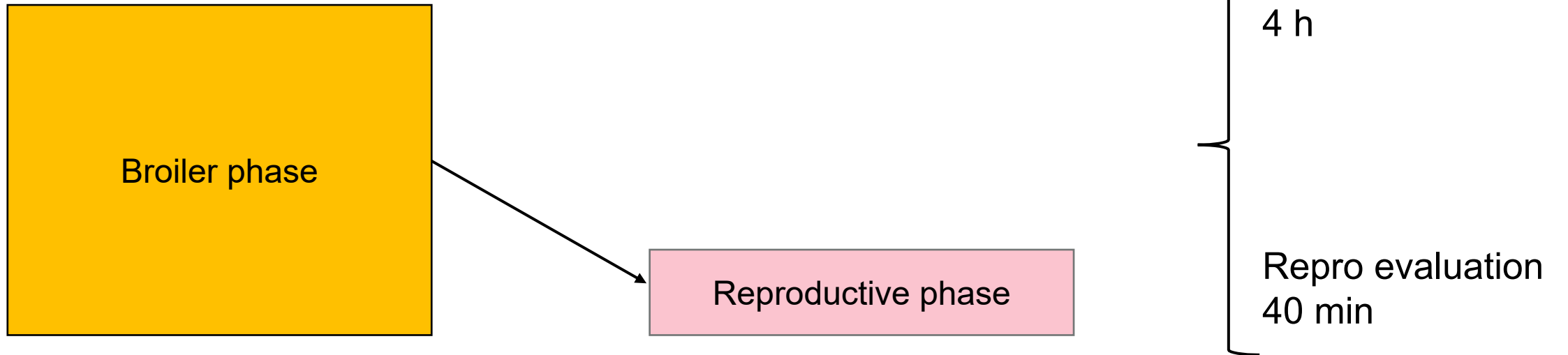


# **Accounting for sequential genomic selection in broiler breeding**

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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 <sup>2</sup>
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

