Department of
Agriculture,
Food and the Marine
An Roinn
Talmhaíochta,
Bia agus Mara

Multi-breed beef genomics

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[3] Wageningen, [4] Weatherbys

ICBF Industry Meeting, Roganstown, Nov 2014

teagasc
Agriculture and Food Development Authority

The Irish Agriculture and Food Development Authority

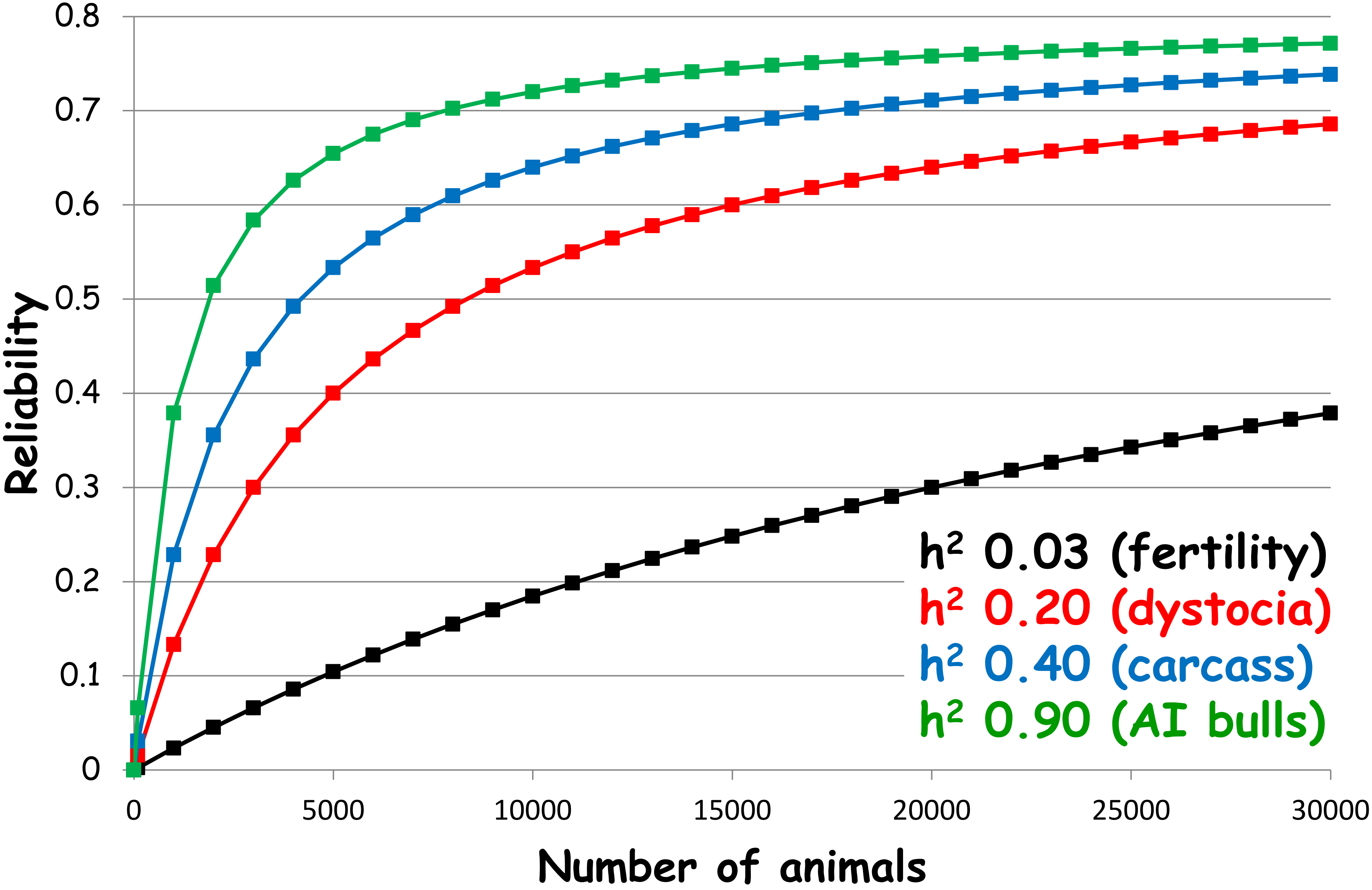
Beef genomics scheme

- Financial incentive to genotype at least 15% of cows (plus natural mating bull) in particip
- All natu genotyped
- Cows ch
- Objective
  - To d -breed beef urebred and crossbred) cattle
    - Must be across all breeds (big and small)

