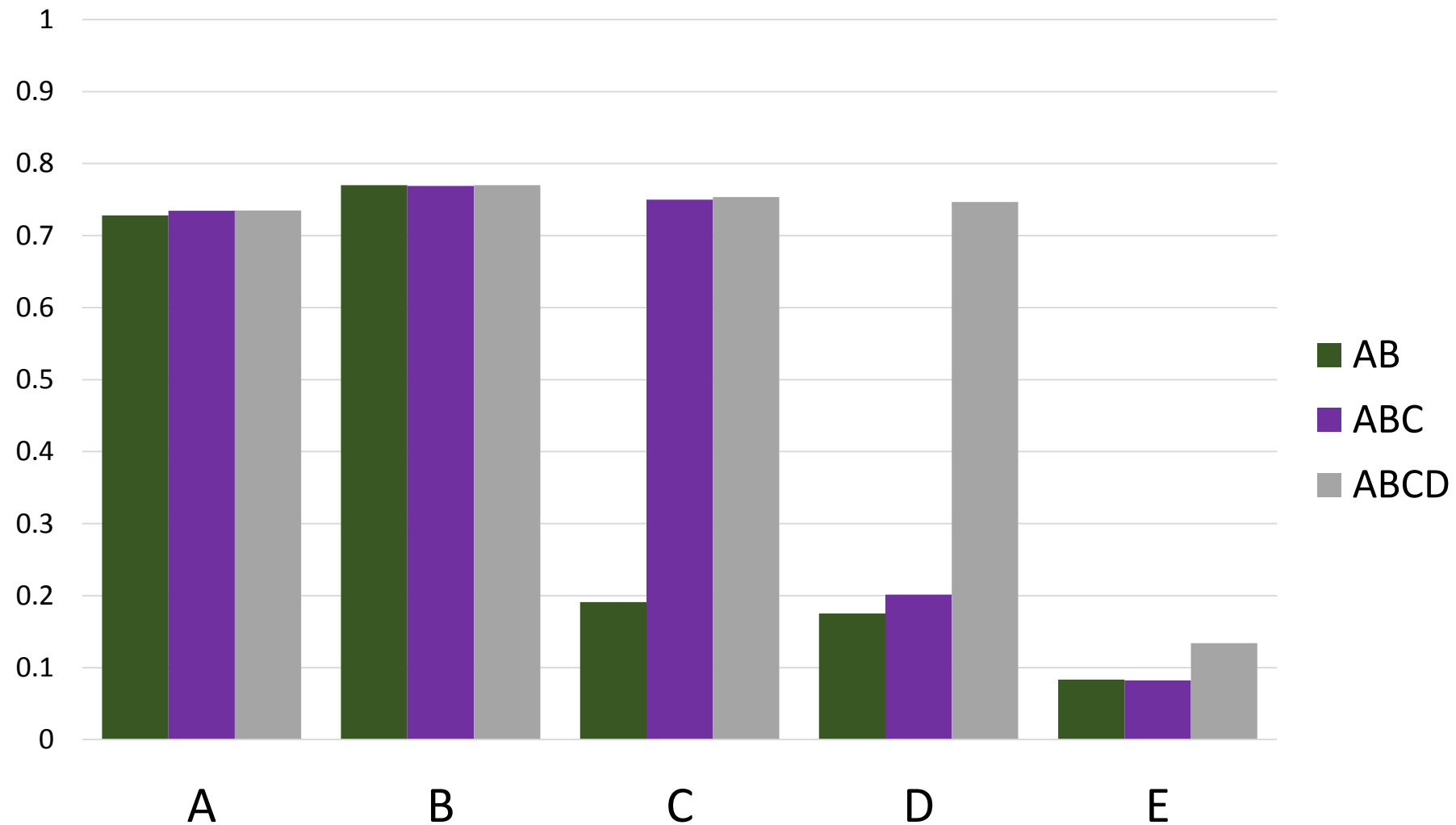
Accuracy using phenotypes of AB - 40K



Accuracy using phenotypes of ABC - 40K

