Future Beef cross

"to calculate accurate breeding values for feed efficiency, methane emission and eating quality"

2019-2023

Mahmoud Shirali

2023.08.18

Experimental setup

Project started January 2020

Beef on Dairy crosses on Holstein dams

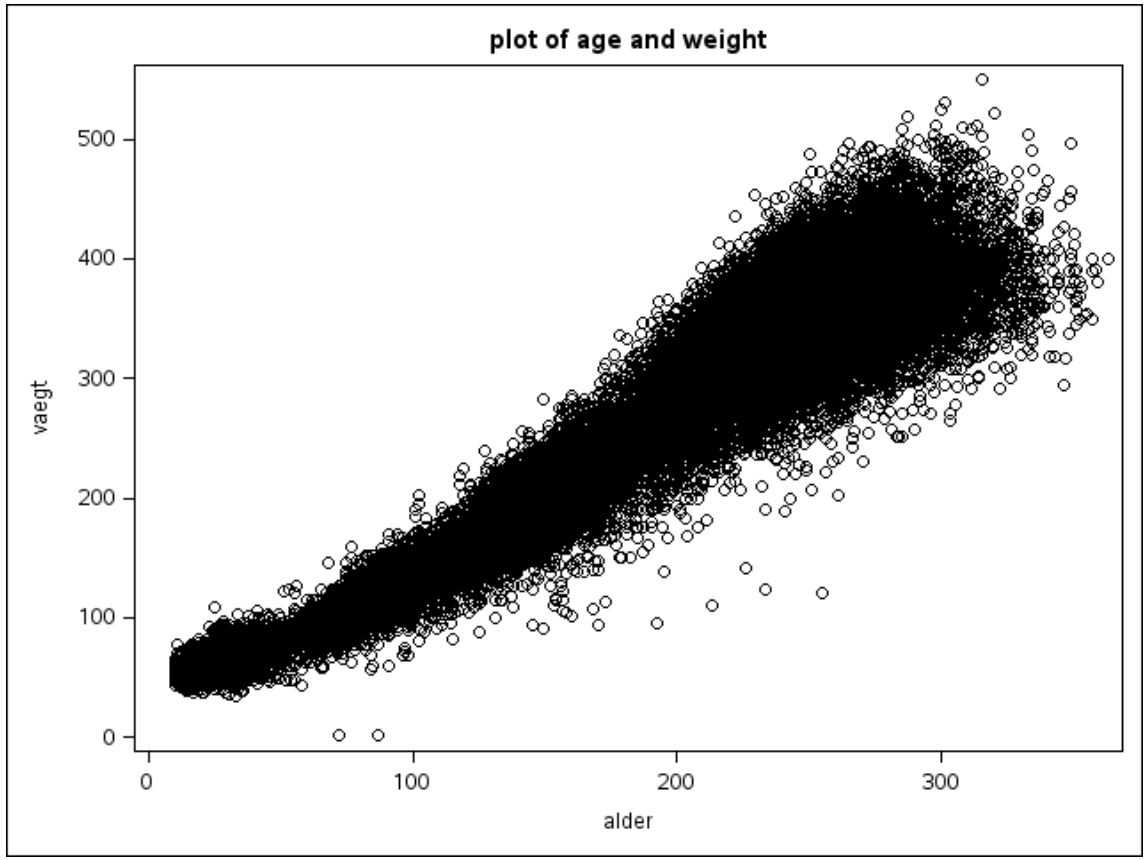
- Belgian Blue
- Charolaise
- Angus

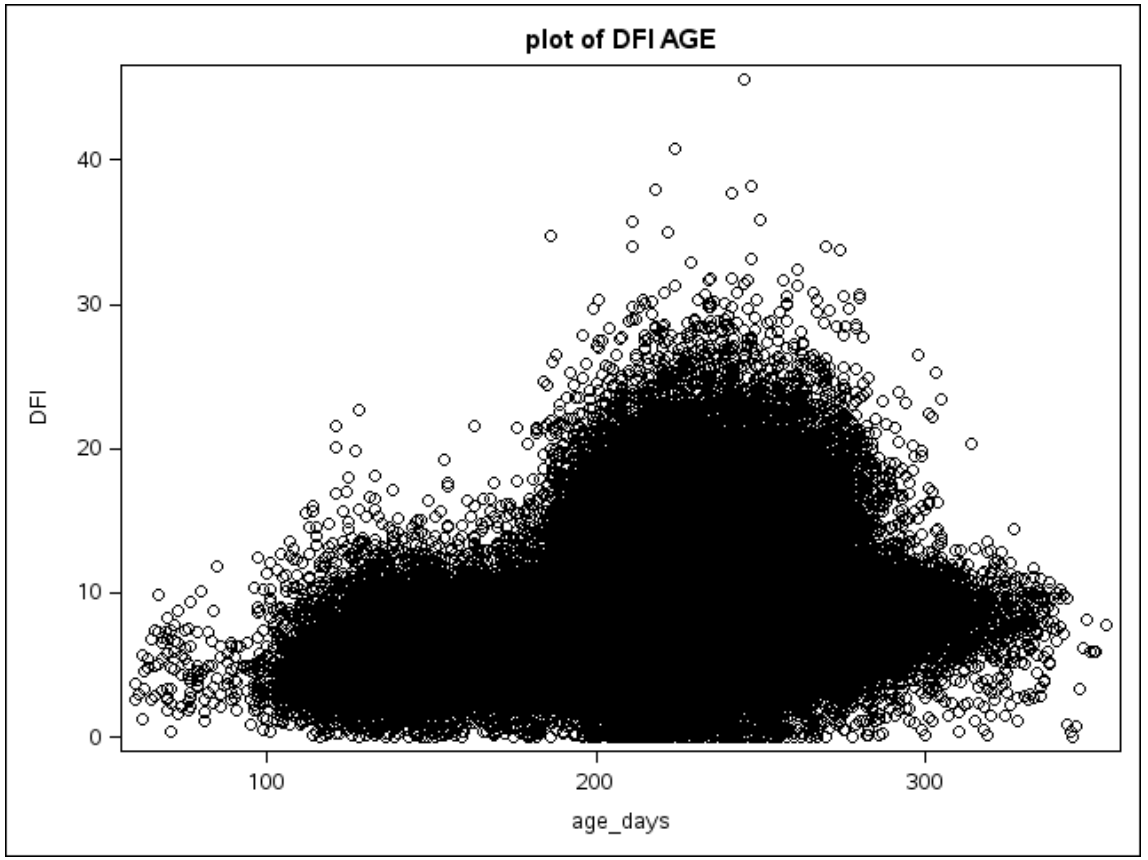
5 commercial slaughter calf herds

- 8 sniffers connected to 6 feed boxes each
- Calves enter for 21 days on average

