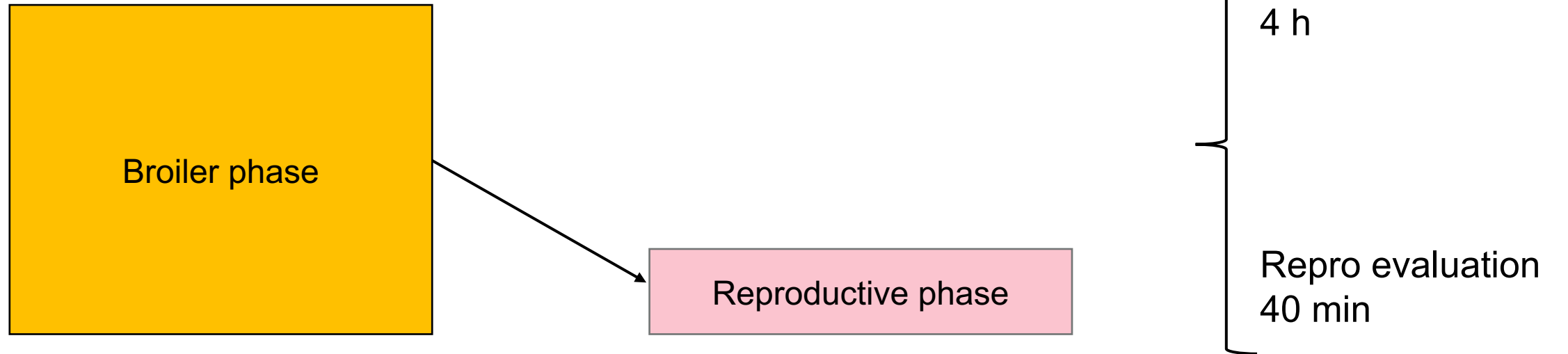


Accounting for sequential genomic selection in broiler breeding

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Introduction



What are the benefits of combining both evaluations?

Data

Data from 30 selection rounds
(212 – 242)

Pedigree included 576,609 birds

Trait	n
Egg Production	8,776
Fertility	8,619
Hatch of fertile eggs	8,536
Body Weight	518,673
Breast Meat Percent	23,679
Fat Percent	23,545
Residual Feed Intake	97,749

APY - Breeders Core (BC) = all parents + selection candidates (last 2 selection rounds)

RE (baseline scenario)

- included pedigrees, genotypes, and phenotypes for reproductive traits of selected animals for reproduction
- BC with 12,458 animals
- total number of genotypes = 18,179

RE2

- included RE + broiler phenotypes of those selected animals
- BC with 12,458 animals
- total number of genotypes = 18,179

RE_BR

- included RE2 + broiler phenotypes of those *unselected* animals
- BC with 12,458 animals
- total number of genotypes = 18,179

RE_BR_GE

- included RE_BR + genotypes of those *unselected* animals
- BC with 19,121 animals
- total number of genotypes = 146,084

Genetic parameters

Trait	h ²
Egg Production	0.31
Fertility	0.02
Hatch of fertile eggs	0.32
Body Weight	0.23
Breast Meat Percent	0.44
Fat Percent	0.42
Residual Feed Intake	0.33

Gen Corr	Egg P	Fert	Hatch	BW	BMP	FP	RFI
Egg P	1.00						
Fert	0.84	1.00					
Hatch	0.46	0.76	1.00				
BW	0.28	0.69	0.46	1.00			
BMP	-0.06	0.16	0.16	0.32	1.00		
FP	0.15	0.09	0.03	-0.10	-0.38	1.00	
RFI	0.19	0.30	0.08	0.29	-0.30	0.42	1.00

Validation using LR method

$$\text{Accuracy} = \sqrt{\frac{\text{cov}(\hat{u}_w, \hat{u}_p)}{(1-\bar{F})\sigma_u^2}}$$

$$\text{Bias} = \bar{\hat{u}}_p - \bar{\hat{u}}_w$$

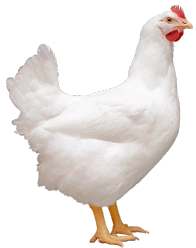
$$\text{Dispersion} = \frac{\text{cov}(\hat{u}_p, \hat{u}_w)}{\sigma_{\hat{u}_p}^2}$$

565 hens

212	213	214	233	234	235	236	237	238	239	240	241	242
212	213	214	233	234	235	236	237	238	239	240		