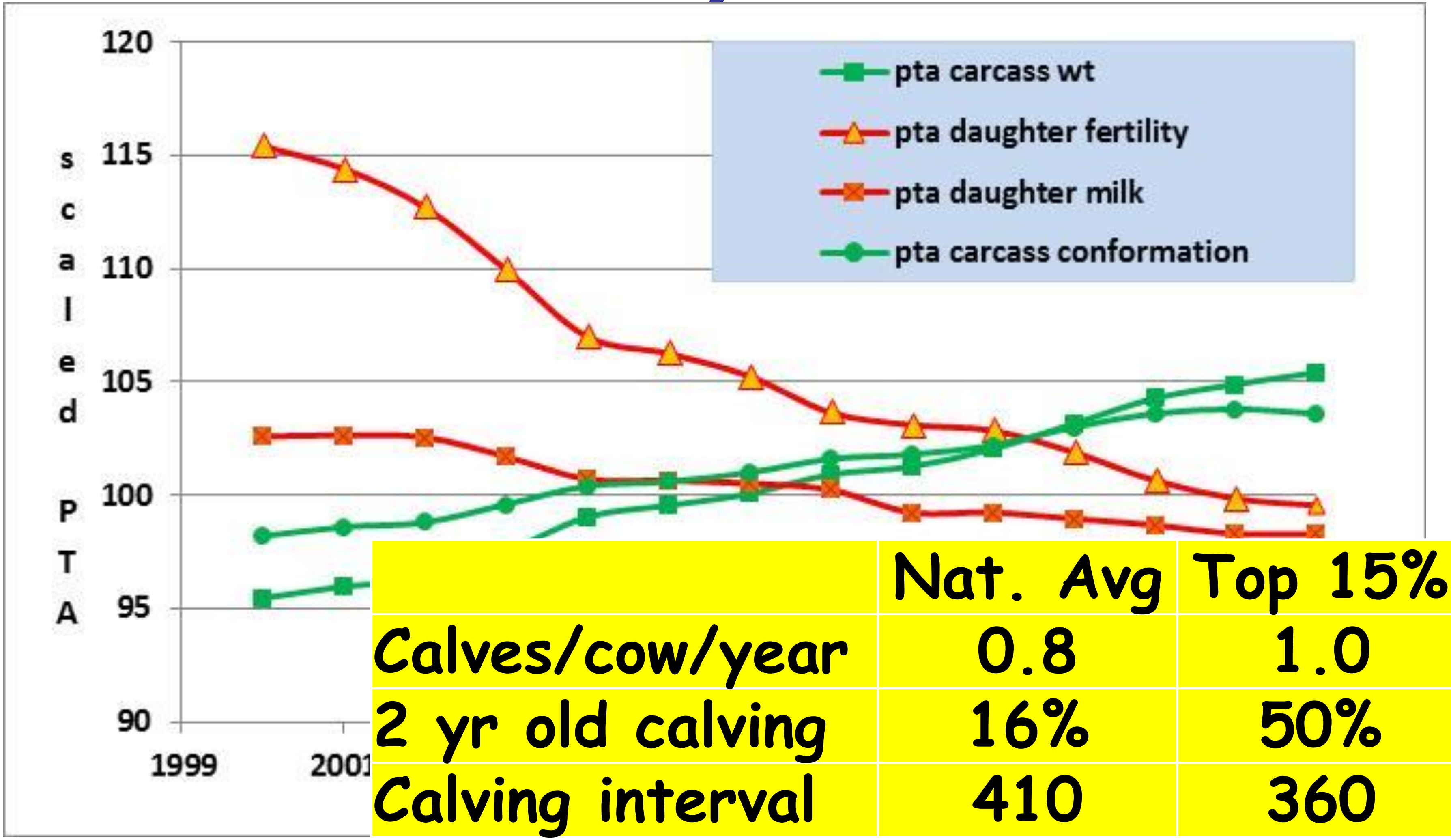
- 89,662 animals
  - 20,608 males
  - 69,054 females

69,753,628,844 SNPs!!