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

565 hens

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

$$\text{Dispersion} =$$



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

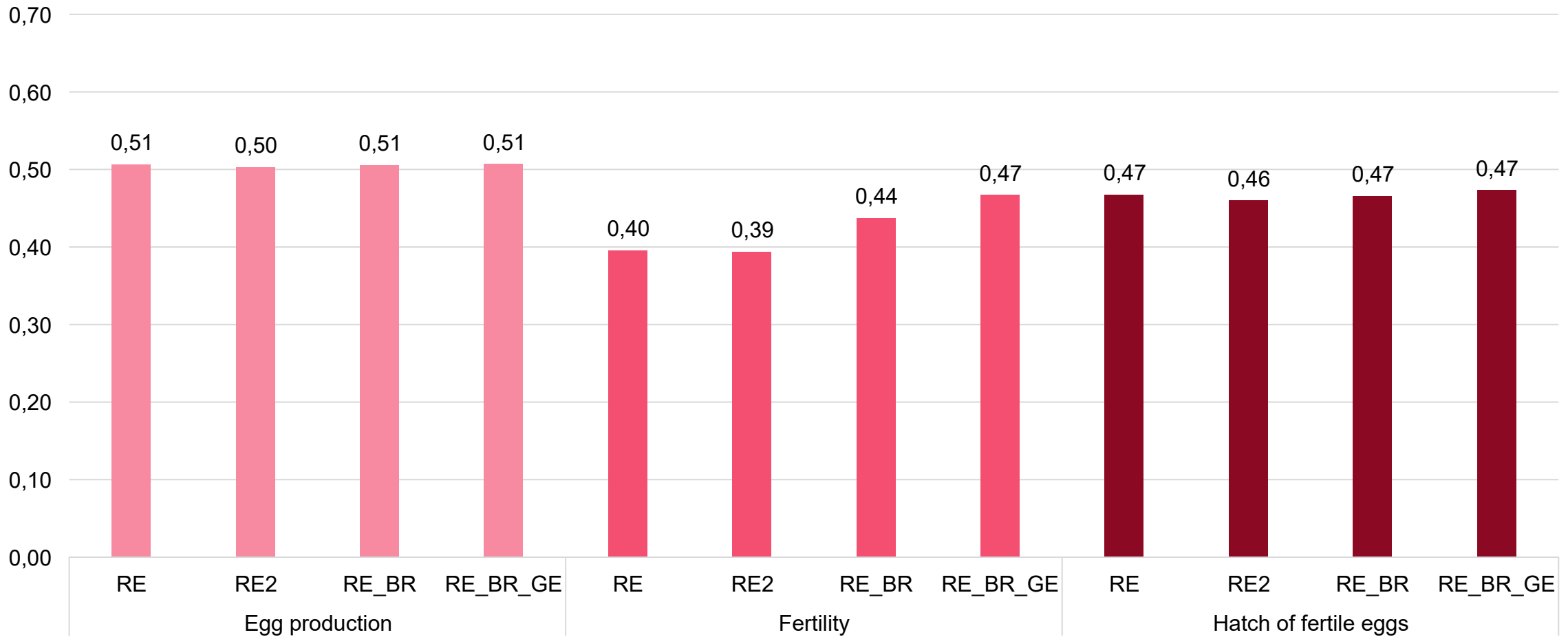


38 roosters, number of progeny from 10 to 43

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