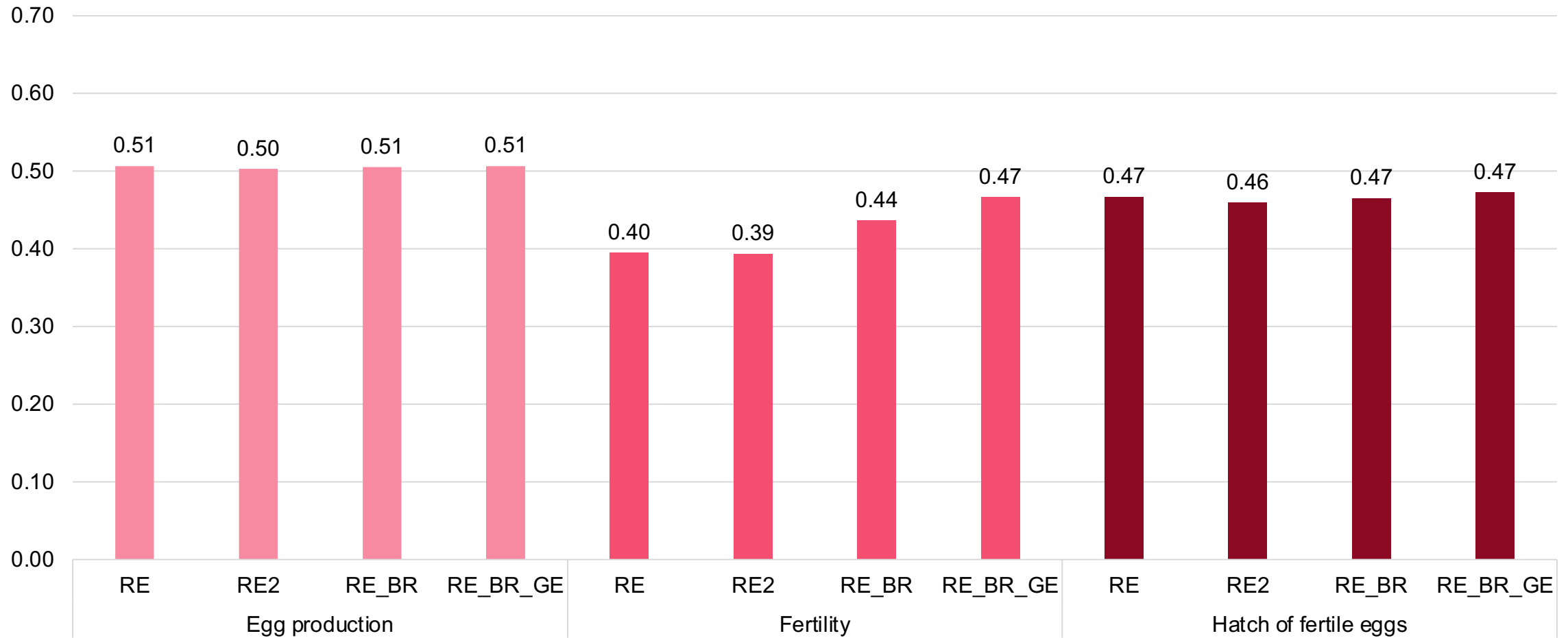
38 roosters, number of progeny from 10 to 43

212	213	214	233	234	235	236	237	238	239	240	241	242
212	213	214	233	234	235	236	237	238	239	240		