Accuracy v number of animals

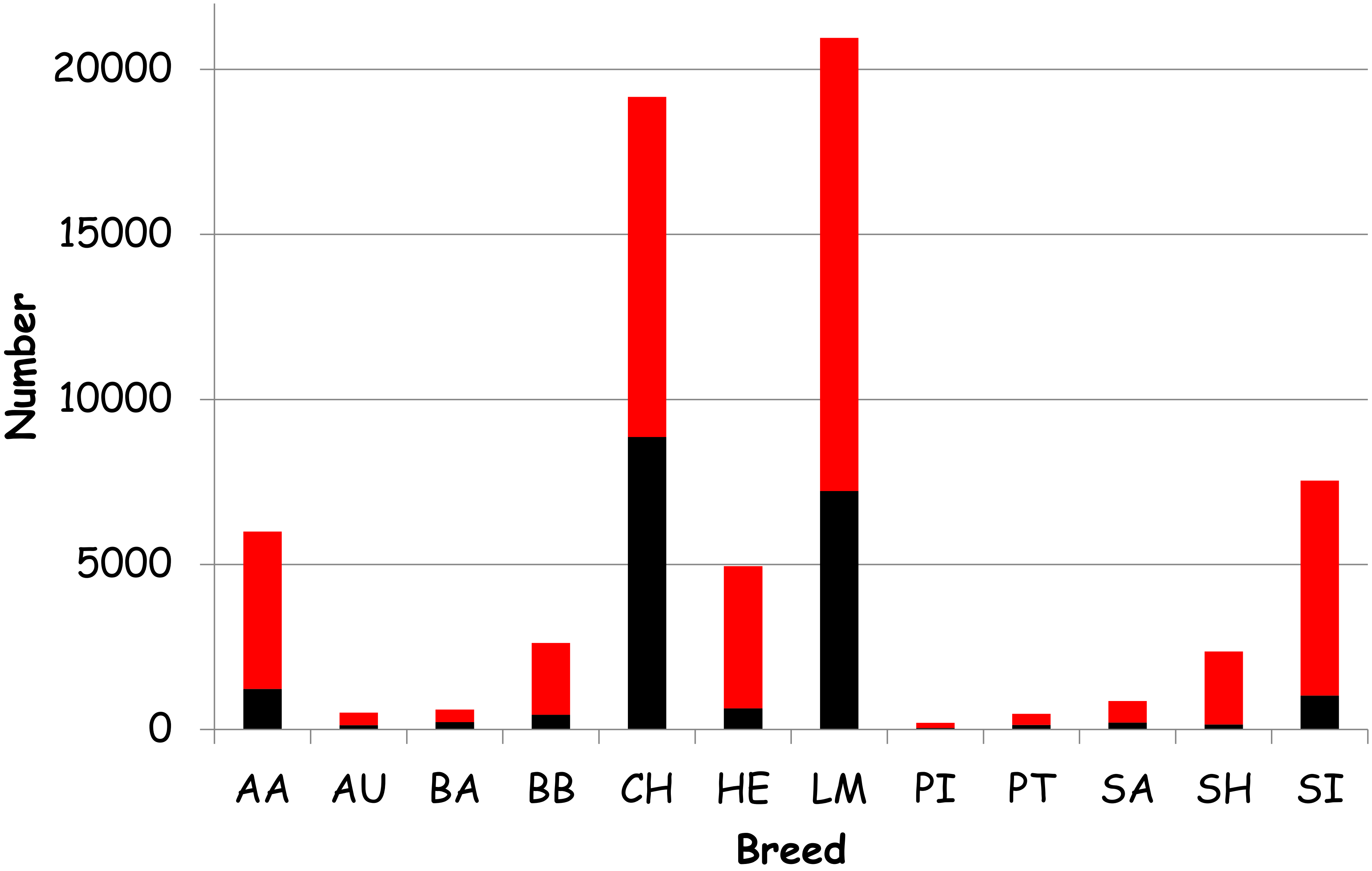


Why???

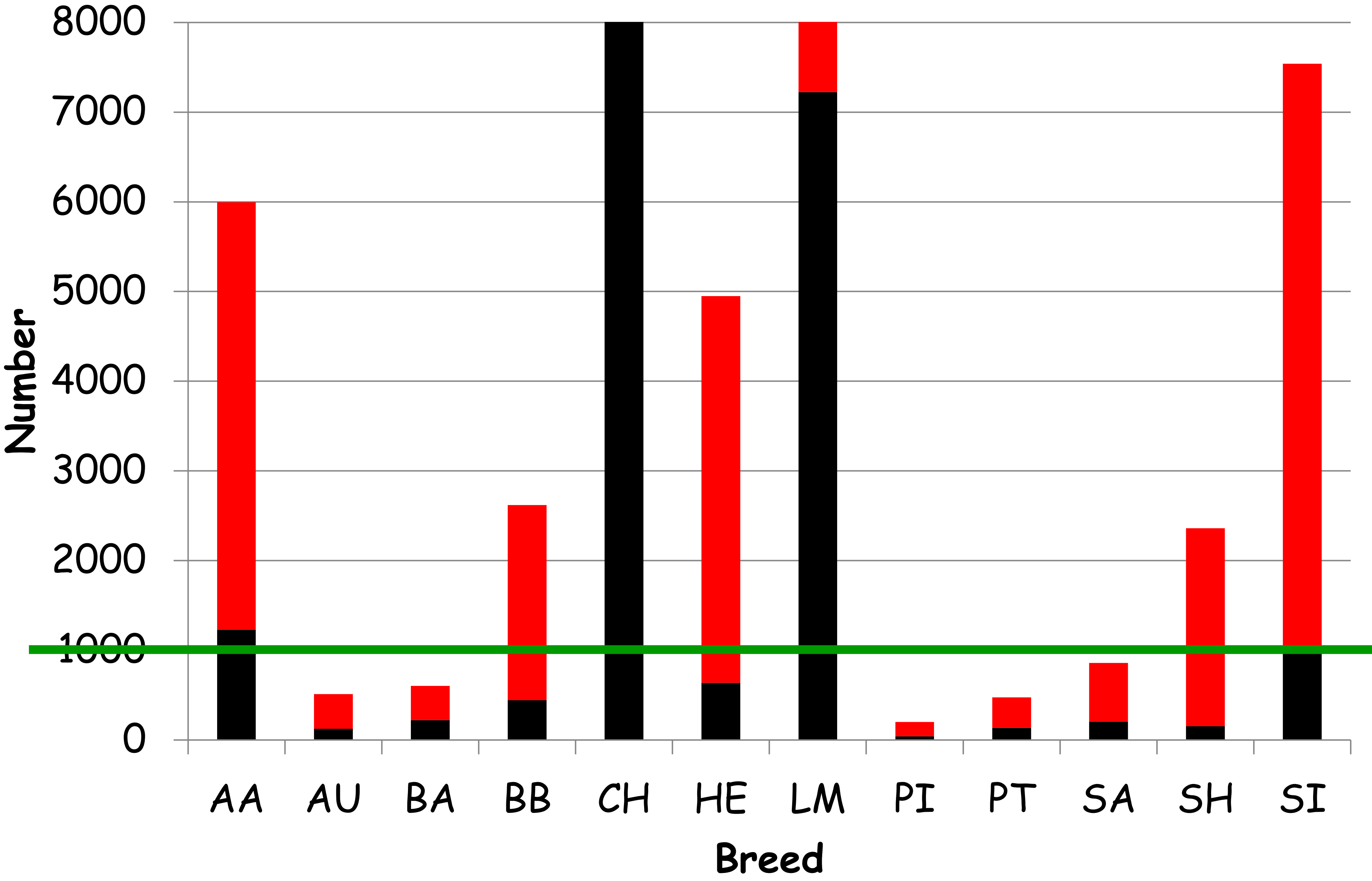


	Nat. Avg	Top 15%
Calves/cow/year	0.8	1.0
2 yr old calving	16%	50%
Calving interval	410	360