Feedboxes from Allflex danmark

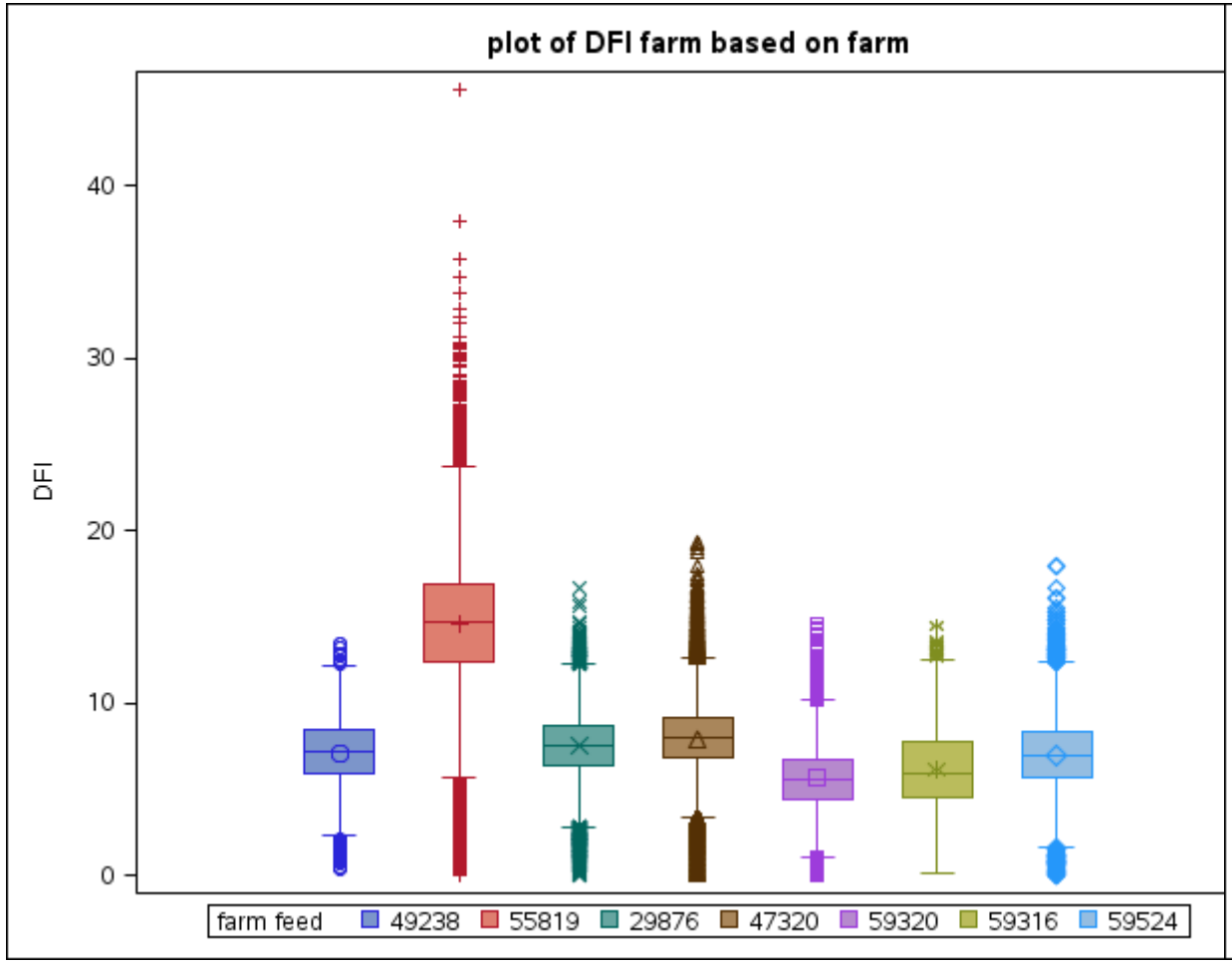
Raw daily feed and body weight data

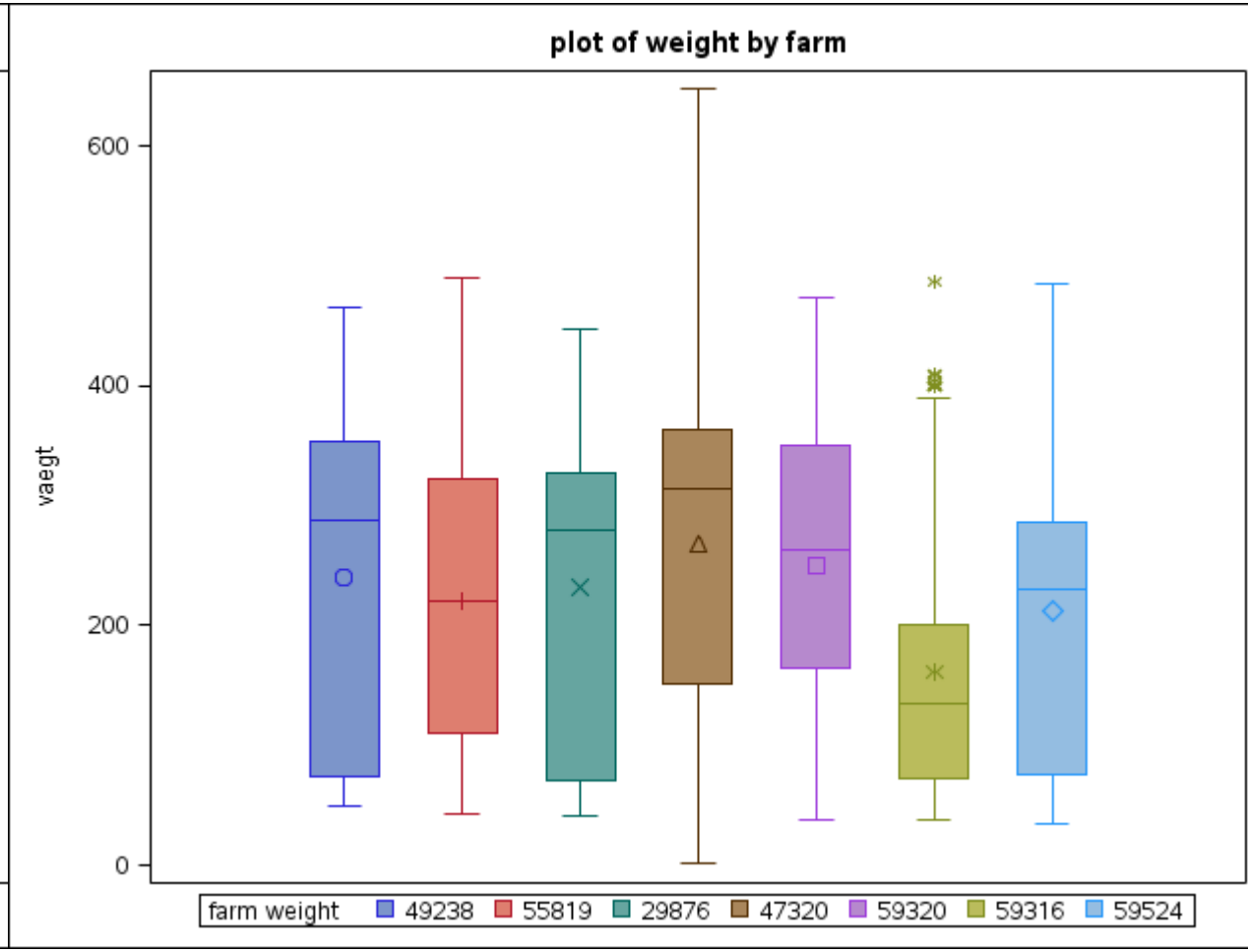




SEGES INNOVATION

Data overview





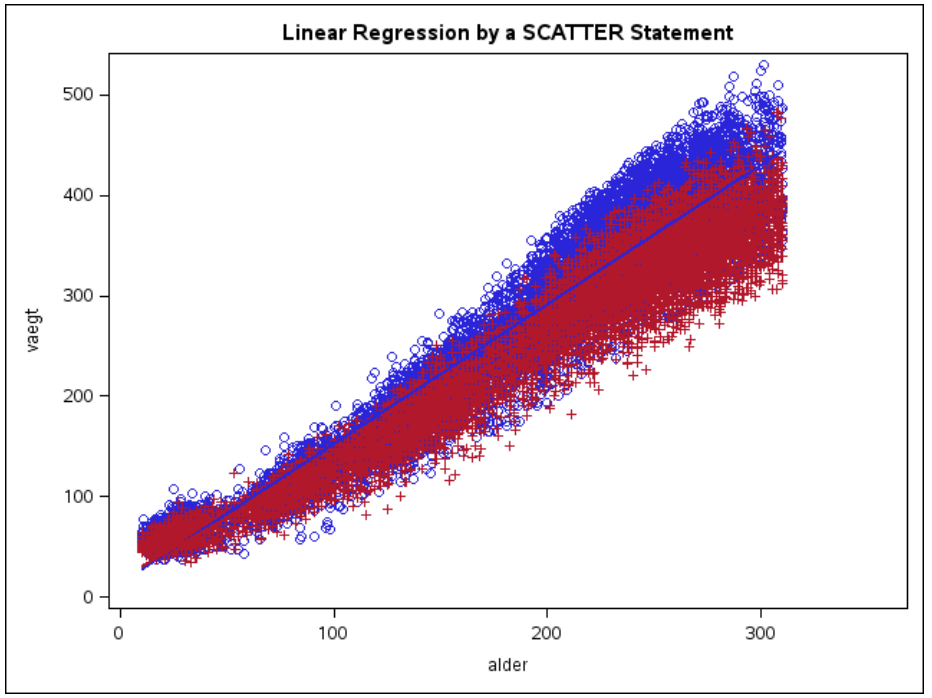
SEGES INNOVATION

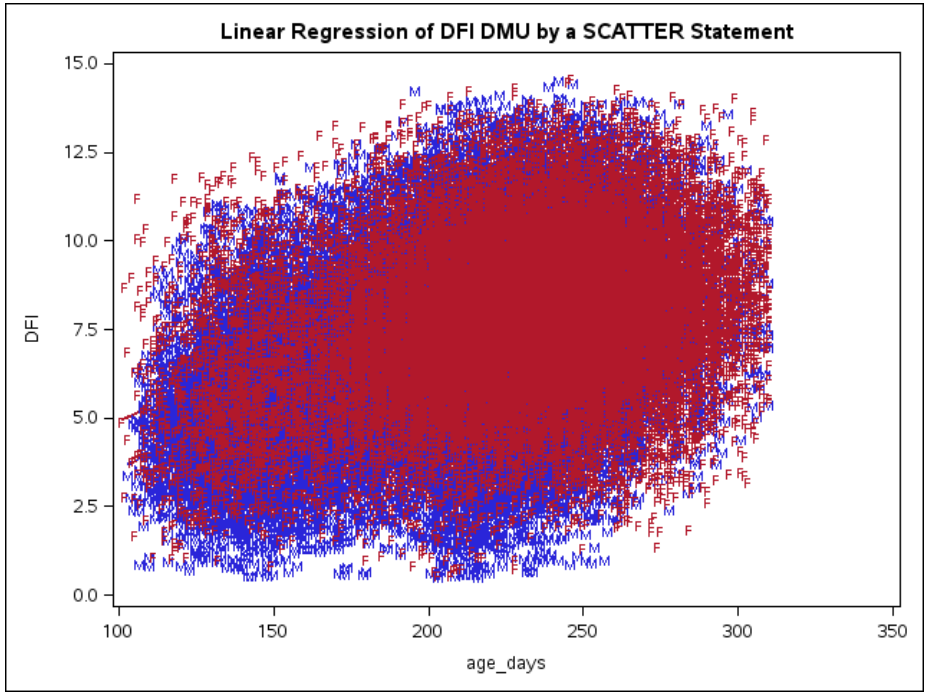
Data overview

Sire breeds	N crossbreds
BBL	4266
ANN	1124
CHA	898

Sex	N crossbreds
Male	3899
Female	2389

Year	N crossbreds
2020	1321
2021	1933
2022	2227
2023	807





SEGES INNOVATION

Bivariate random regression model

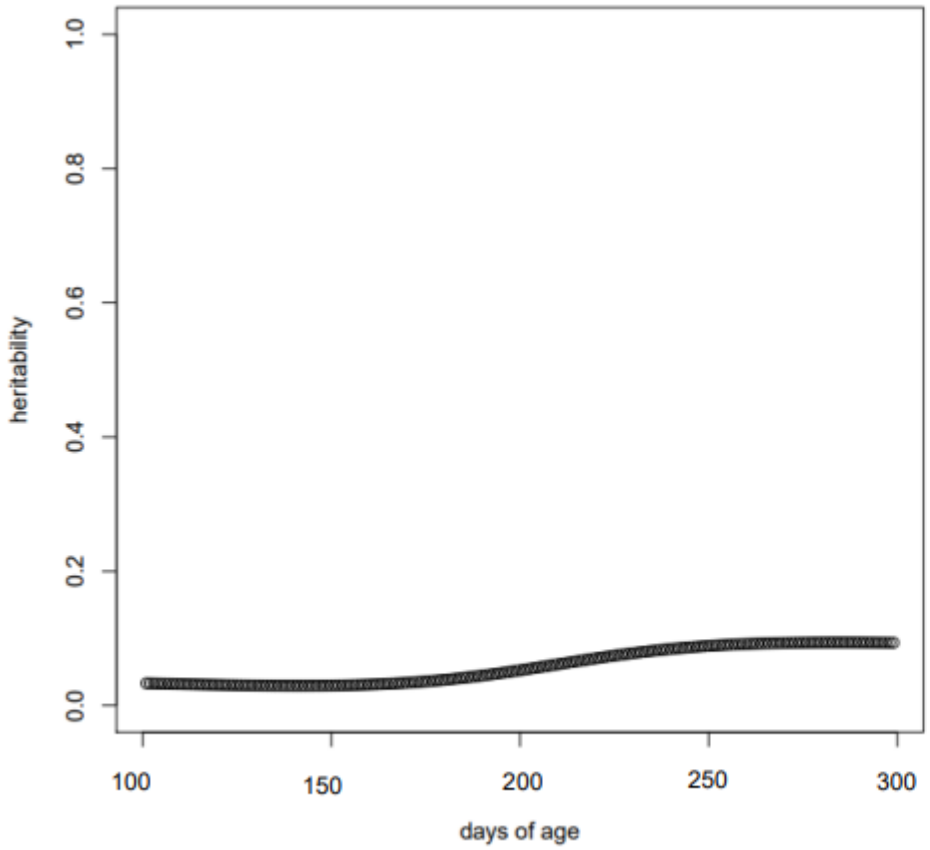
$$DDMI = HerdYearMonthGender + Sirebreed + Startage + Startagequadratic + lg1(Sirebreed + Gender + HerdYear) + lg1(genetics) + lg1(permanent\ environment) + e$$

$$BW = HerdYear + Gender + Sirebreed + lg1(Sirebreed + Gender + HerdYear) + lg2(Sirebreed + Gender + HerdYear) + lg1(genetics) + lg1(permanent\ environment) + e$$