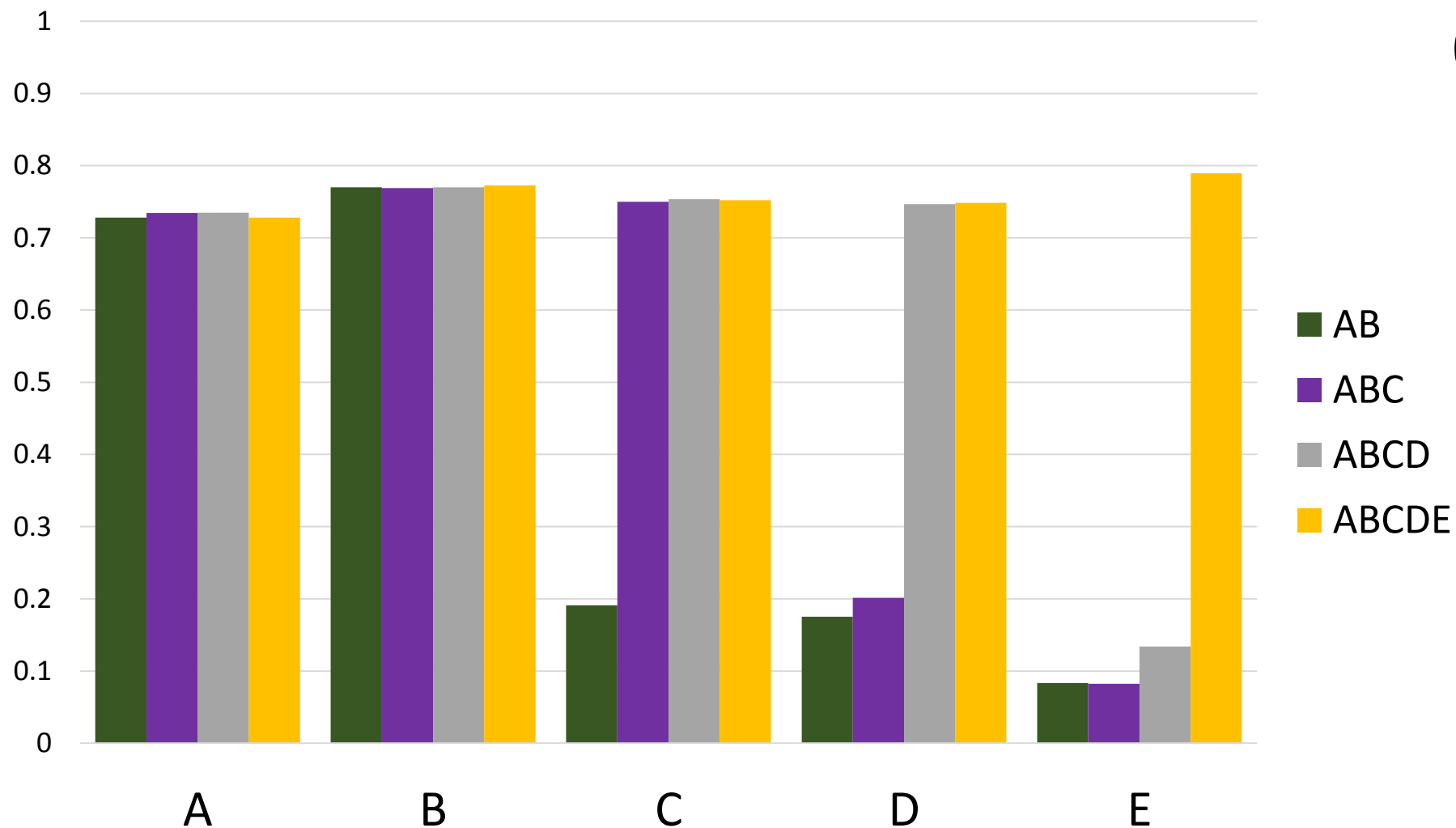


Accuracy using phenotypes of ABCD - 40K



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