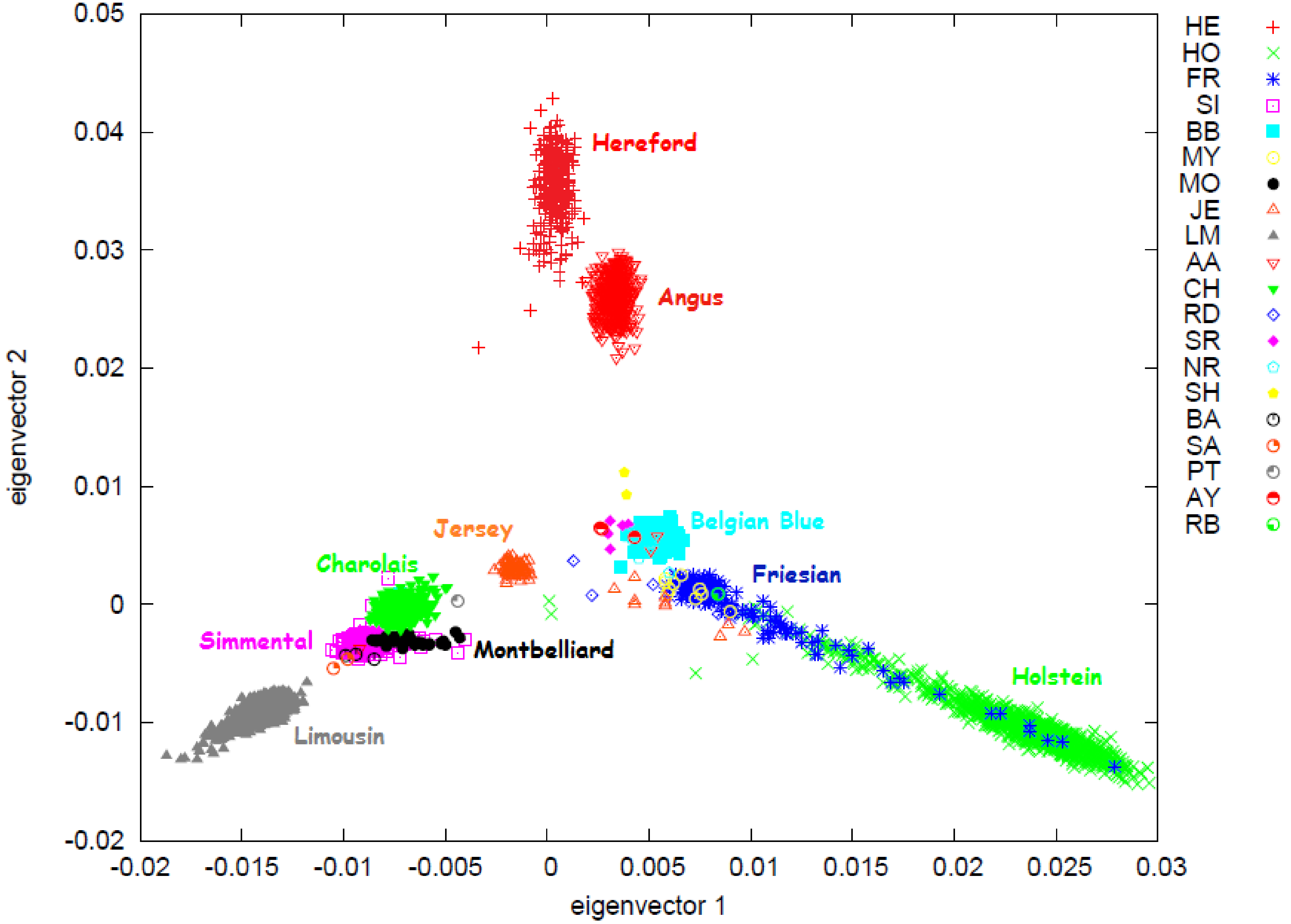
Breed representation



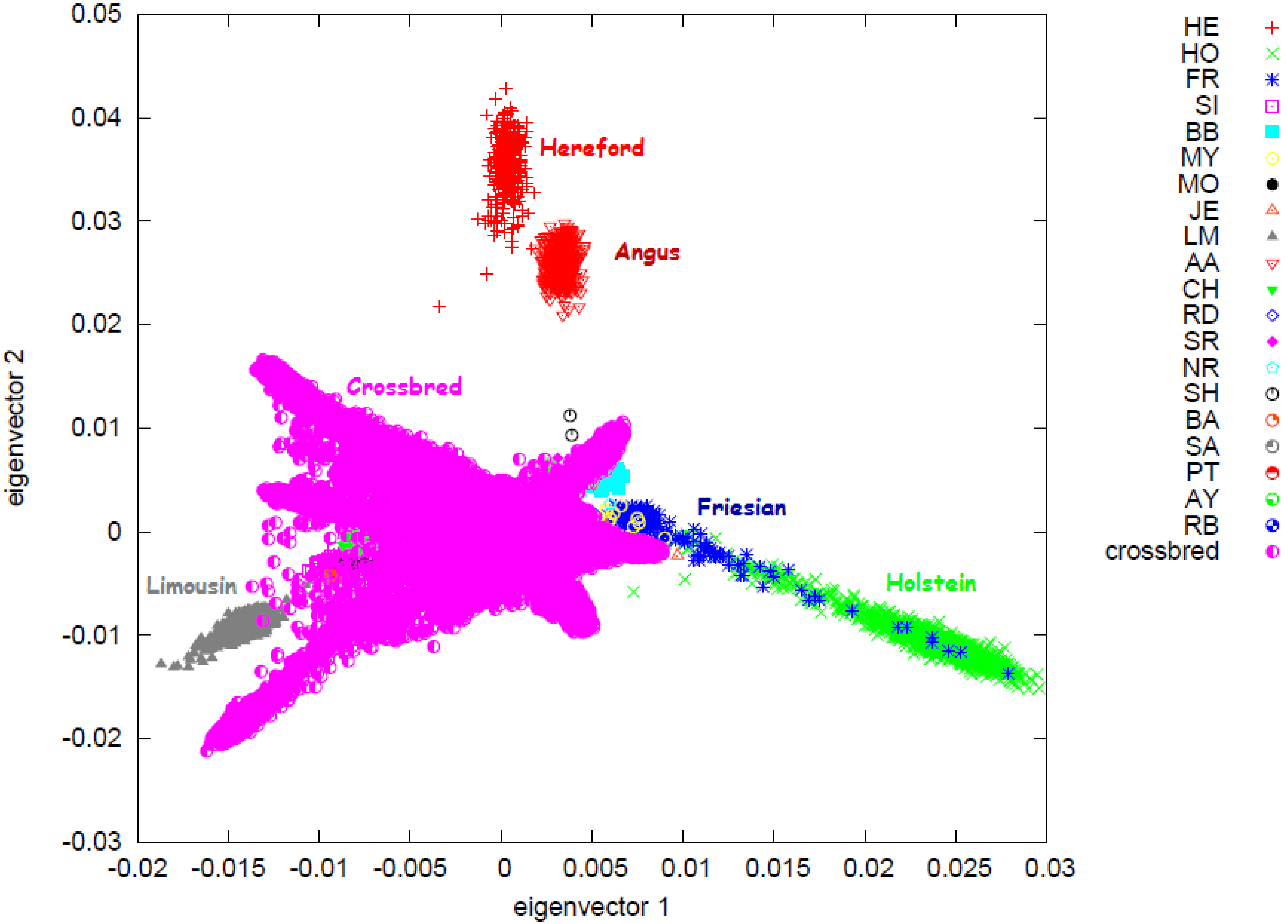
Breed representation



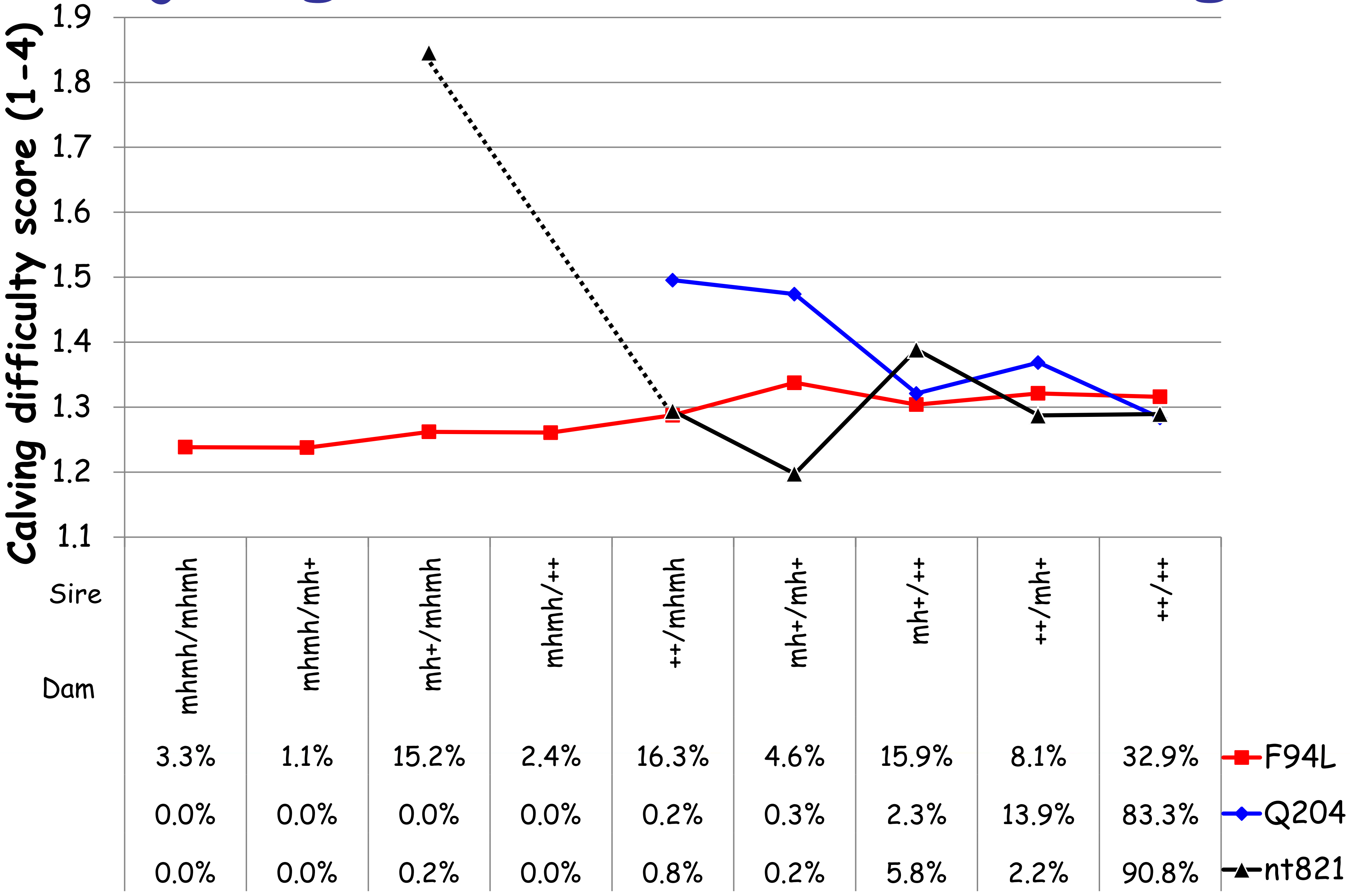
Population structure



Population structure



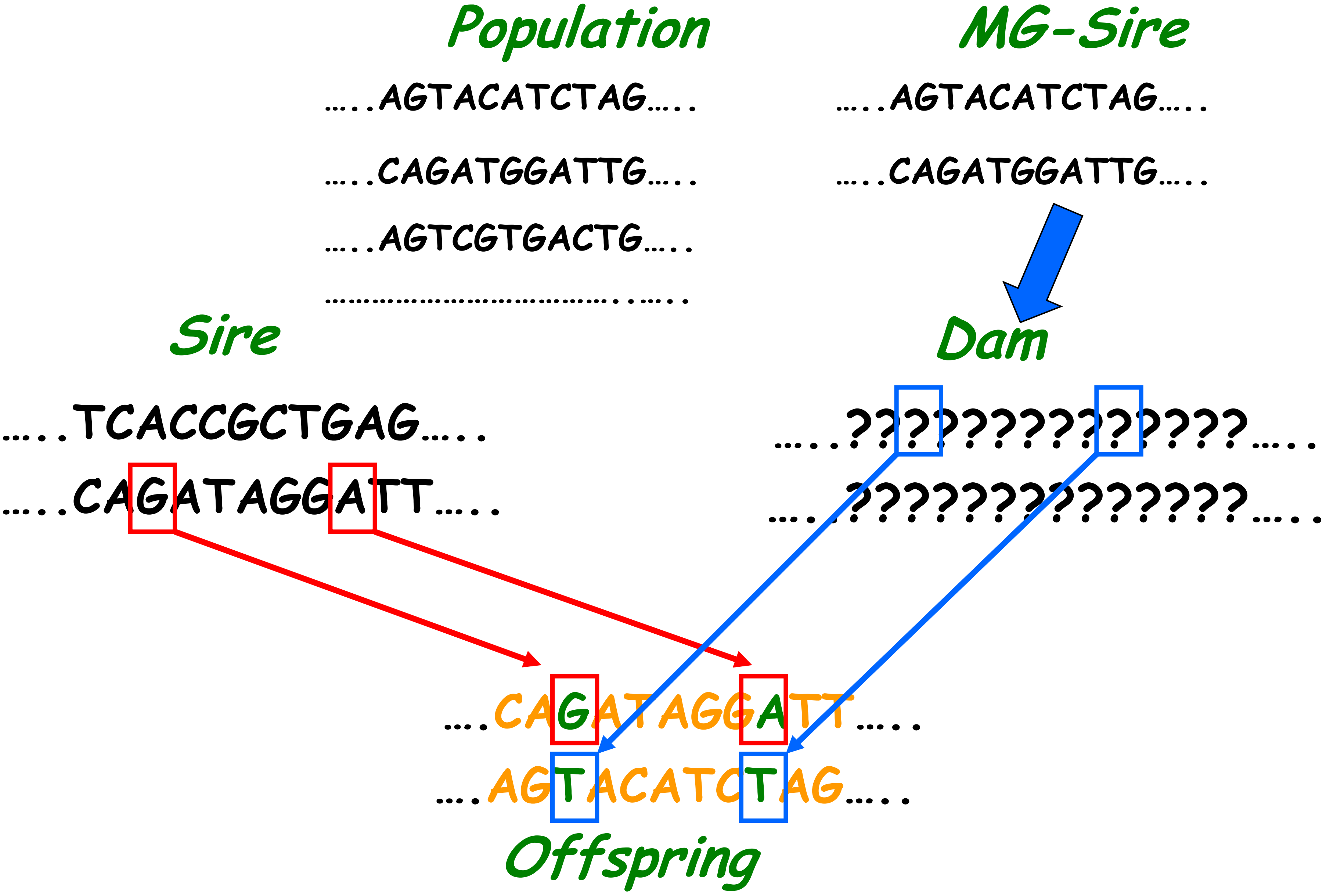
Major genes (>20,000 calvings)



Sire Dam	mhmh/mhmh	mhmh/mh+	mh+/mhmh	mhmh/++	++/mhmh	mh+/mh+	mh+/++	++/mh+	++/++
F94L	3.3%	1.1%	15.2%	2.4%	16.3%	4.6%	15.9%	8.1%	32.9%
Q204	0.0%	0.0%	0.0%	0.0%	0.2%	0.3%	2.3%	13.9%	83.3%
nt821	0.0%	0.0%	0.2%	0.0%	0.8%	0.2%	5.8%	2.2%	90.8%

Imputation

(prediction of “missing” genotypes)



Population

…..AGTACATCTAG…..

…..CAGATGGATTG…..

…..AGTCGTGACTG…..

……………………………………..……..

MG-Sire

…..AGTACATCTAG…..

…..CAGATGGATTG…..

Sire

…..TCACCGCTGAG…..

…..CAGATAGGATTT…..

Dam

…..???????????????…..