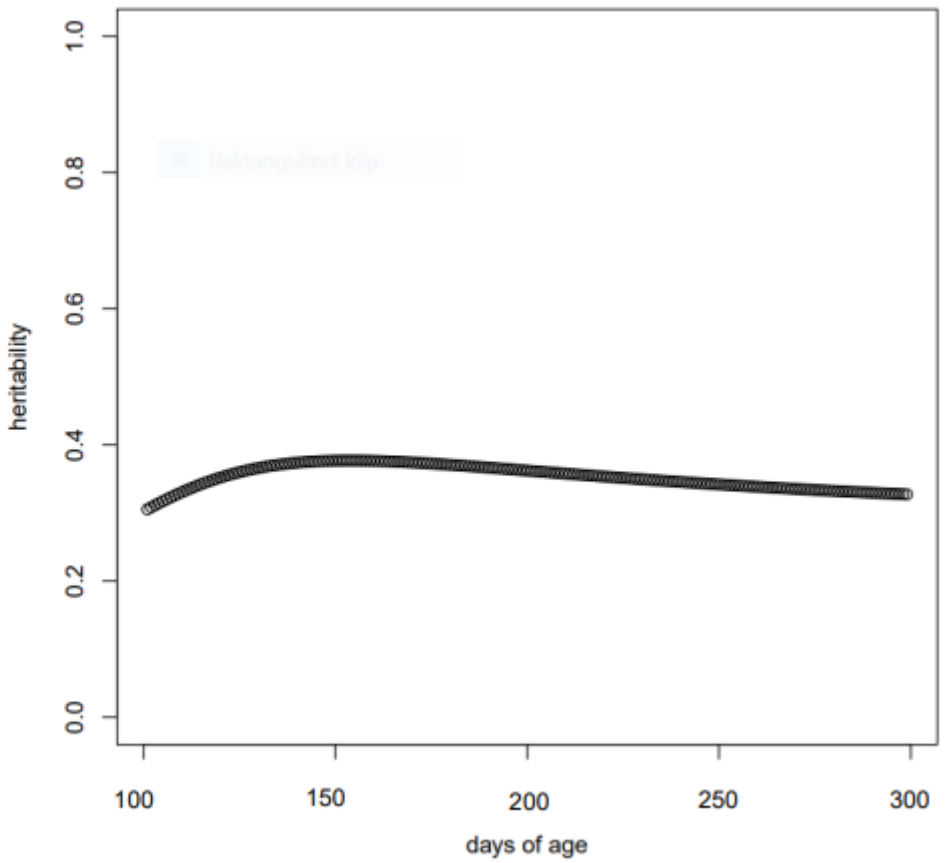
SEGES INNOVATION

Heritability graphs

DMI



BW



SEGES INNOVATION

RFI Calculation

Genetic RFI was calculated following Esfandiari and Jensen (2021) and Shirali et al. (2018).

$$RFI = TDMI - b_{gain}GAIN - b_{mbw}MBW$$

TDMI was the sum of DMI from 200 to 280 days of age.

$$a_{TDMI} = \sum_{t=200}^{280} l_{q1}(t)a_{DDMI}$$

GAIN was the total body weight gain during 200 to 280 days of age.

$$a_{GAIN} = (l_{q1}(t_{280}) - l_{q1}(t_{200}))'a_{BW}$$

MBW was the average body weight during 200 to 280 days of age.

$$a_{MBW} = \frac{1}{2}(l_{q1}(t_{280}) + l_{q1}(t_{200}))'a_{BW}$$

b_{gain} and b_{mbw} are the regression coefficients obtained from Genetic variance covariance matrix.

$$b_{TDMI|\mathrm{GAIN,MBW}} = G_{TDMI|\mathrm{GAIN,MBW}}G^{-1}_{GAIN,MBW}$$

SEGES INNOVATION

Feed efficiency complex

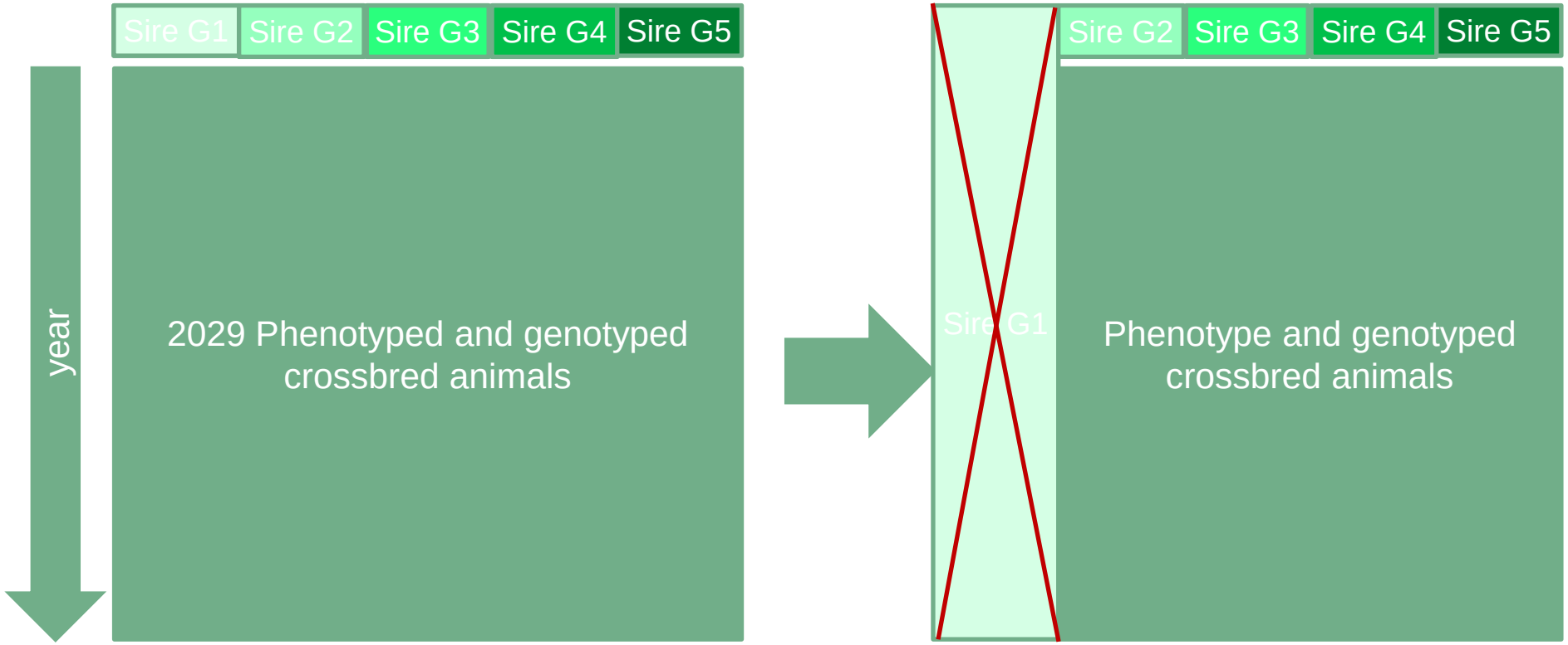
The heritabilities (diagonal) and genetic correlations (off diagonal) are as follow:

	TDMI	RFI	GAIN	MBW
TDMI	0.24			
RFI	0.84	0.21		
GAIN	0.43	-0.12	0.21	
MBW	0.46	0.00	0.80	0.35

$\frac{a^2_{RFI}}{a^2_{TDMI}} = \frac{484}{675}$ 72% of genetic variance in DMI is explained by RFI

SEGES INNOVATION

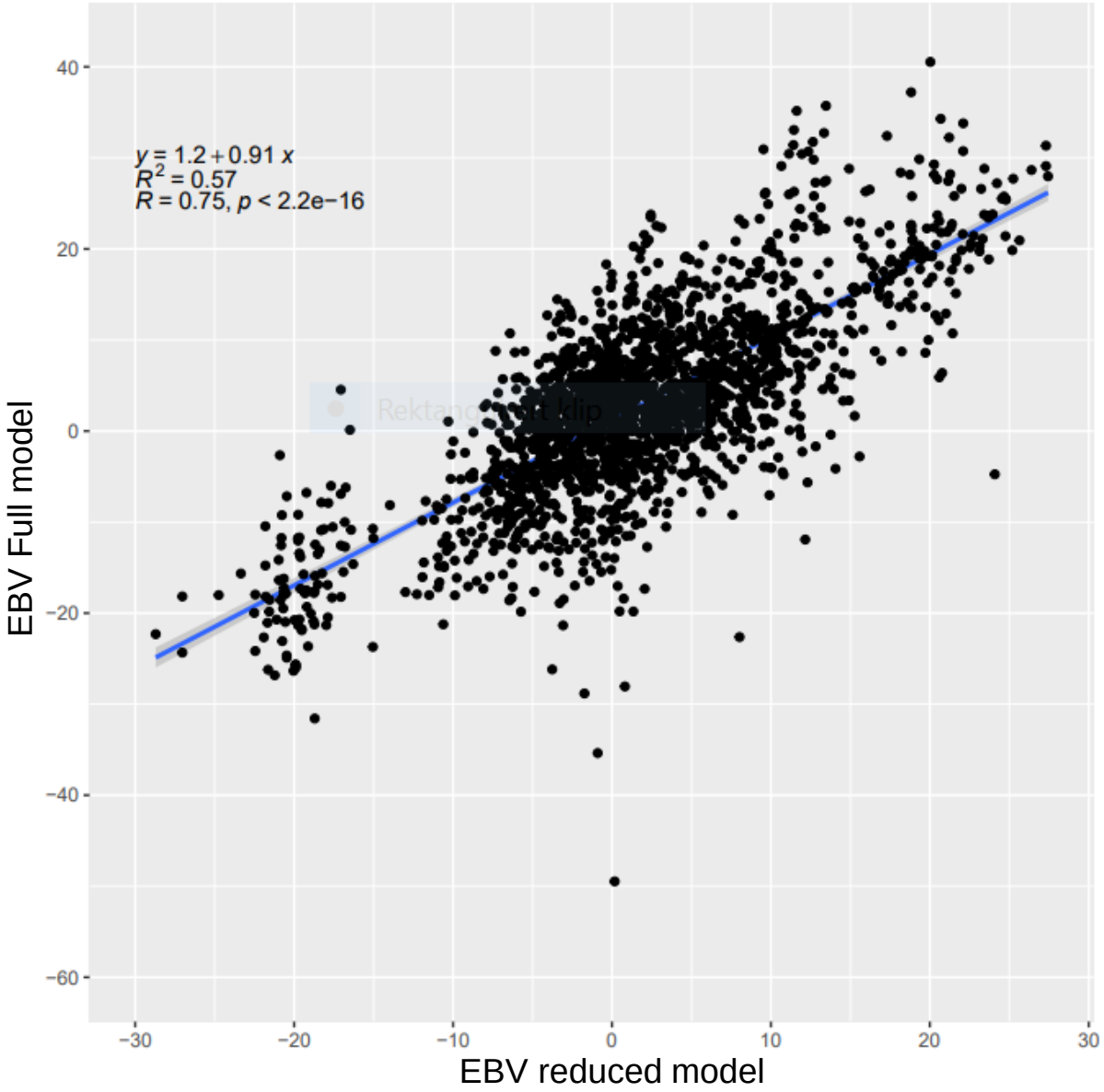
Cross Validation approach for feed efficiency