$$1/2\Delta F$$

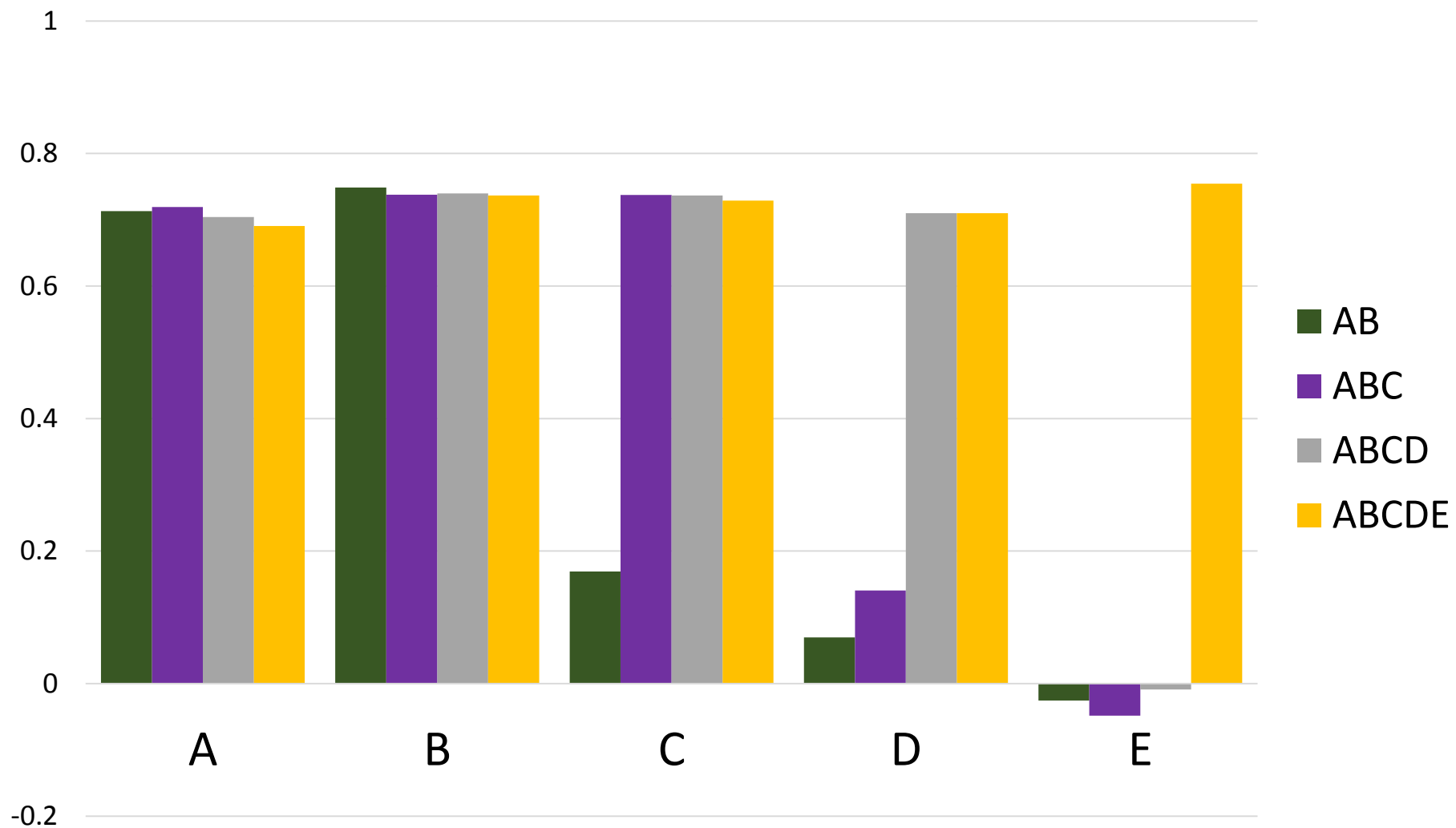
Average = **41**

Eigenvalues