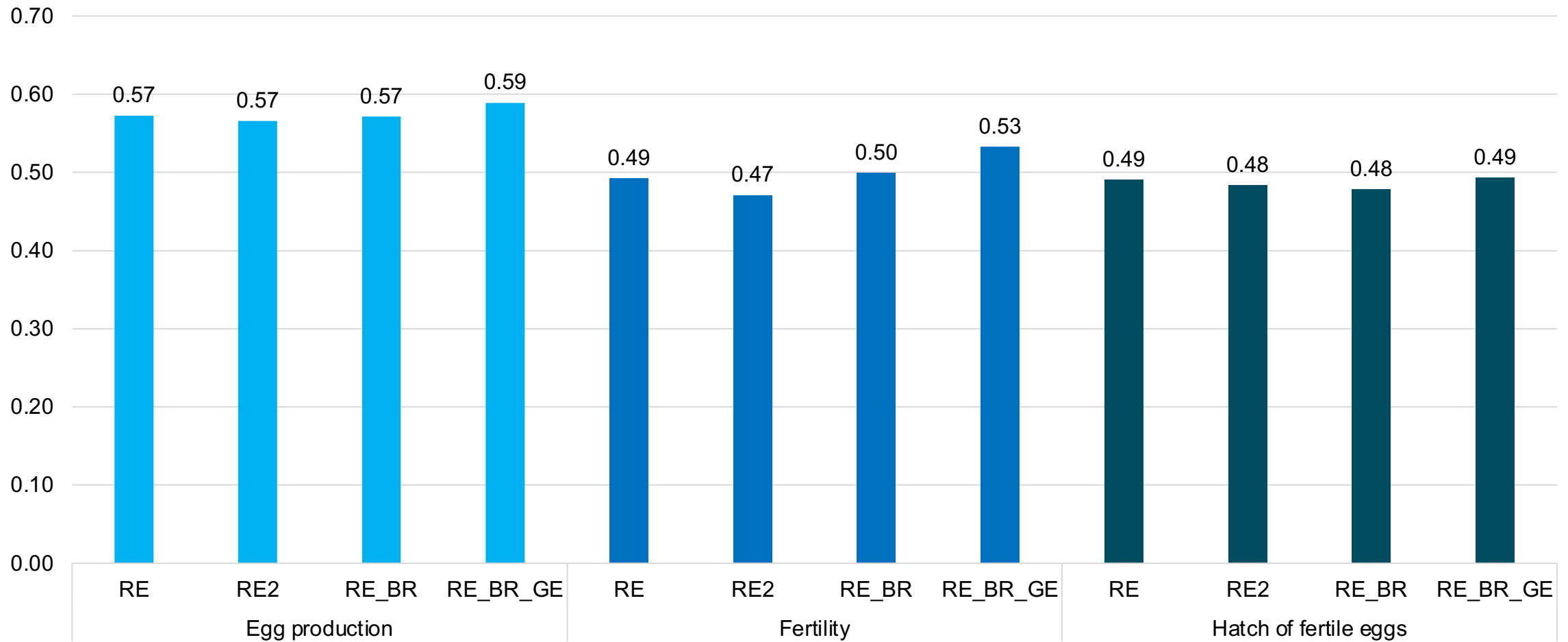
Results - Accuracy

Hens



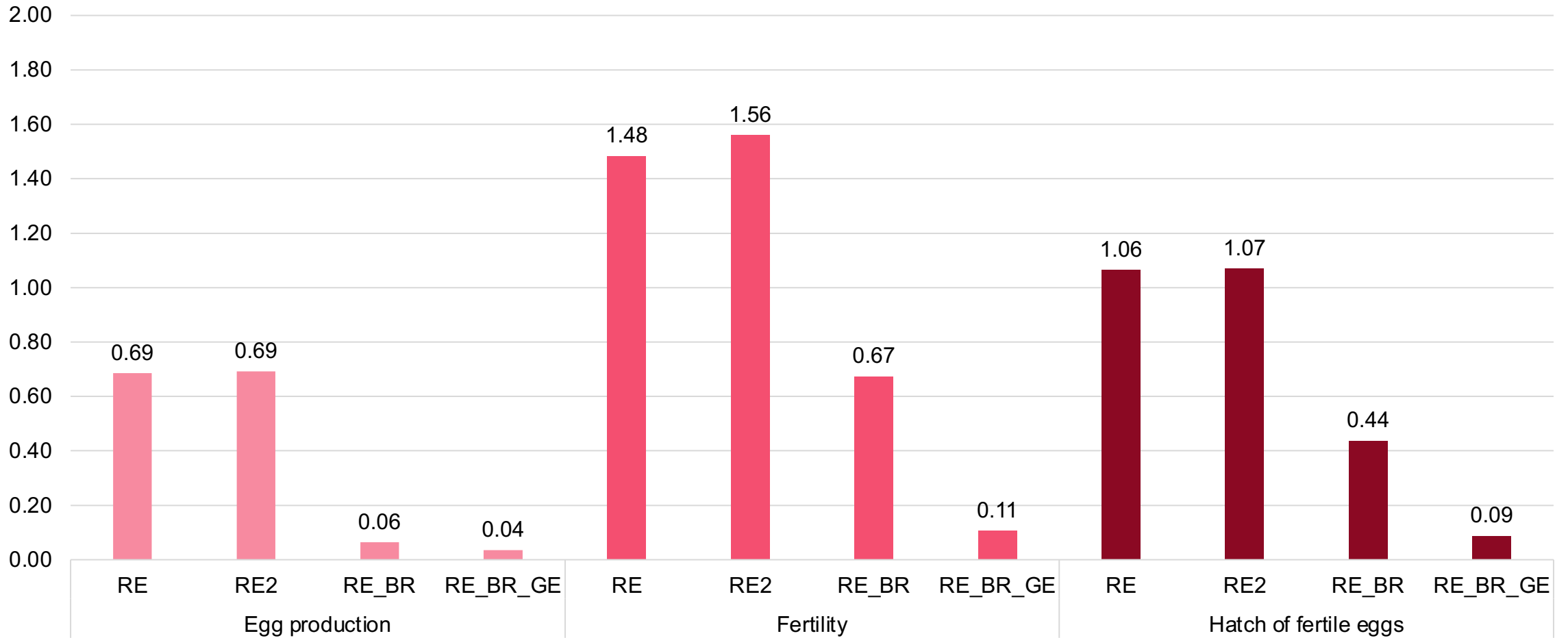