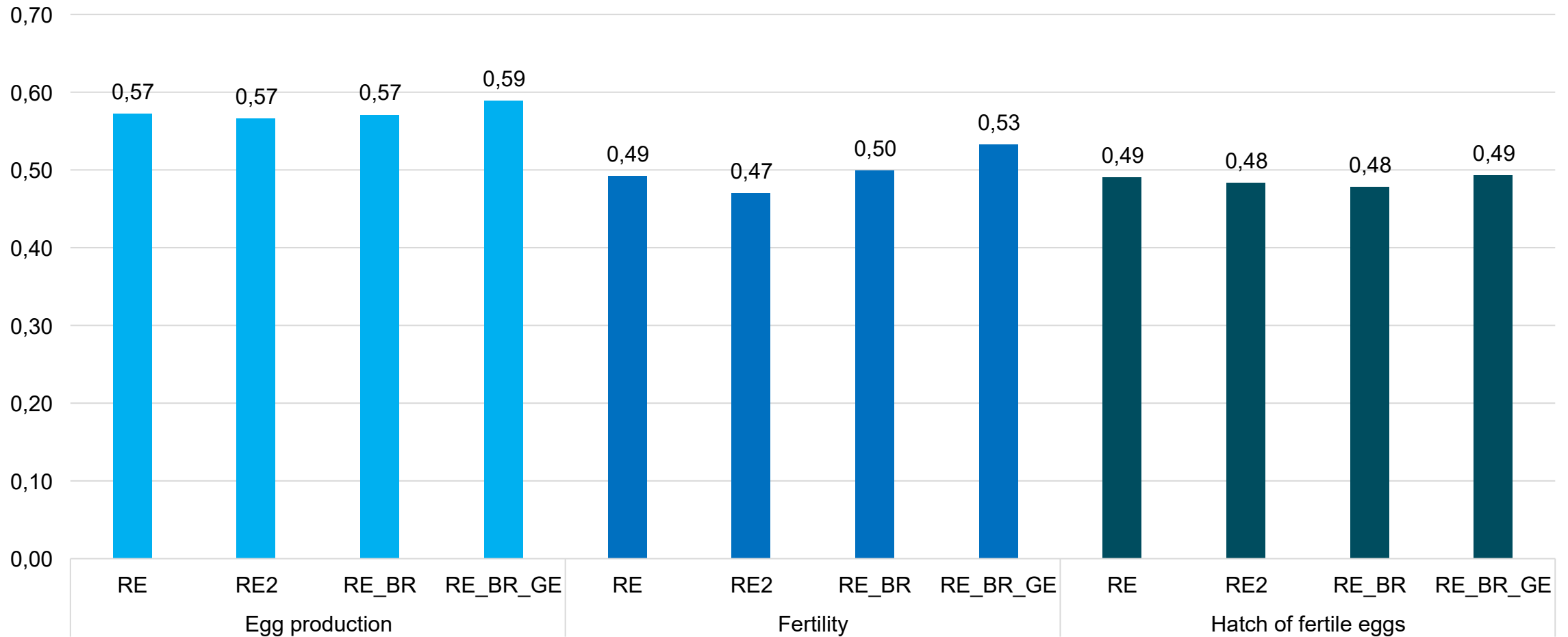
# Results - Accuracy

Hens



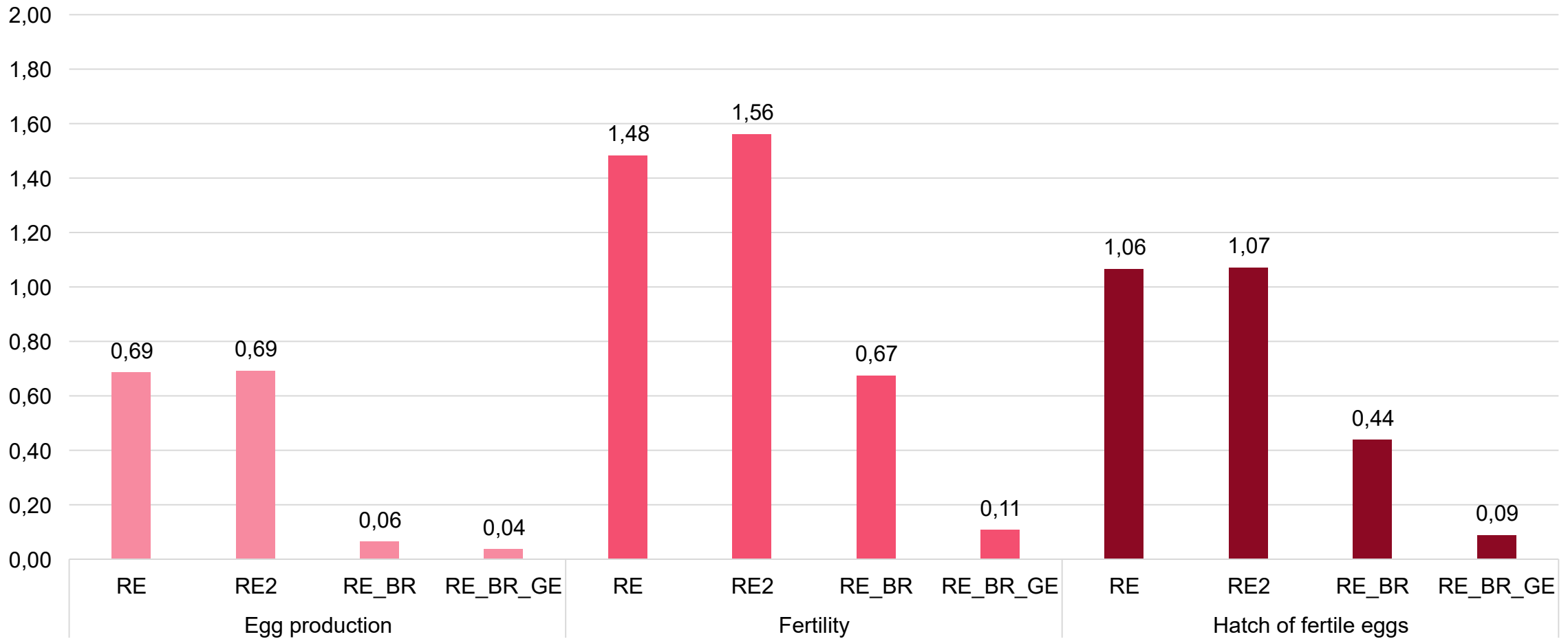
# Results - Accuracy

Roosters