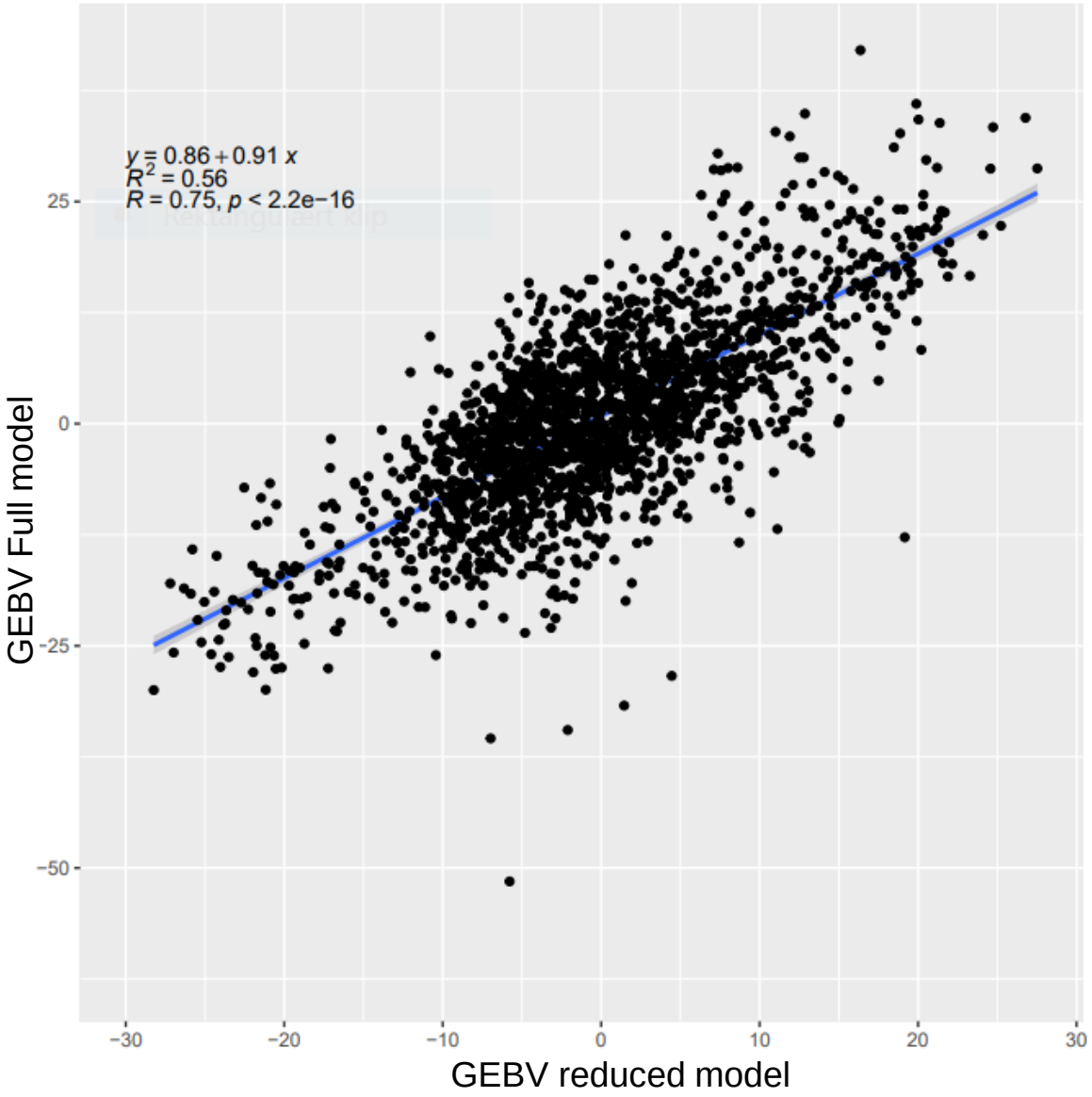


Scenarios	Number of animals	Number of sires
Sire G1	305	10
Sire G2	438	10
Sire G3	479	10
Sire G4	481	10
Sire G5	326	34