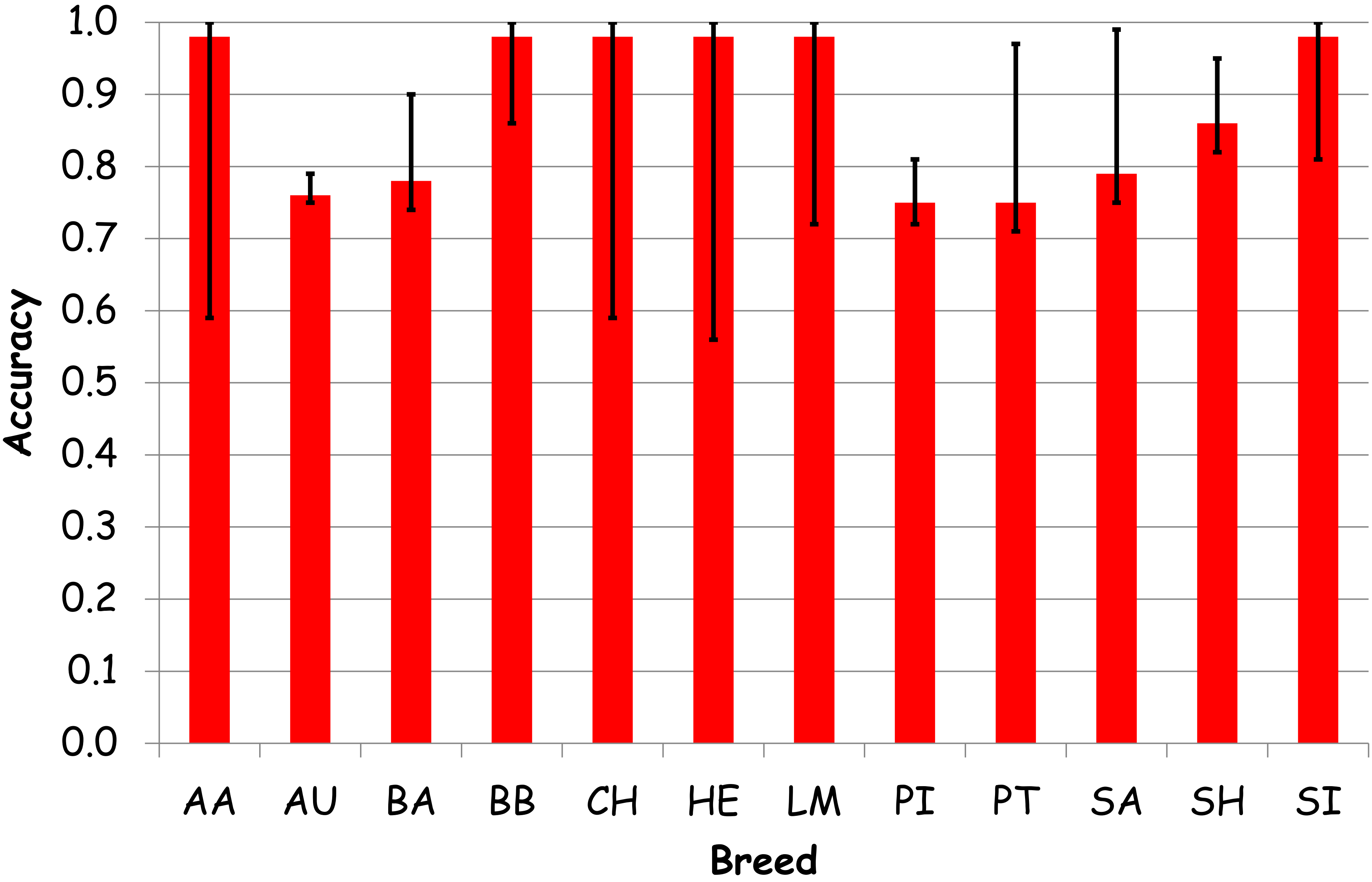
…..???????????????…..

….CAGATAGGATTT…..

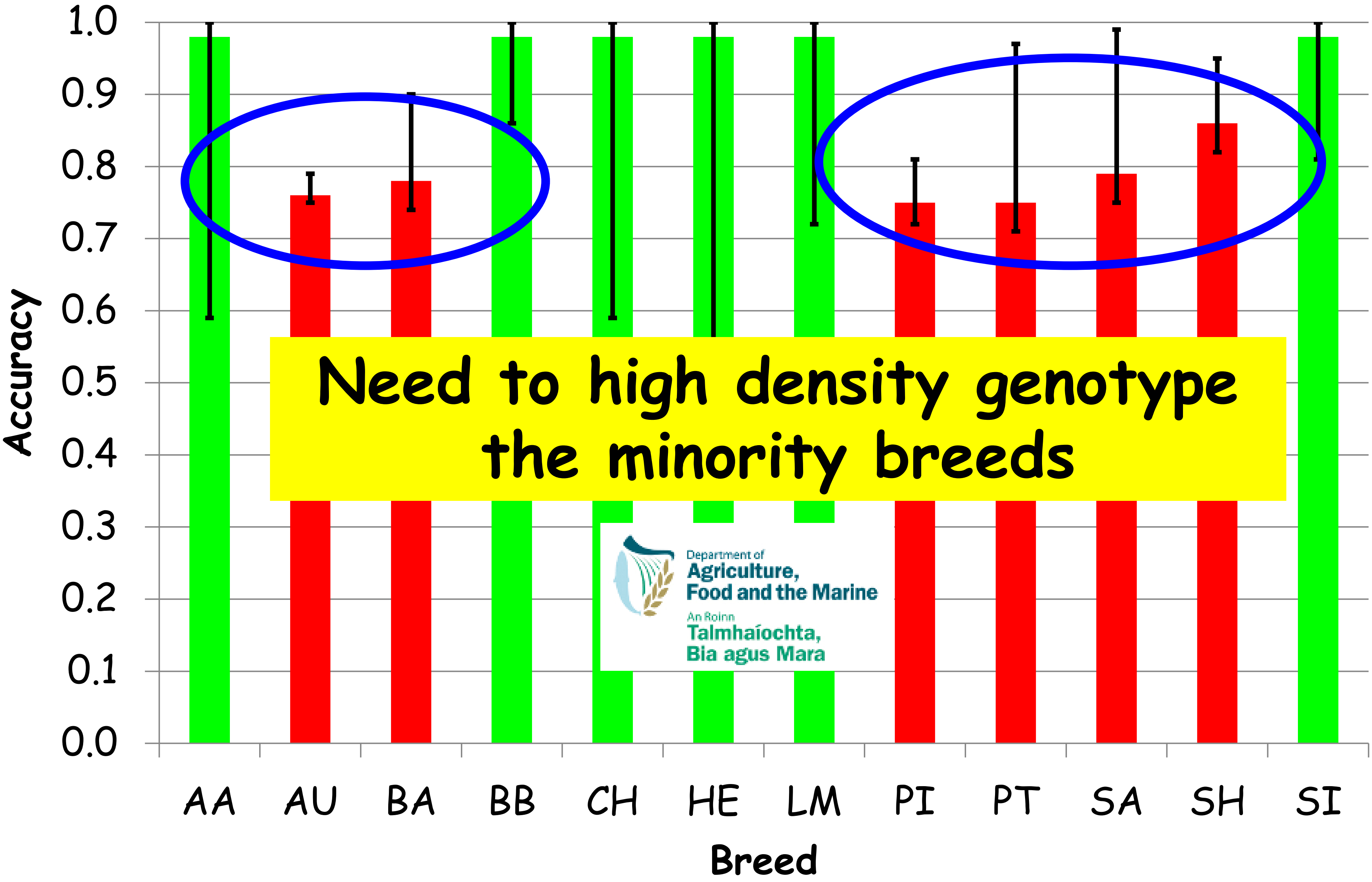
….AGTACATCTAG…..