# Results - Bias

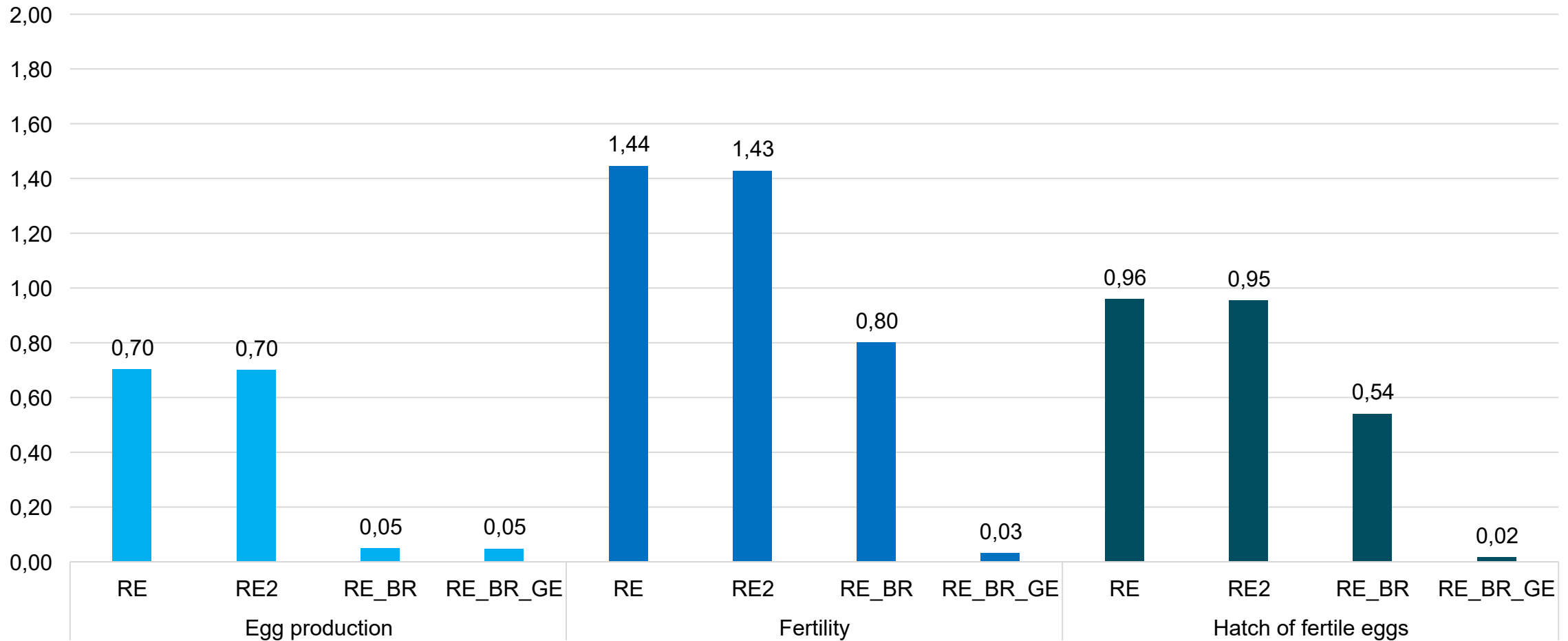
Hens





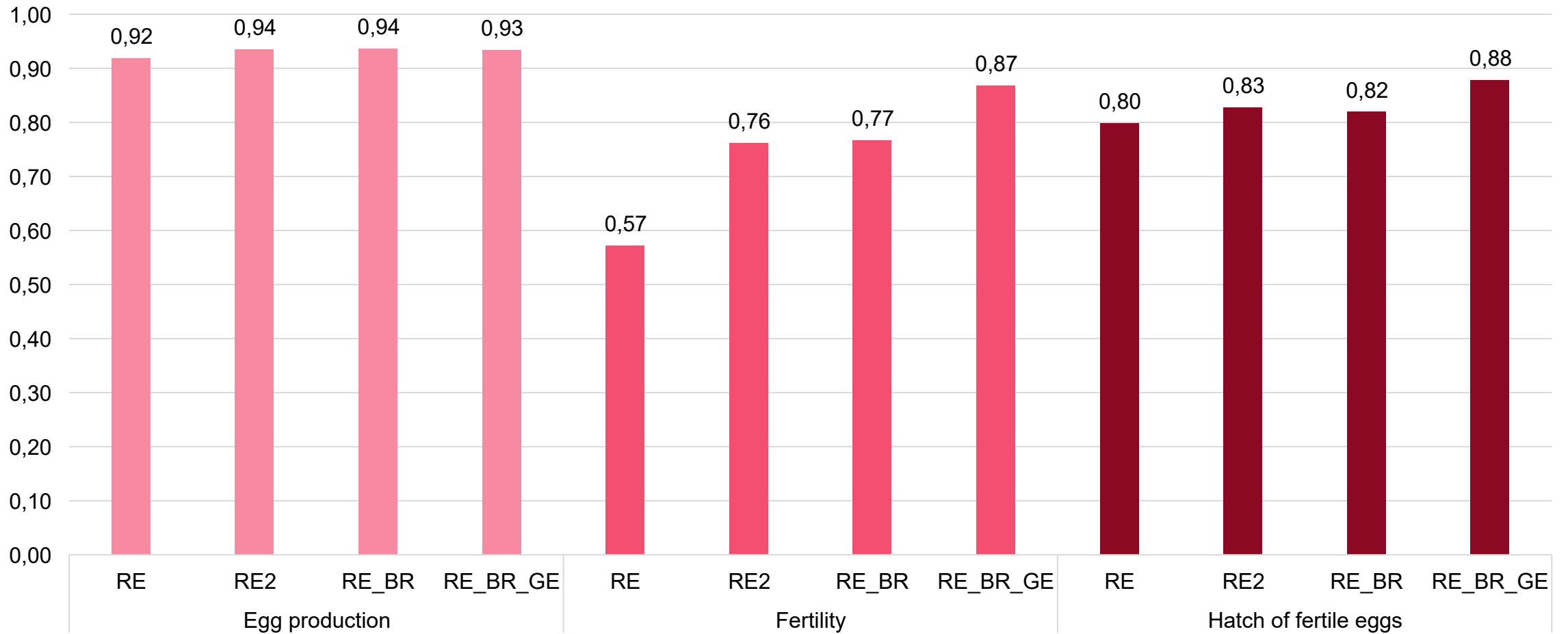
# Results - Bias

Roosters