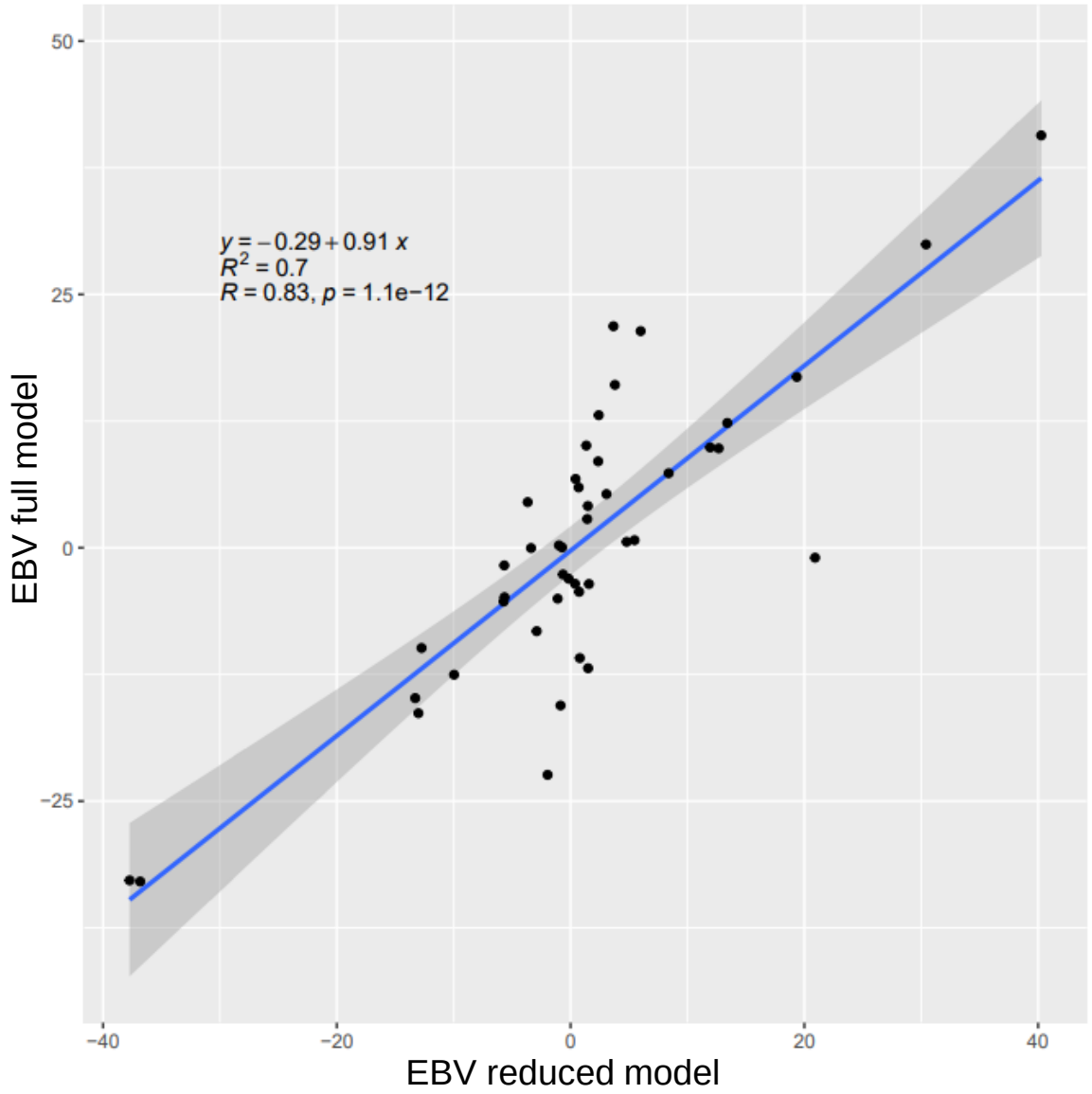
SEGES INNOVATION

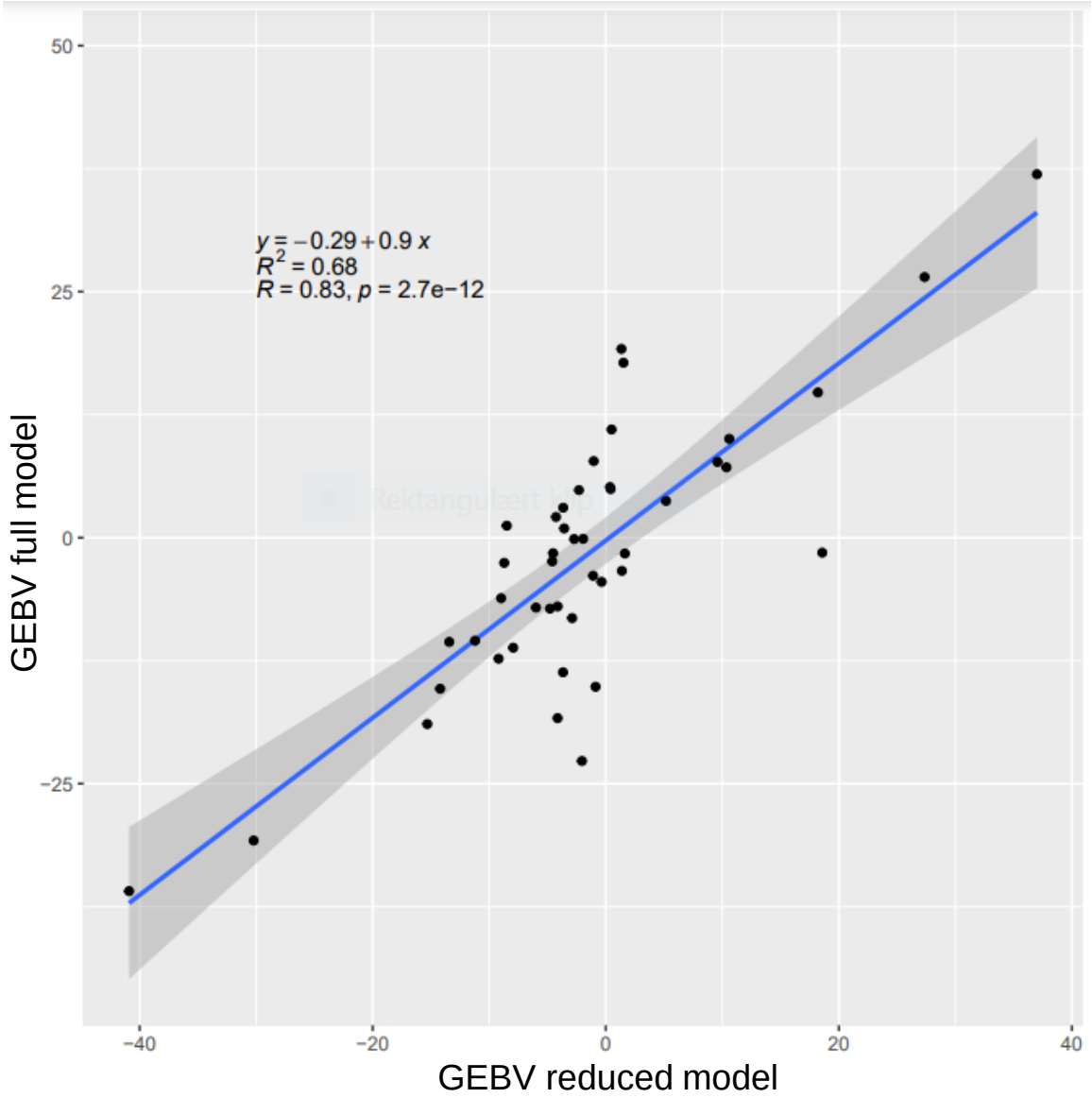
Crossvalidation: Crossbred PBLUP vs SSGBLUP





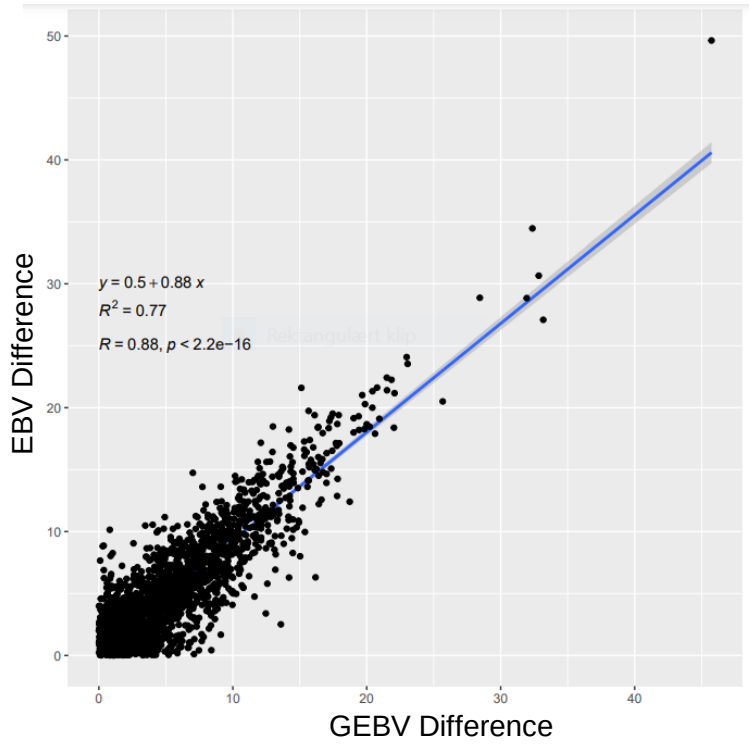
Crossvalidation: BBL Bulls PBLUP vs SSGBLUP

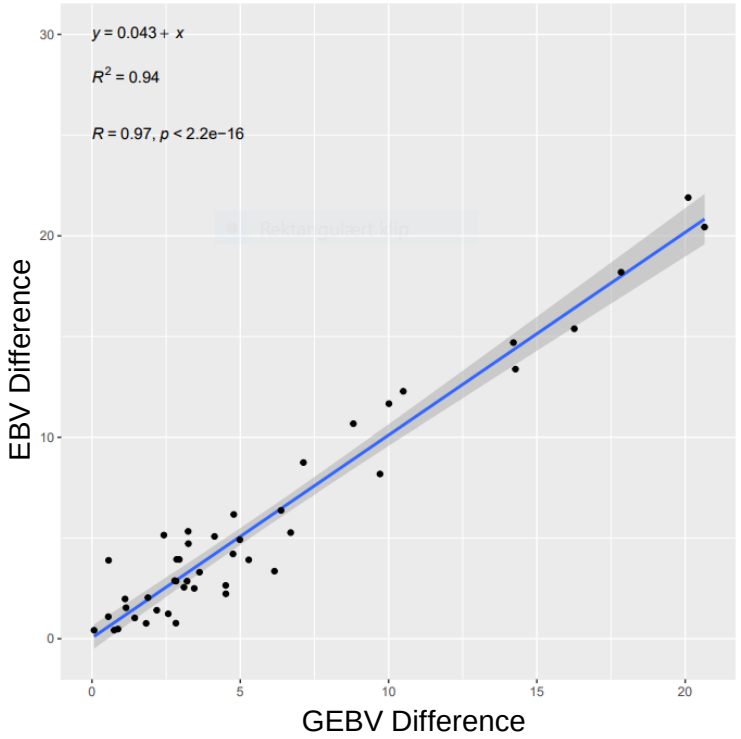




Difference between Breeding values from Full and reduced models for crossbred & bulls: Pedigree vs SSGBLUP

	Crossbreds		Bulls	
	Mean	SD	Mean	SD
PBLUP	5.27	4.58	5.71	5.52
SSGBLUP	5.44	4.59	5.63	5.32





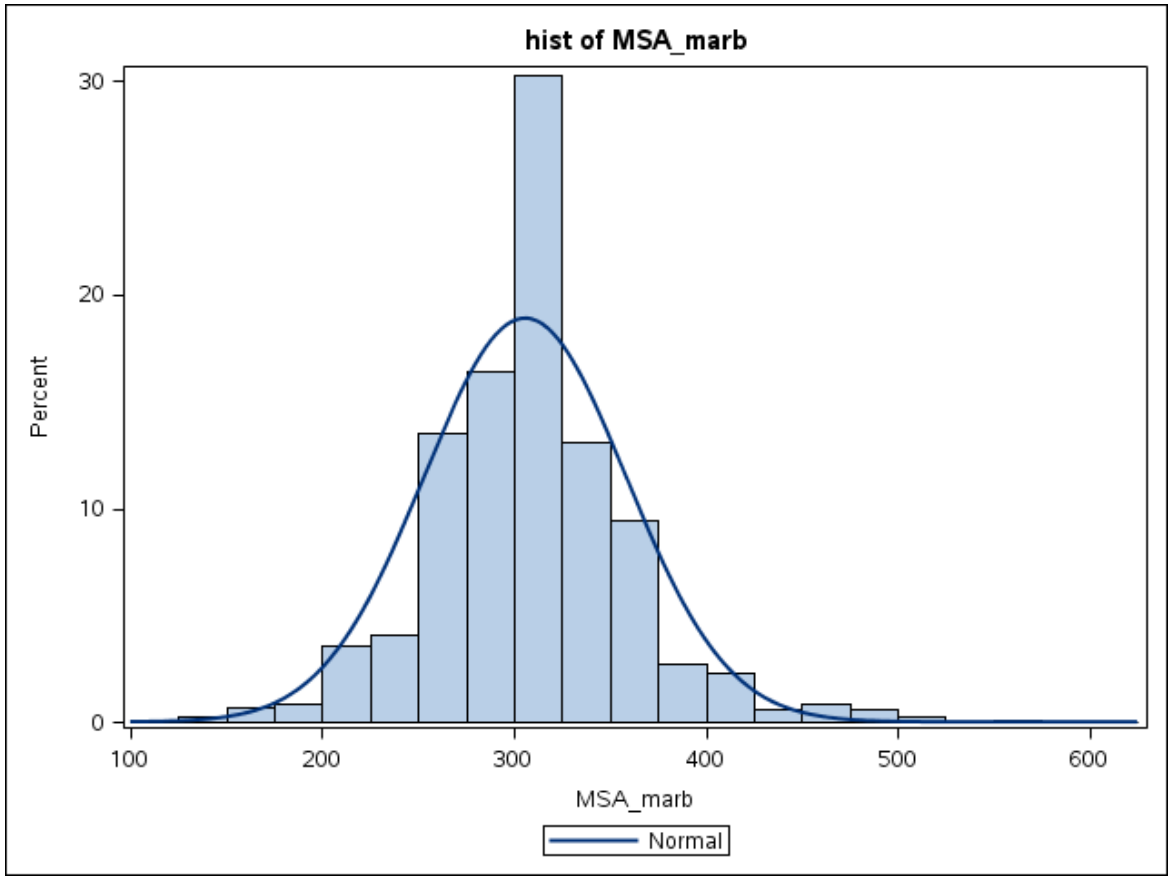
SEGES INNOVATION

Phenotypic performance of elite animals

500 gram feed intake per day less in offspring of top 10 bulls compared to 10 bottom bulls