Results - Accuracy

Roosters



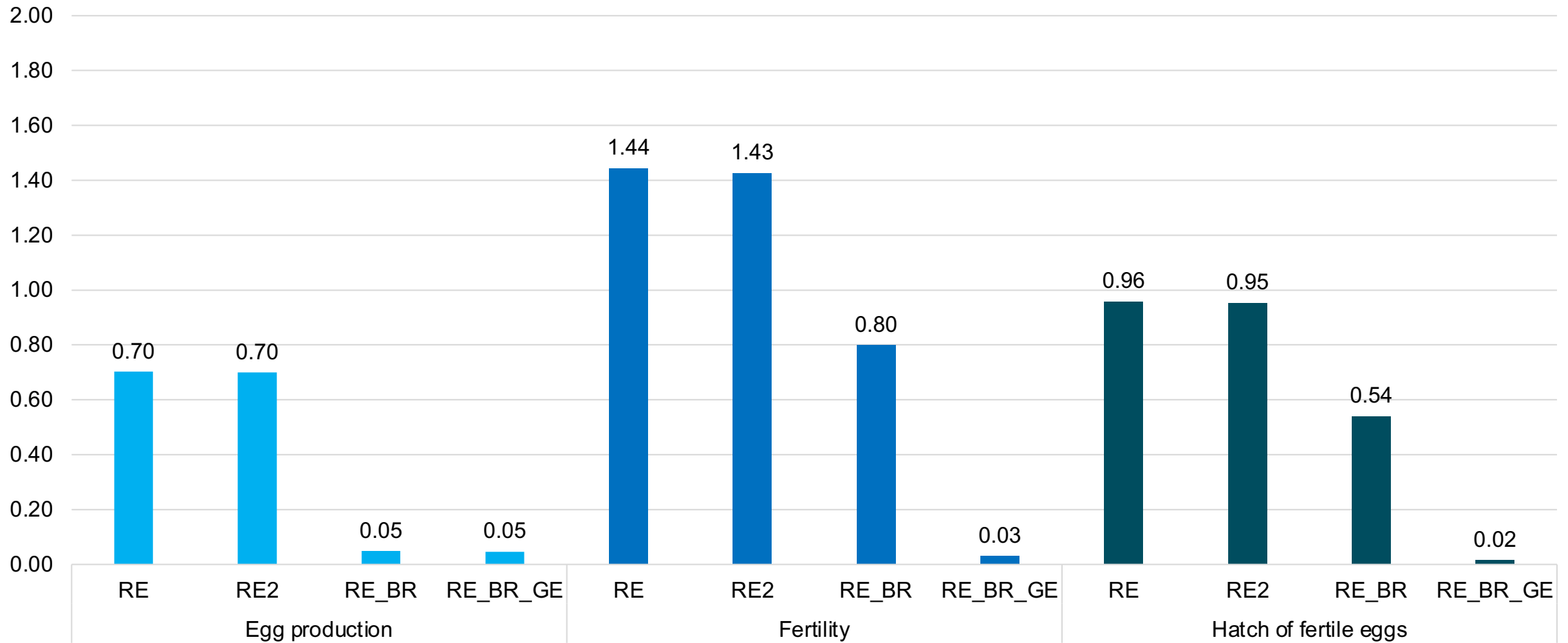
Results - Bias

Hens