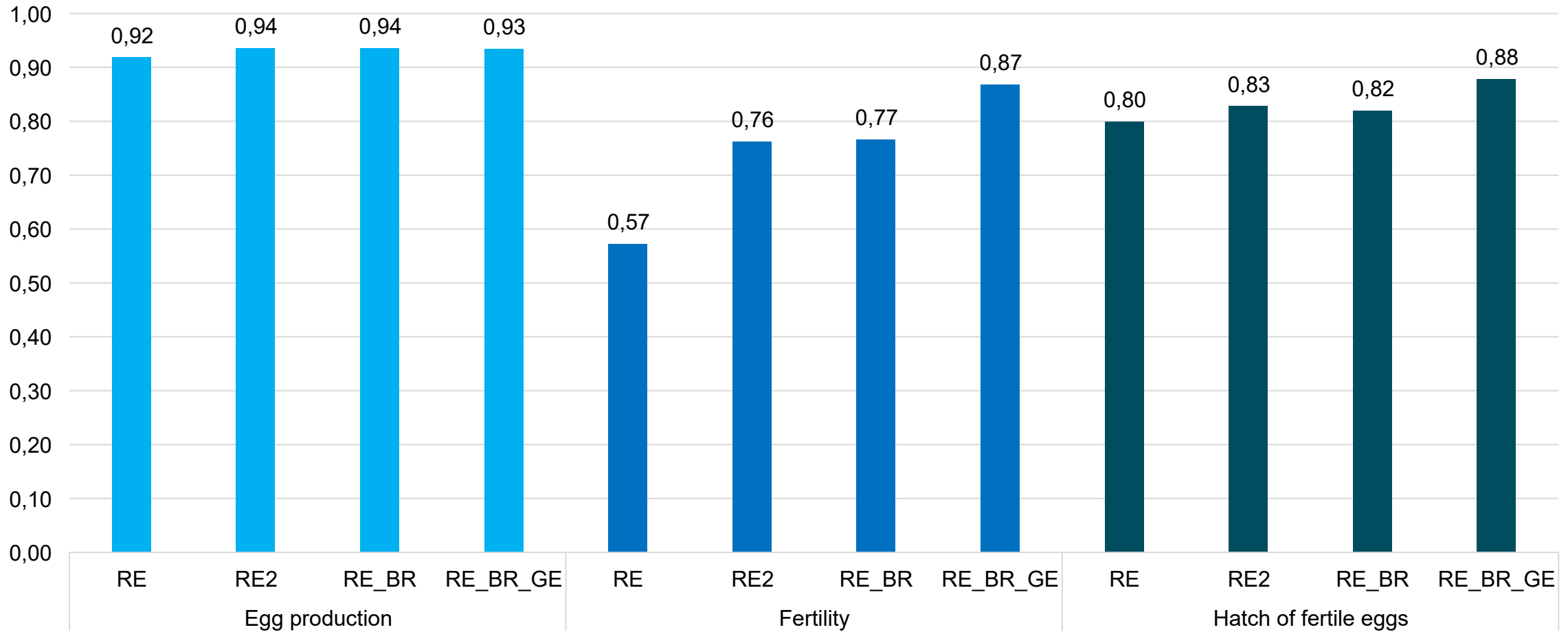
# Results - Dispersion

Hens



# Results - Dispersion

Roosters



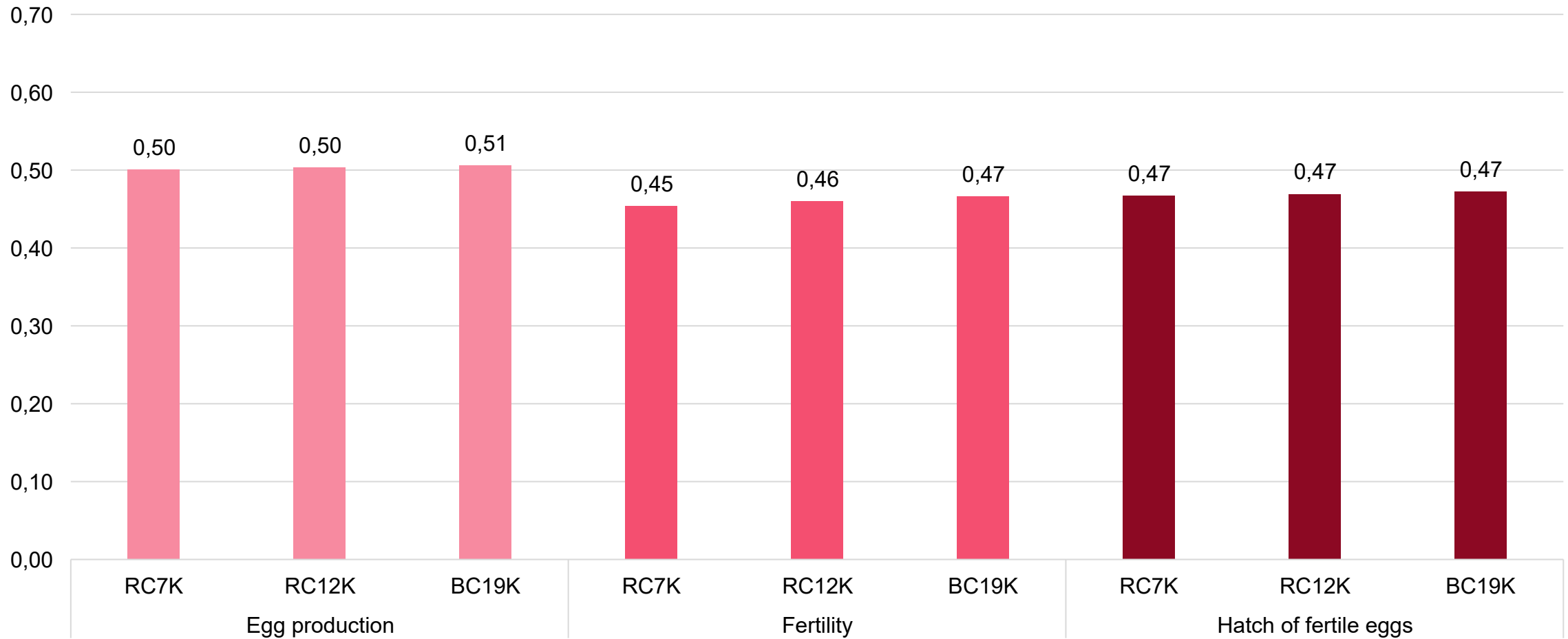
# How to reduce computing time?