SEGES INNOVATION

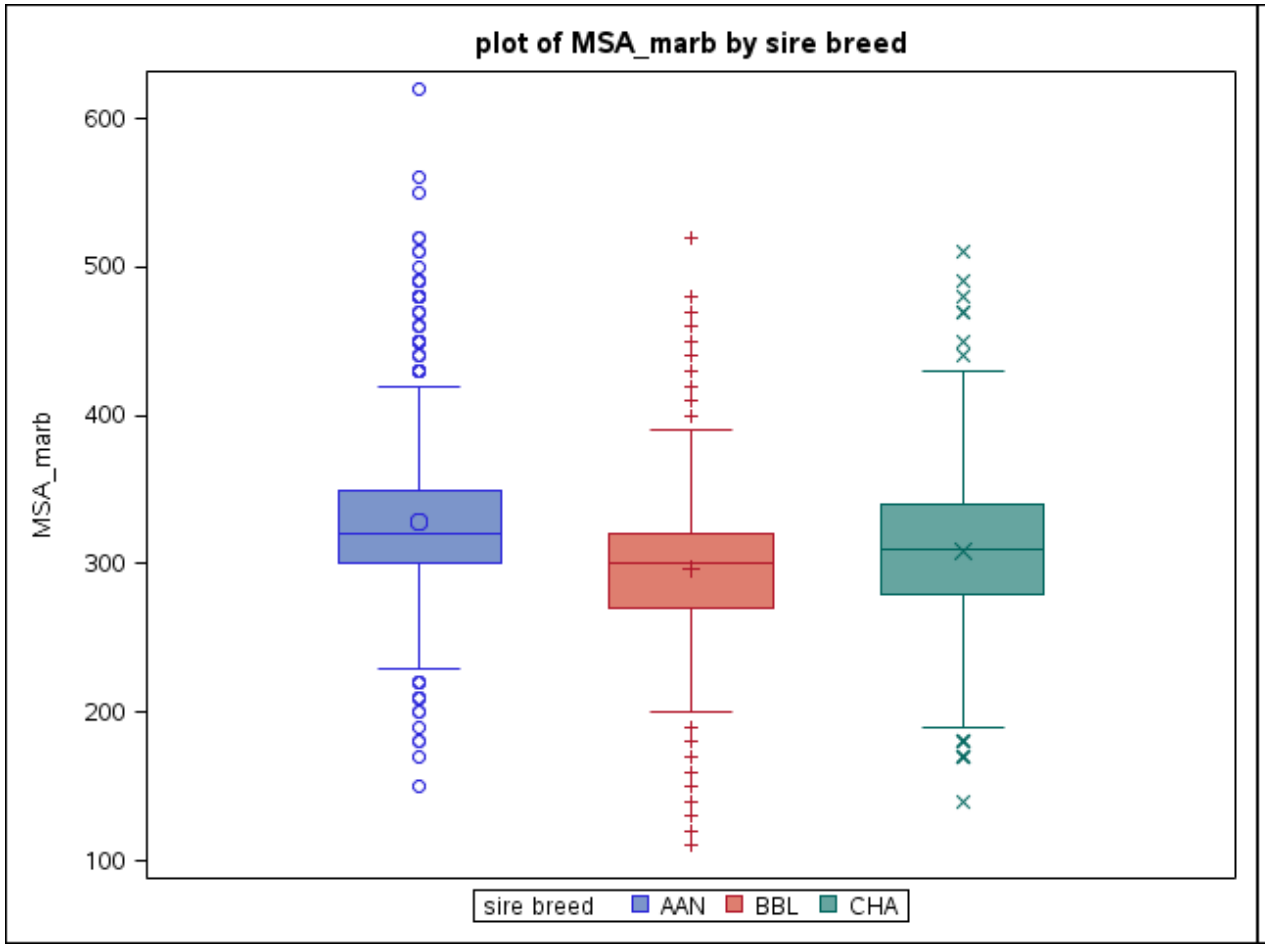
Marbling Score

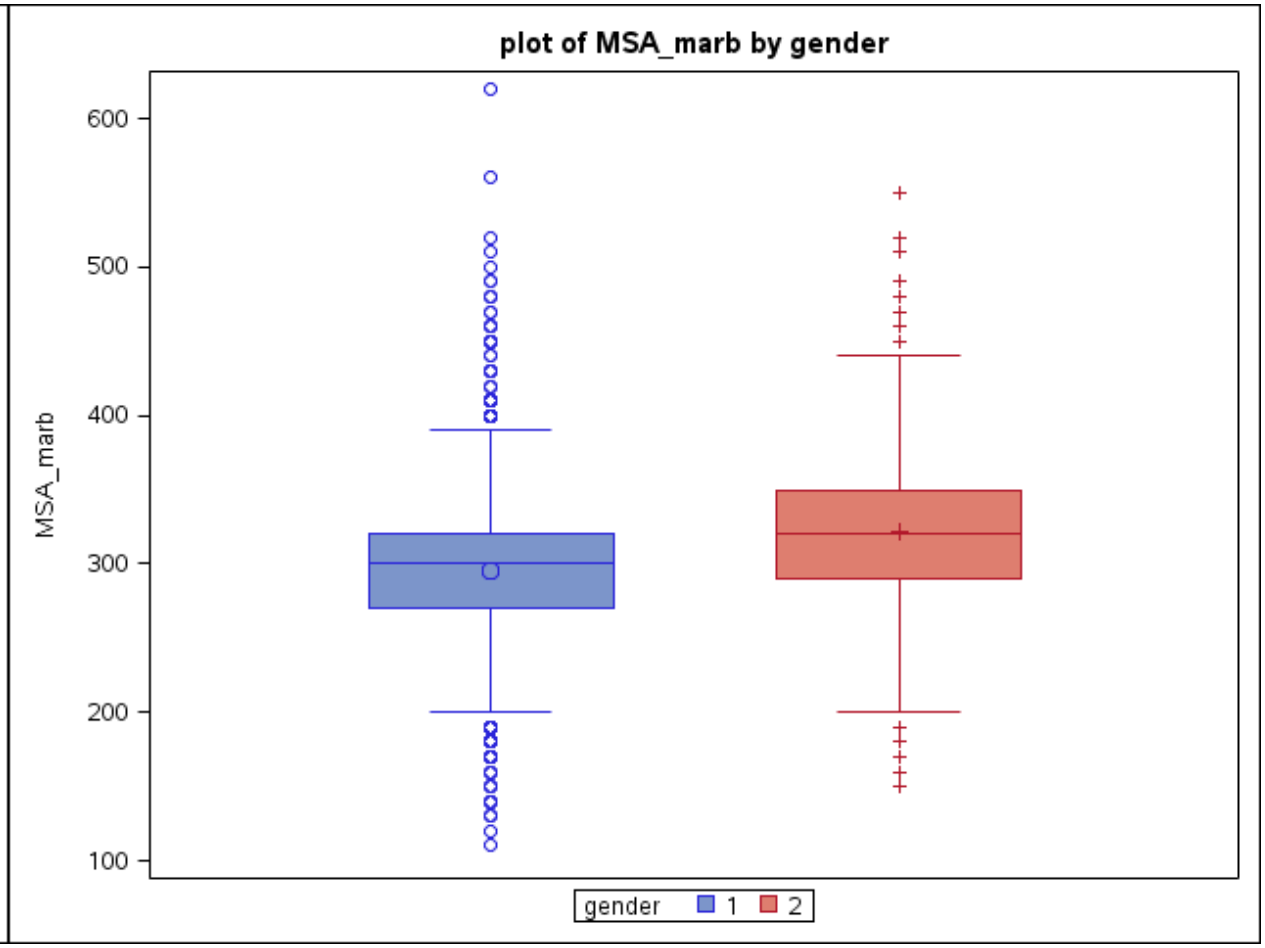


Sire breeds	N crossbreds
BBL	1686
ANN	622
CHA	456

SEGES INNOVATION

Marbling Score





SEGES INNOVATION

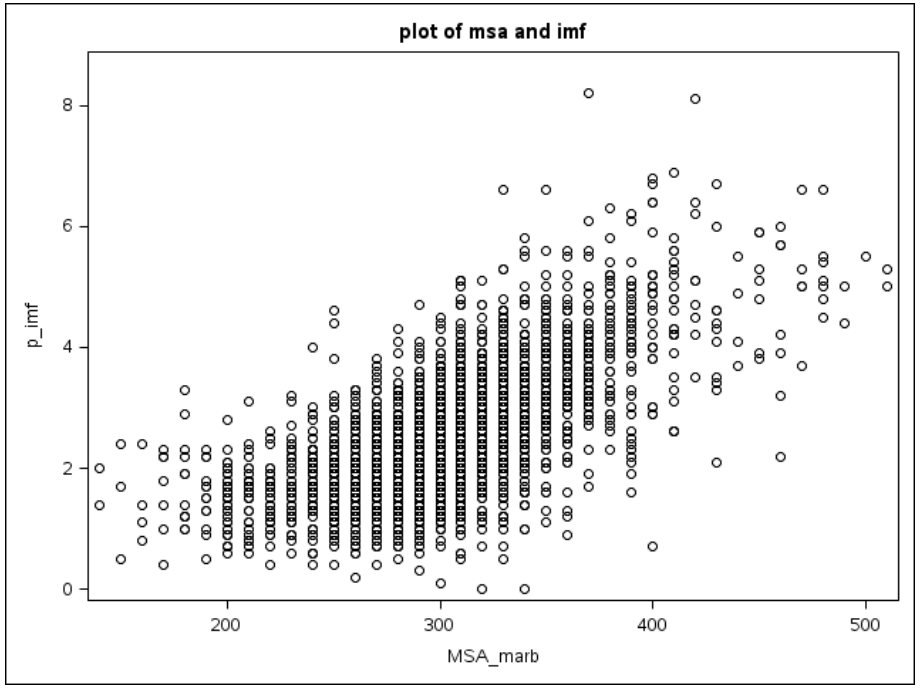
Crossbred animals of BBL sires and HOL dam