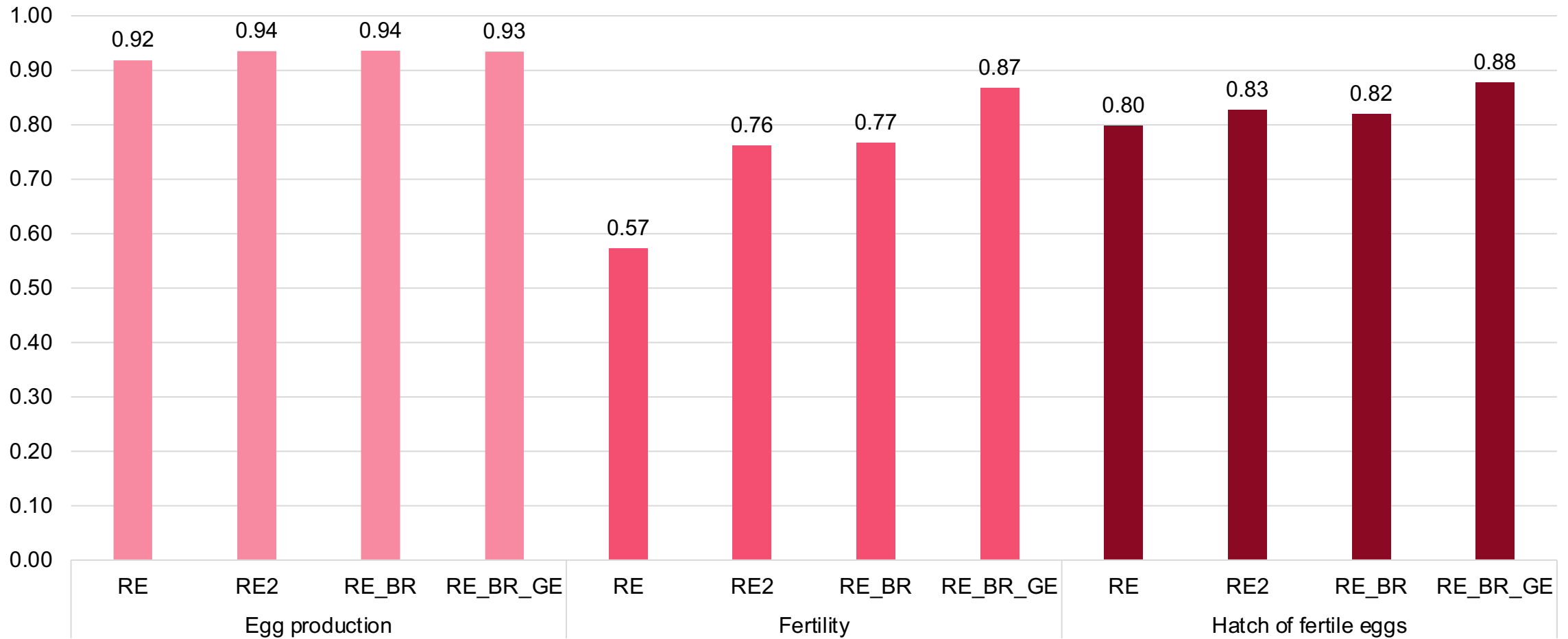
Results - Bias

Roosters



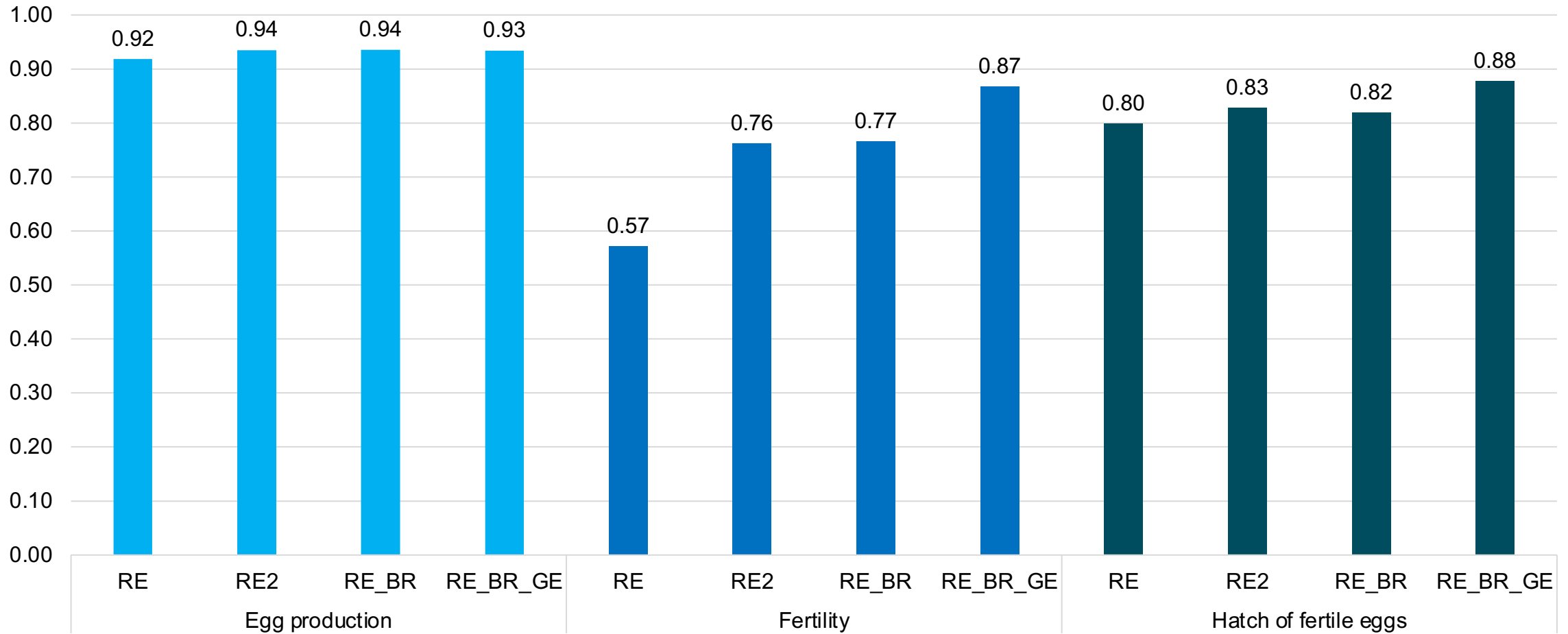
Results - Dispersion