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

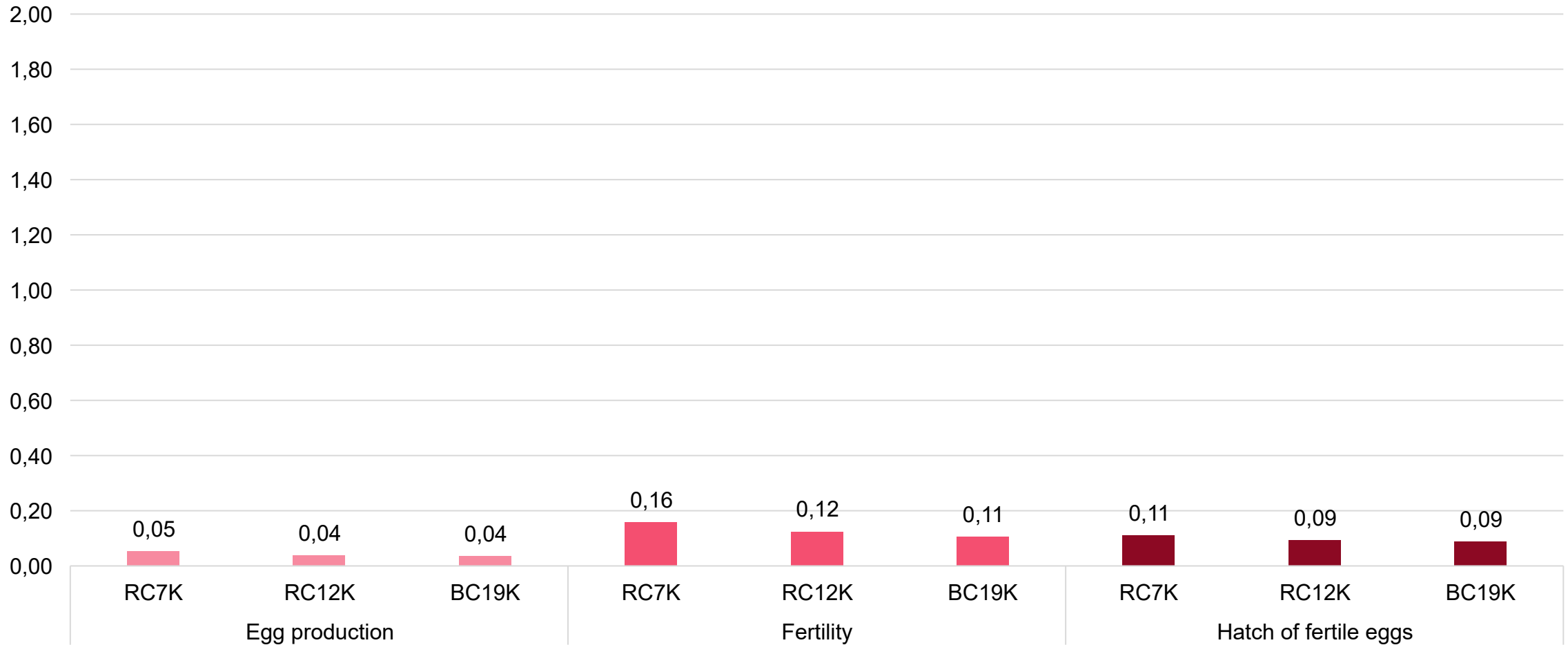
# Results - Accuracy

Hens



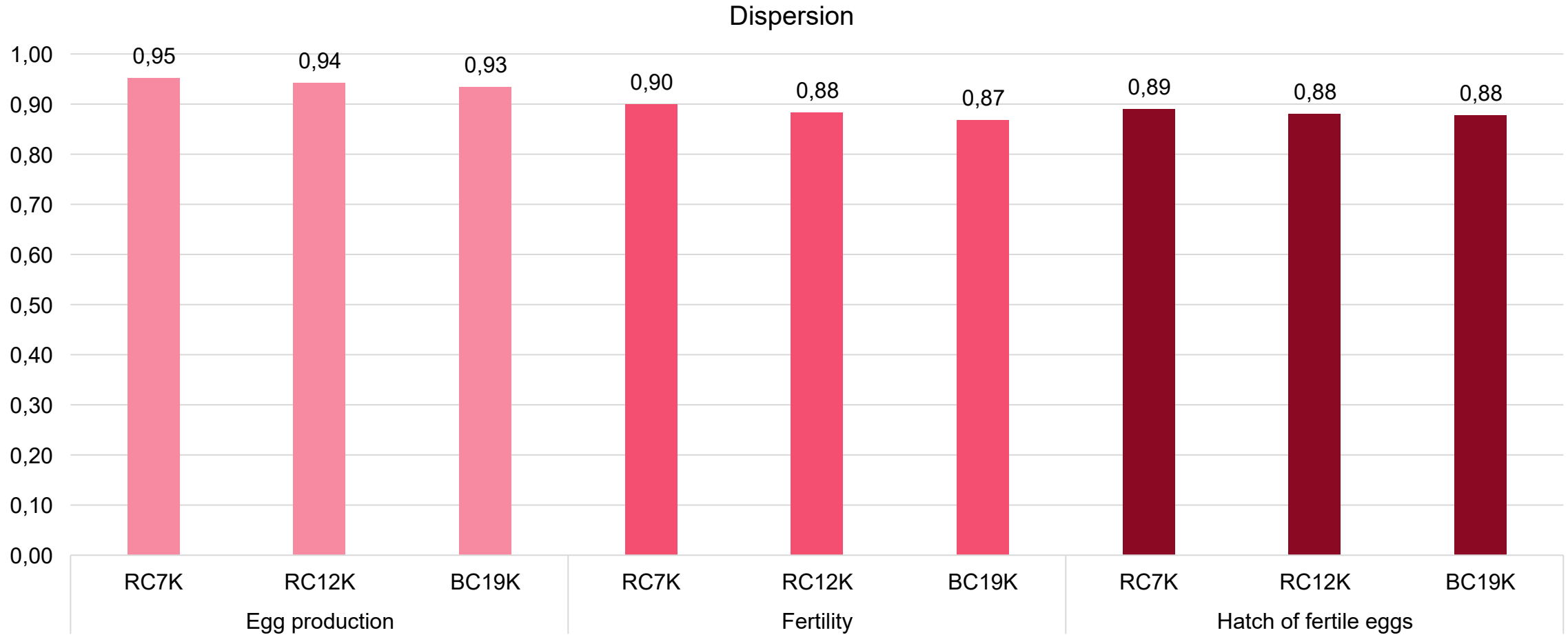