	N Crossbred
Male	1029
Female	657

Herd	N Crossbred
29876	207
47320	931
55819	447
59524	101

Year	N Crossbred
2020	39
2021	465
2022	790
2023	392

	Mean	SD
Marbling score	296	44
IMF	2.3	1
Slaughter age	289	20



SEGES INNOVATION

Univariate BLUP

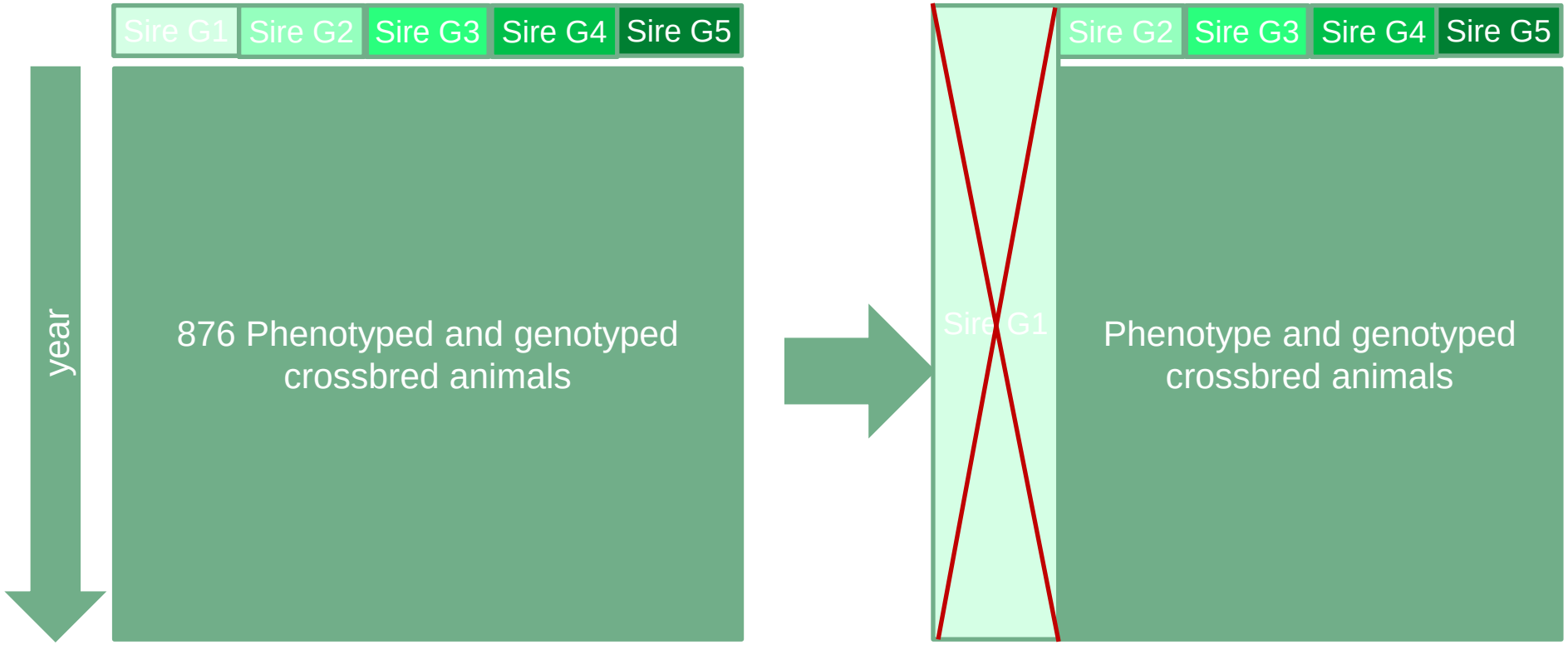
MS = SlaughterYearMonthHerd + Sex + slaugher age + a + e

	Pedigree BLUP	
	Genetic variance	Heritability
Marbling score	243 (96)	0.15
IMF	0.097 (0.038)	0.15

Average heritabilities published for MS : 0.45 (0.12-0.80)
IMF and MS have 0.93 (0.09) genetic correlation

SEGES INNOVATION

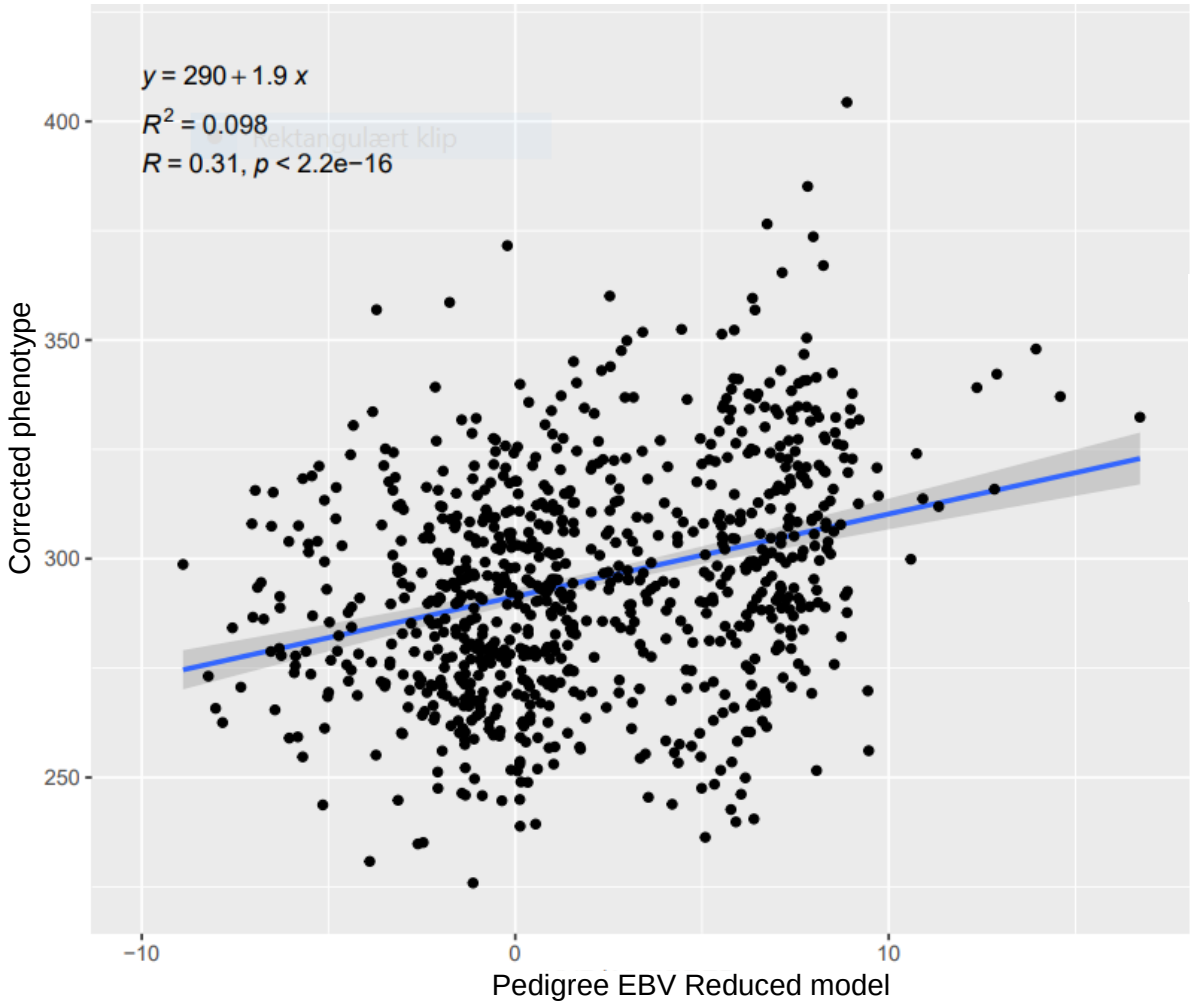
Cross Validation approach for Marblig Score

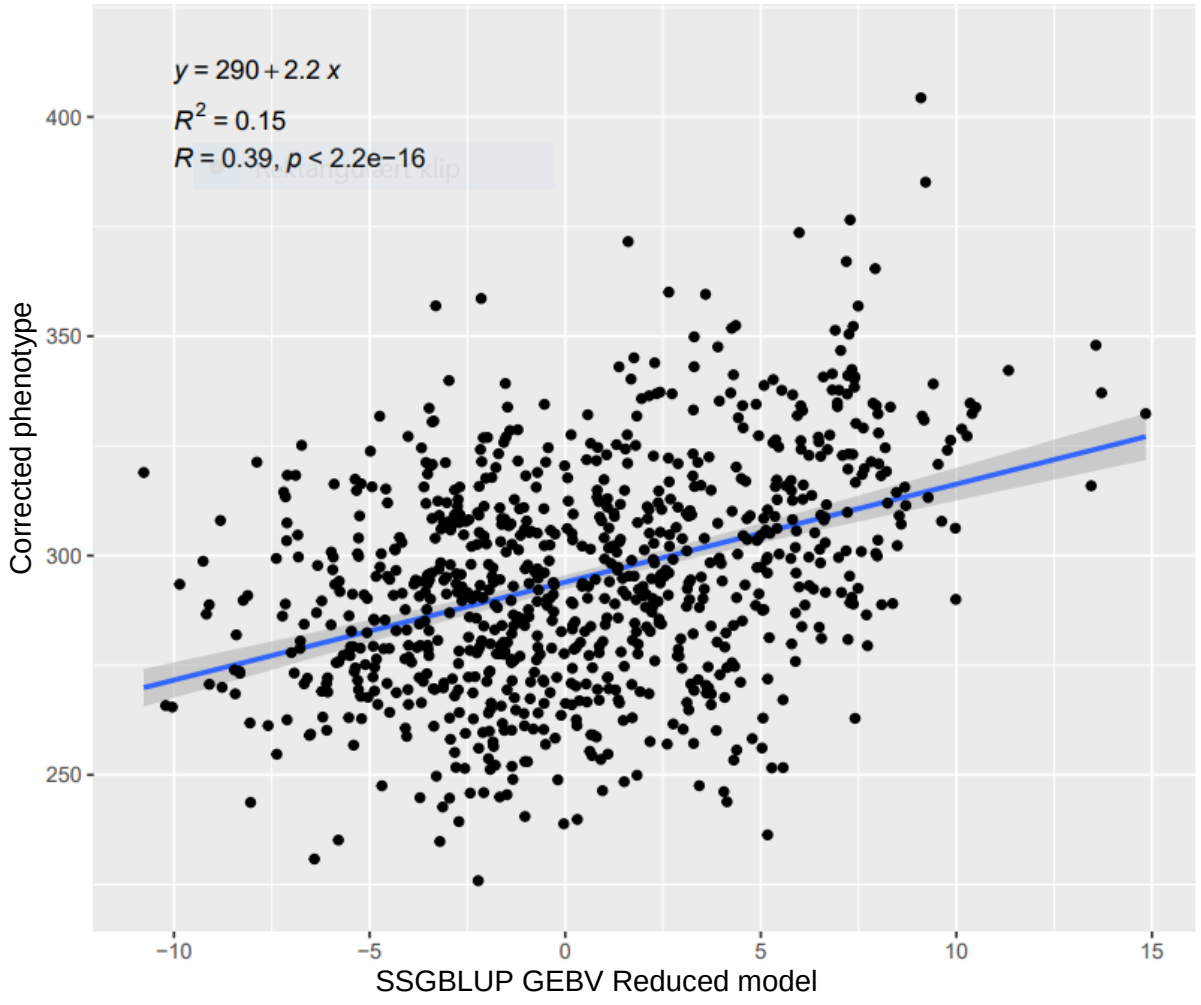


Scenarios	Number of animals	Number of sires
Sire G1	159	10
Sire G2	187	10
Sire G3	84	10
Sire G4	286	10
Sire G5	160	25