Hens



Results - Dispersion

Roosters



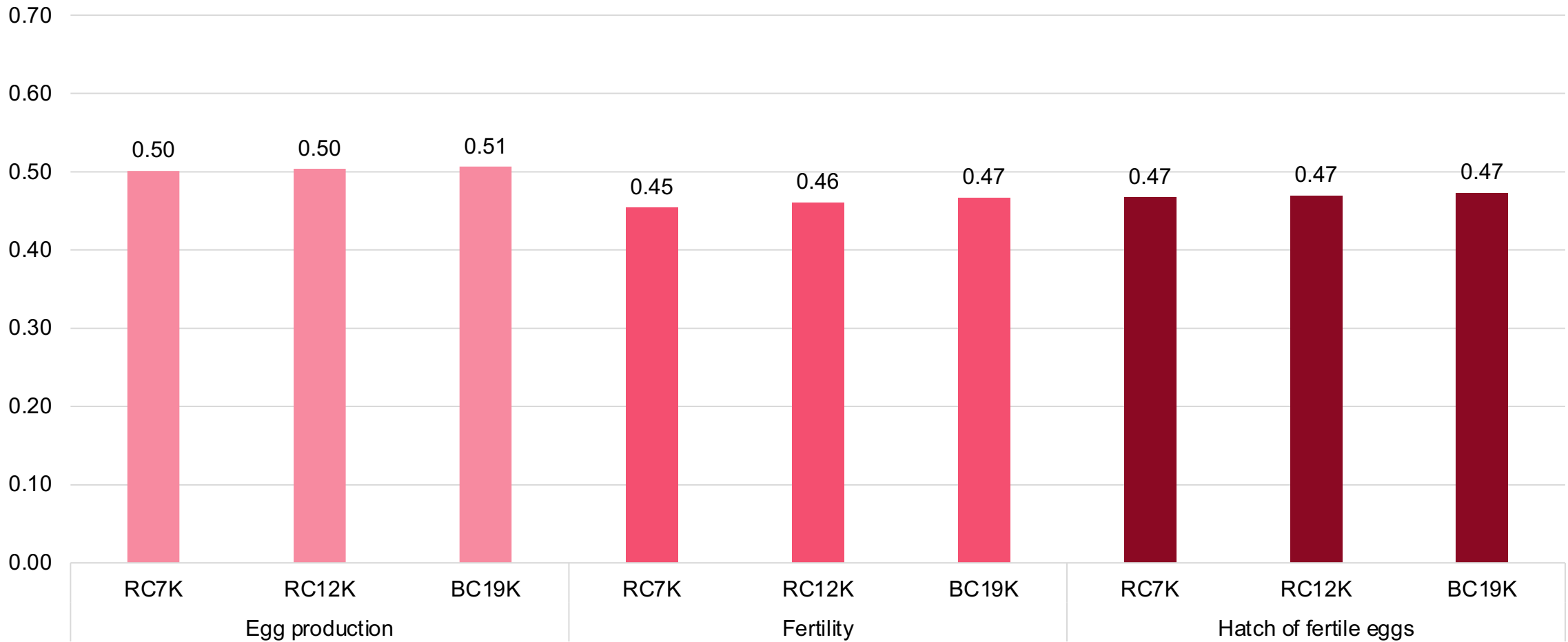
How to reduce computing time?