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

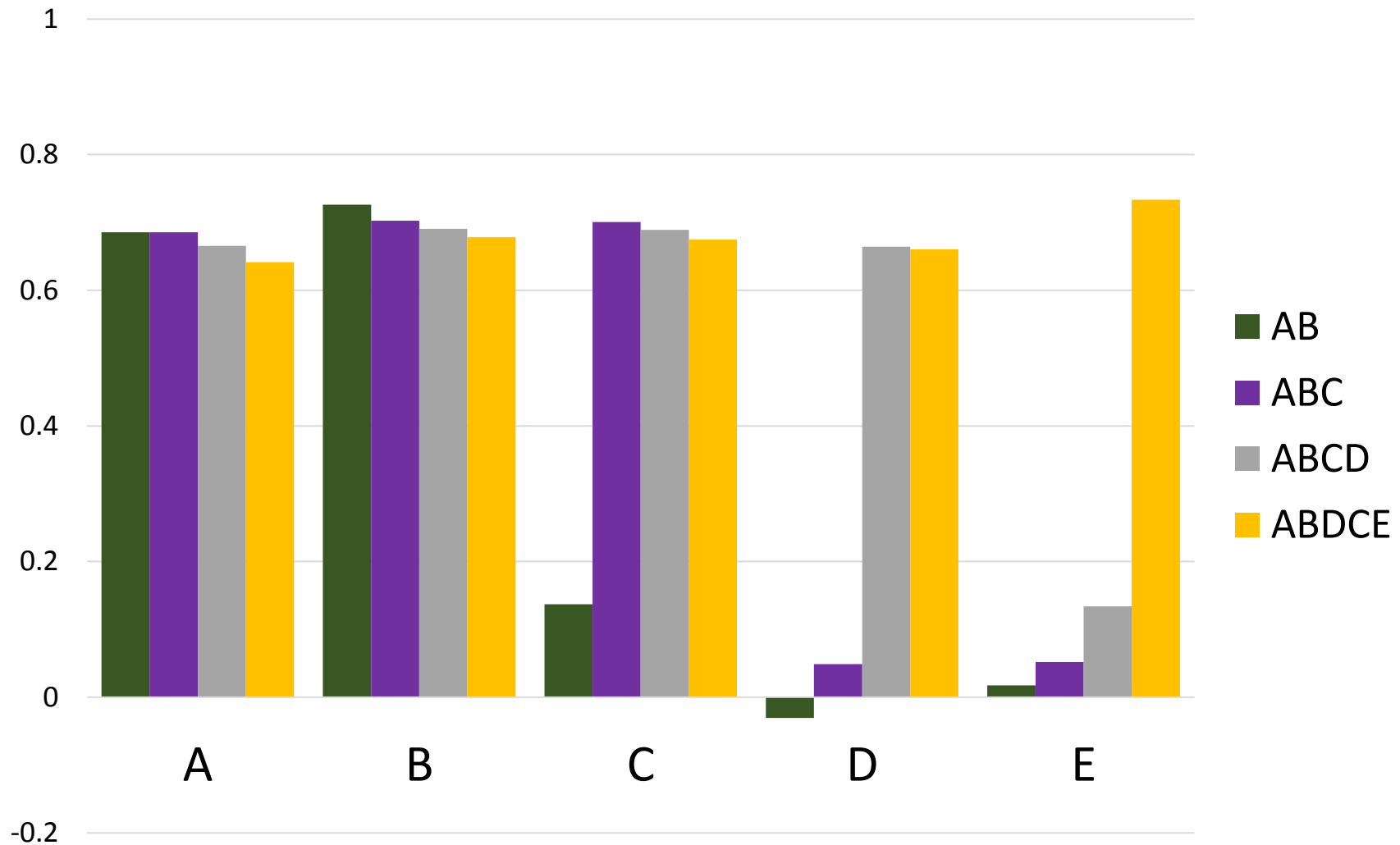
Accuracy using phenotypes of ABCDE - 10K