# Results - Bias

Hens

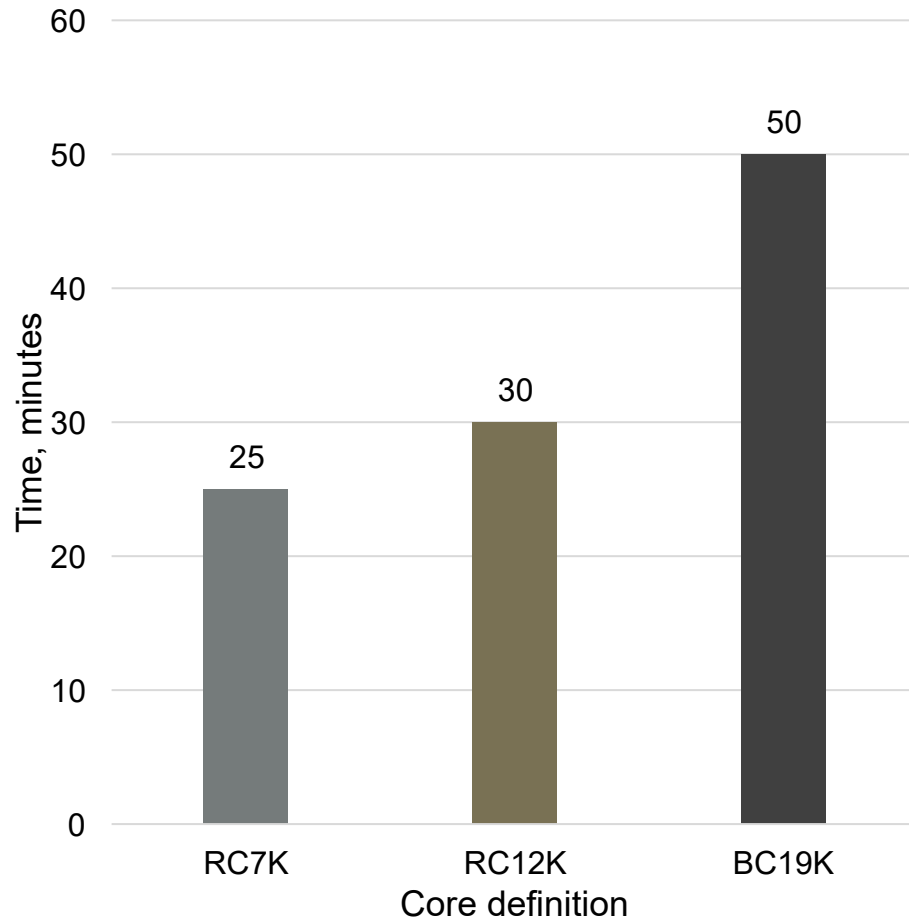


# Results - Dispersion

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!!!