All information, different core definition

1. **BC** 19,121 animals
2. **Random** 7,093 animals (this number was equal to the number of the largest eigenvalues explaining 99% of the variation in **G**)
3. **Random** 12,000 animals

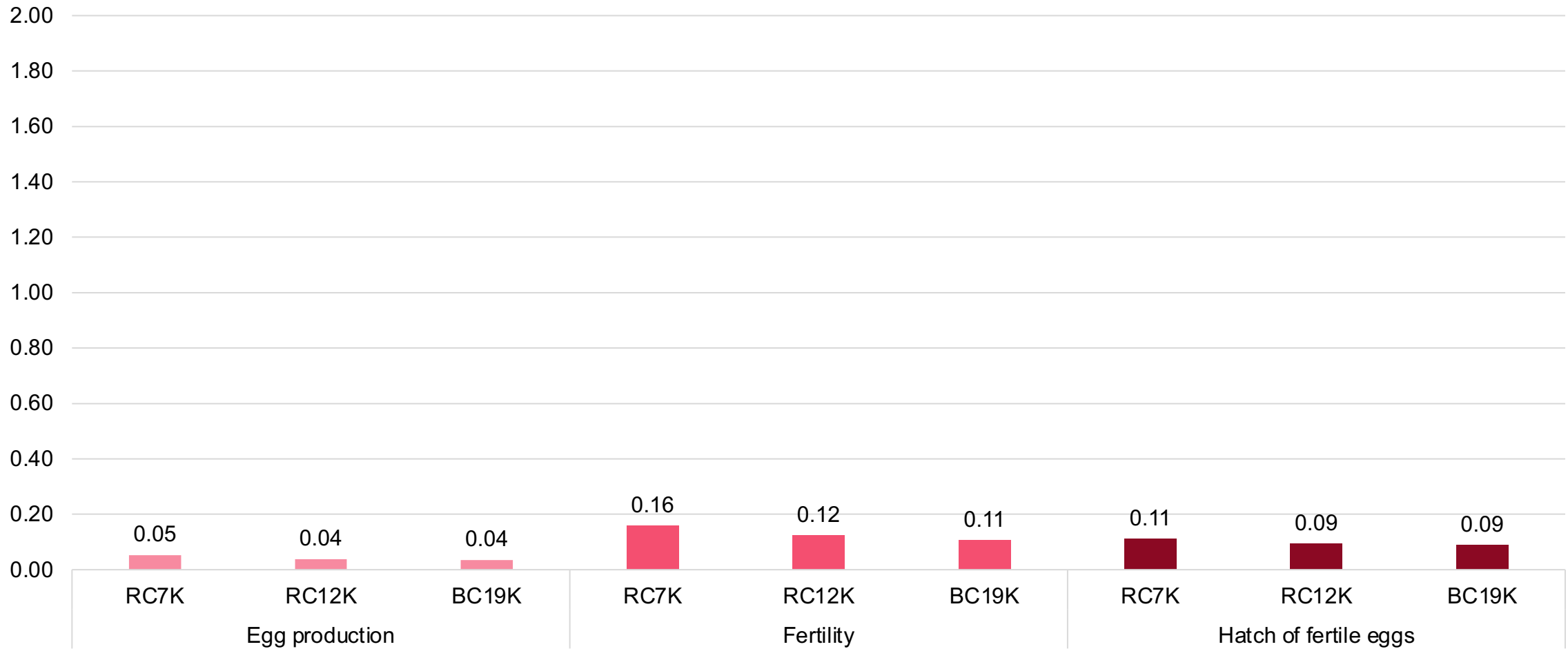
Results - Accuracy

Hens