SEGES INNOVATION

Crossbred animals: Pedigree vs. SSGBLUP

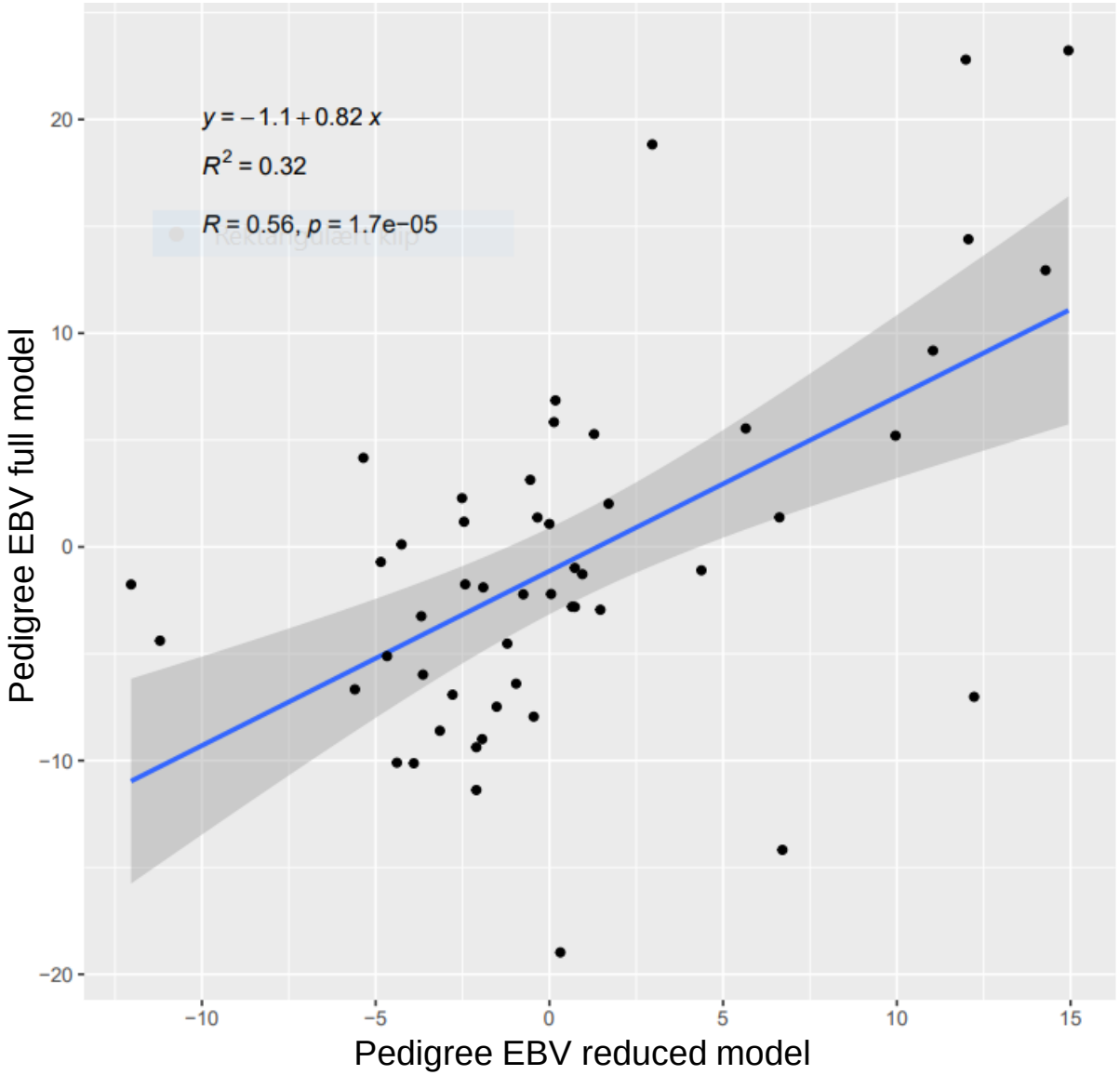


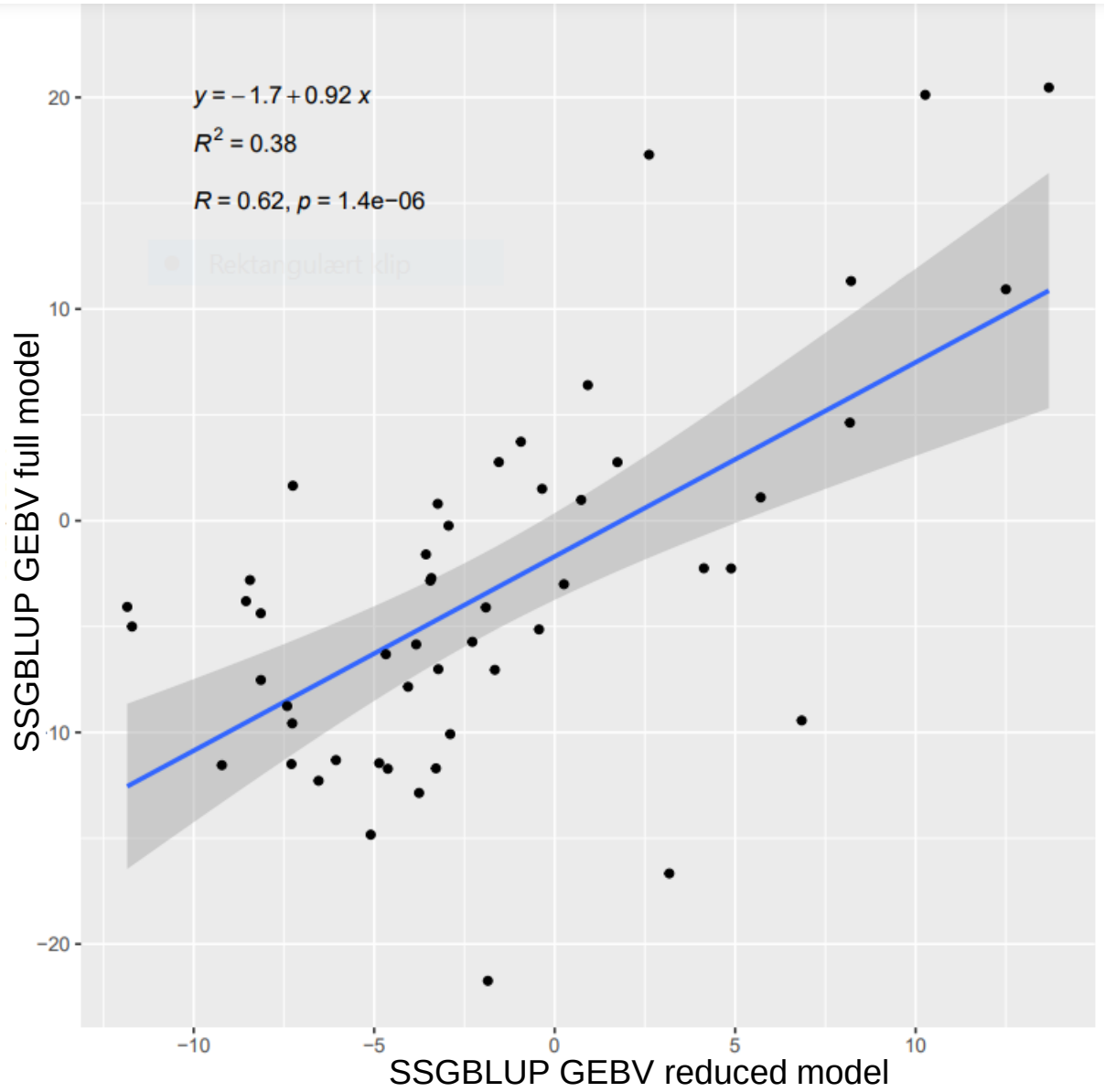


- $r_{g\hat{g}} = cor(g, \hat{y})/\sqrt{h^2}$
- $\hat{y} = GEBV + e$ from SSGBLUP full model

SEGES INNOVATION

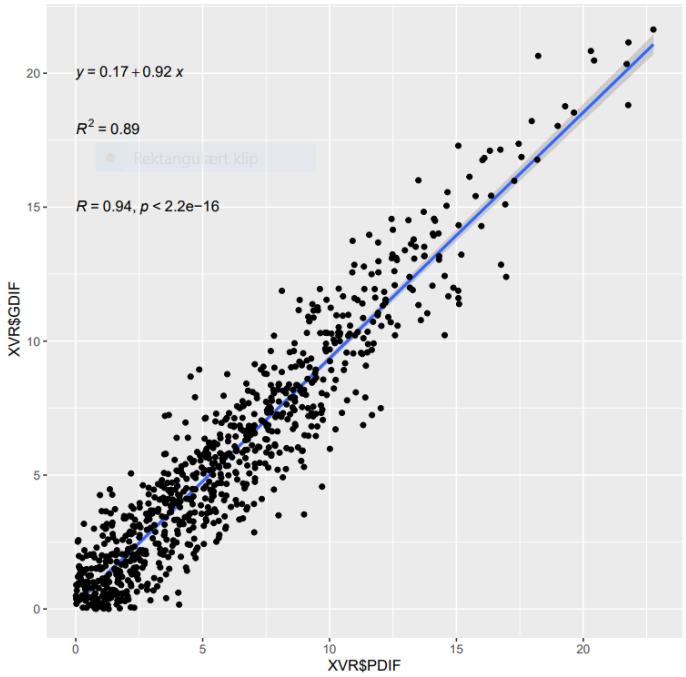
BBL bulls: Pedigree vs. SSGBLUP same analysis as for crossbreds

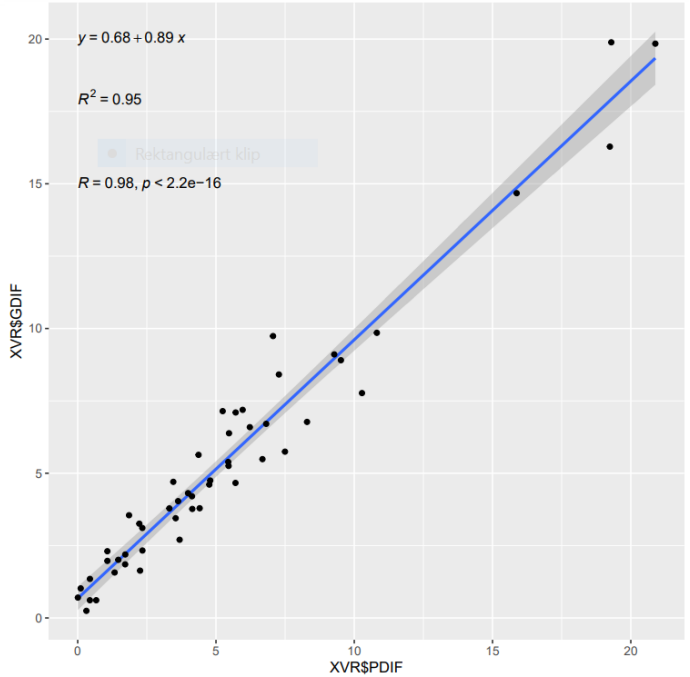




Difference between Full and reduced models for crossbred & bulls: Pedigree vs SSGBLUP

	Crossbreds		Bulls	
	Mean	SD	Mean	SD
PBLUP	5.90	4.35	5.37	4.80
SSGBLUP	5.59	4.23	5.50	4.43





SEGES INNOVATION

Phenotypic performance of elite animals

29 score (0.66 SD) higher Marbling score in offspring of top 10 bulls compared to bottom 10 bulls

SEGES INNOVATION