**Average loss:
0.03**

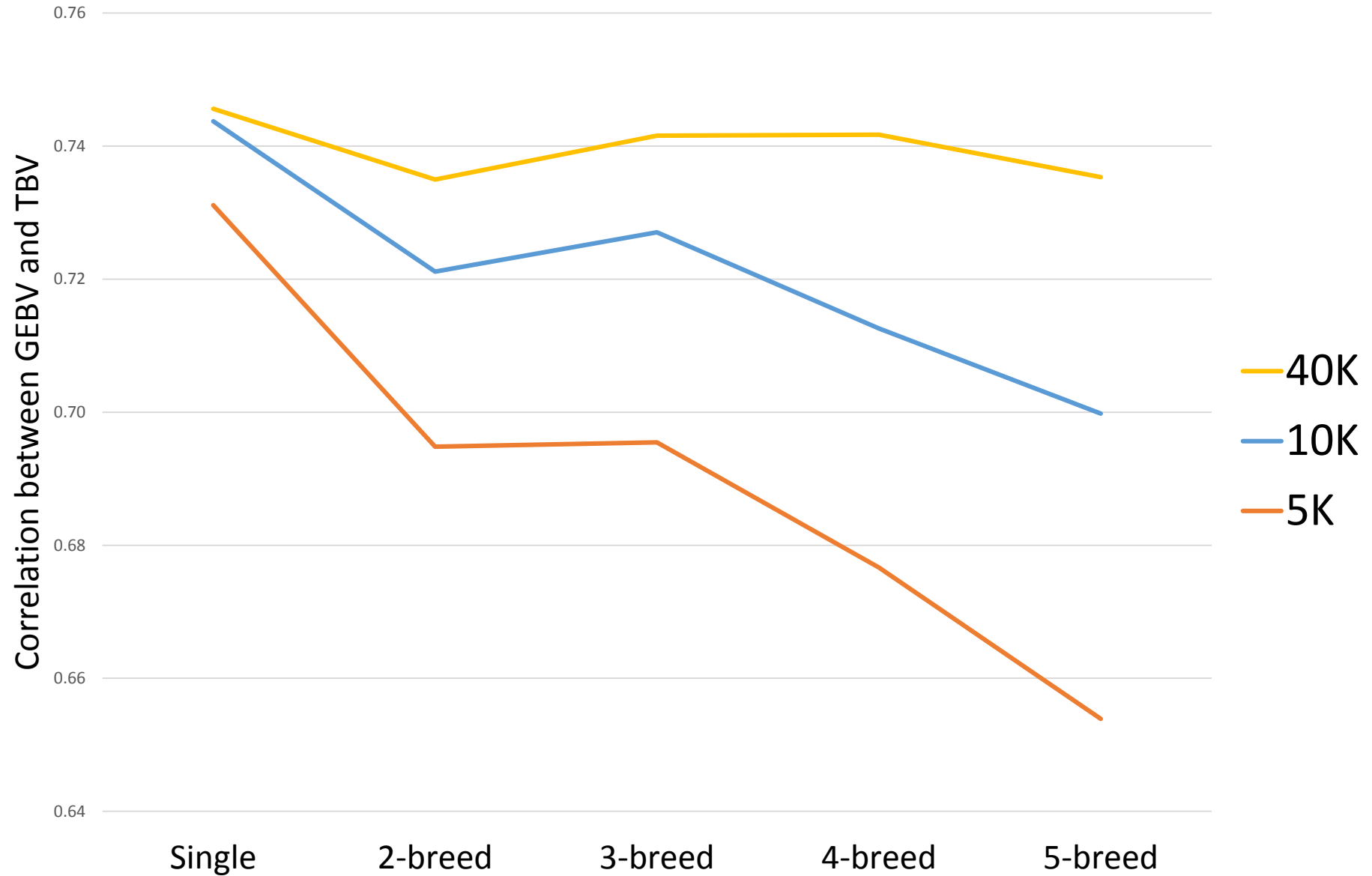


Accuracy using phenotypes of ABCDE- 5K

**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



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