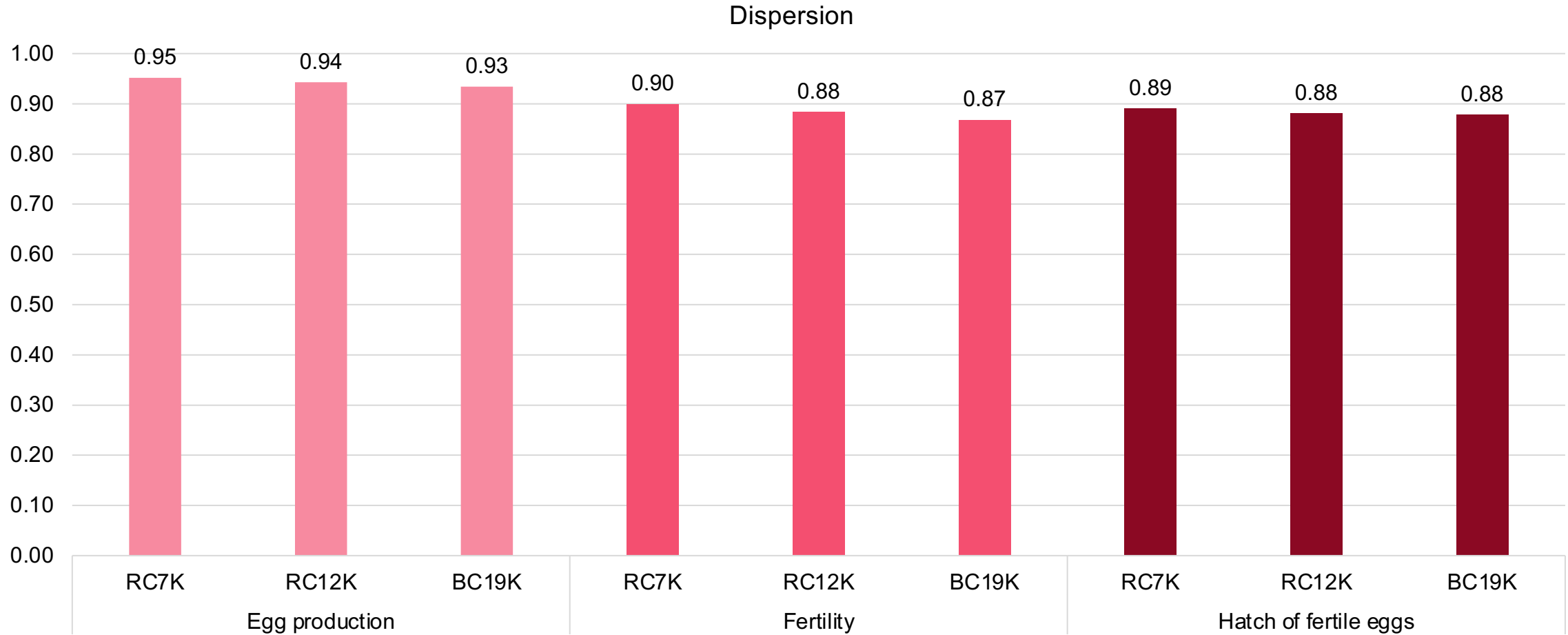
Results - Bias

Hens

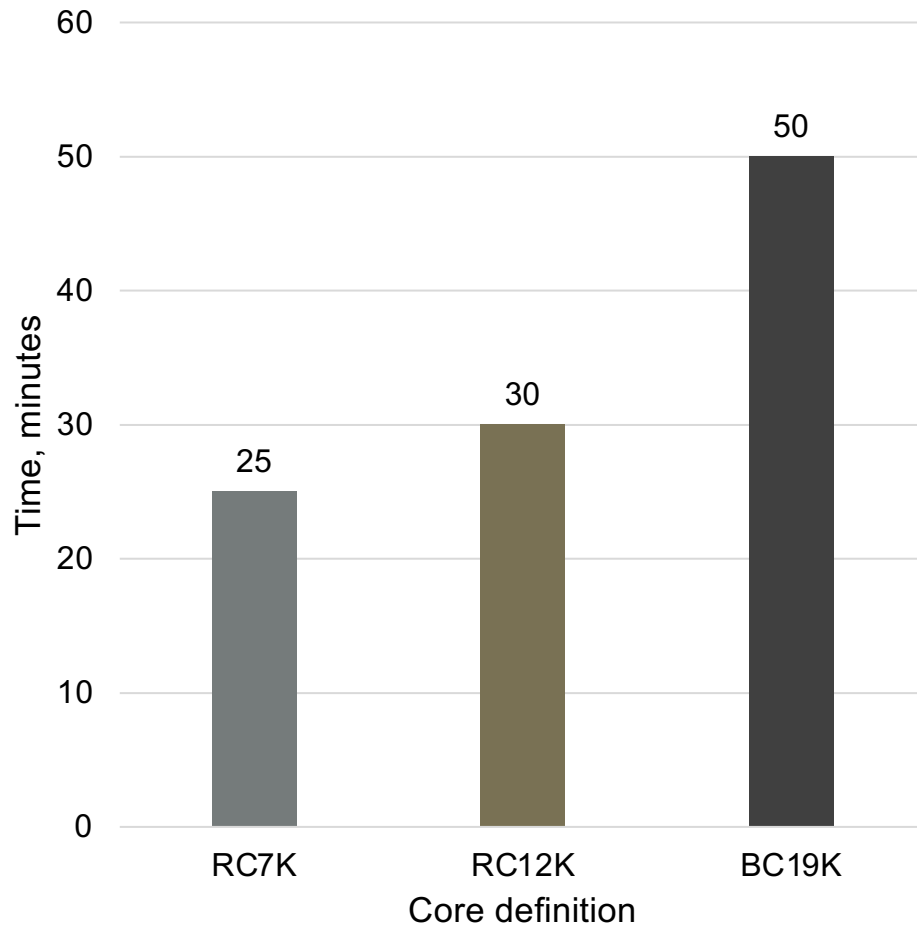


Results - Dispersion

Hens



Time to convergence



GEBV are less biased using all data available, better selection decisions

Computing time can be reduced ~50% using a random core based on SVD

Thank you!!!