Offspring

Imputation by breed



Imputation by breed



Need to high density genotype the minority breeds

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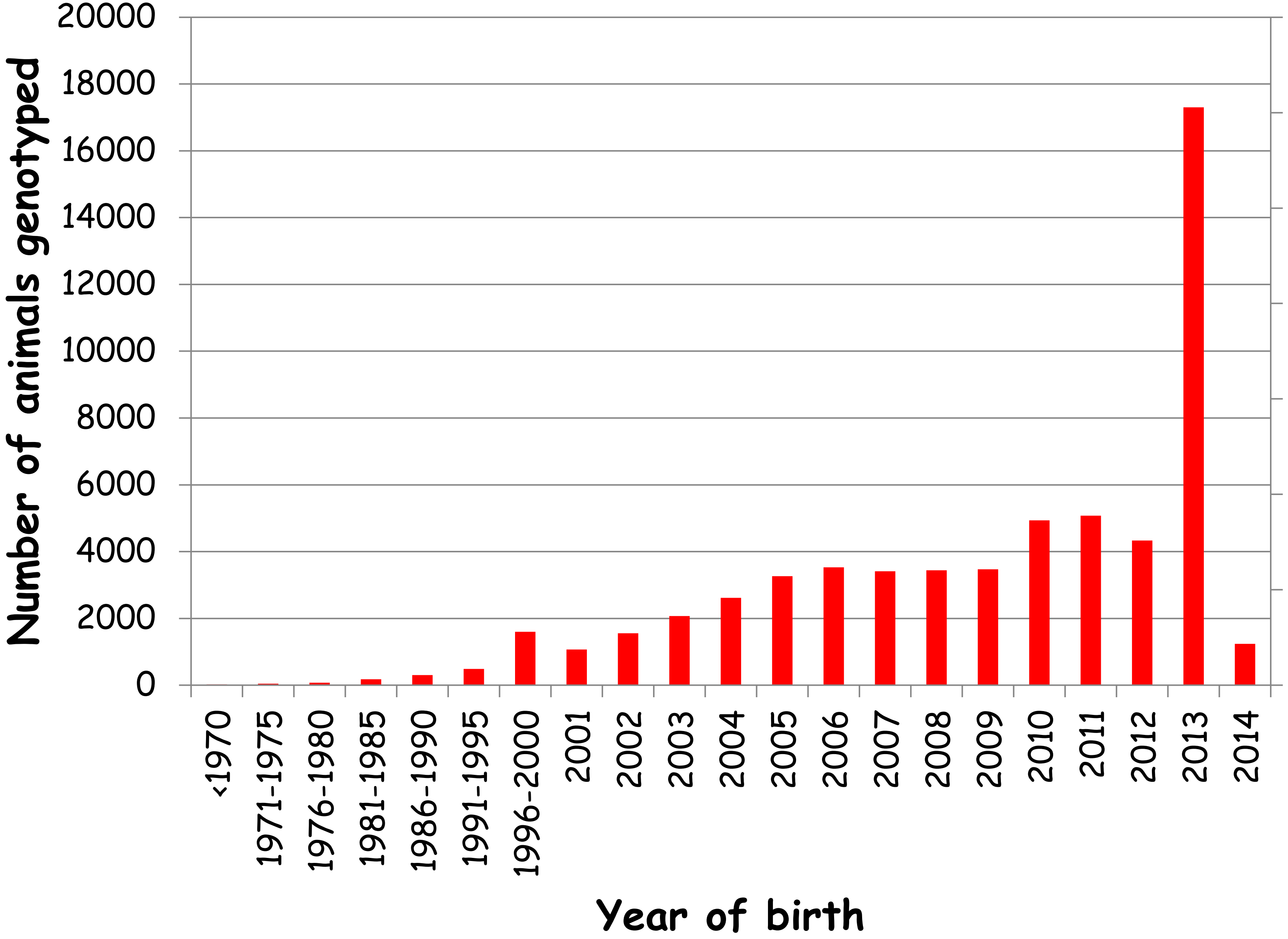
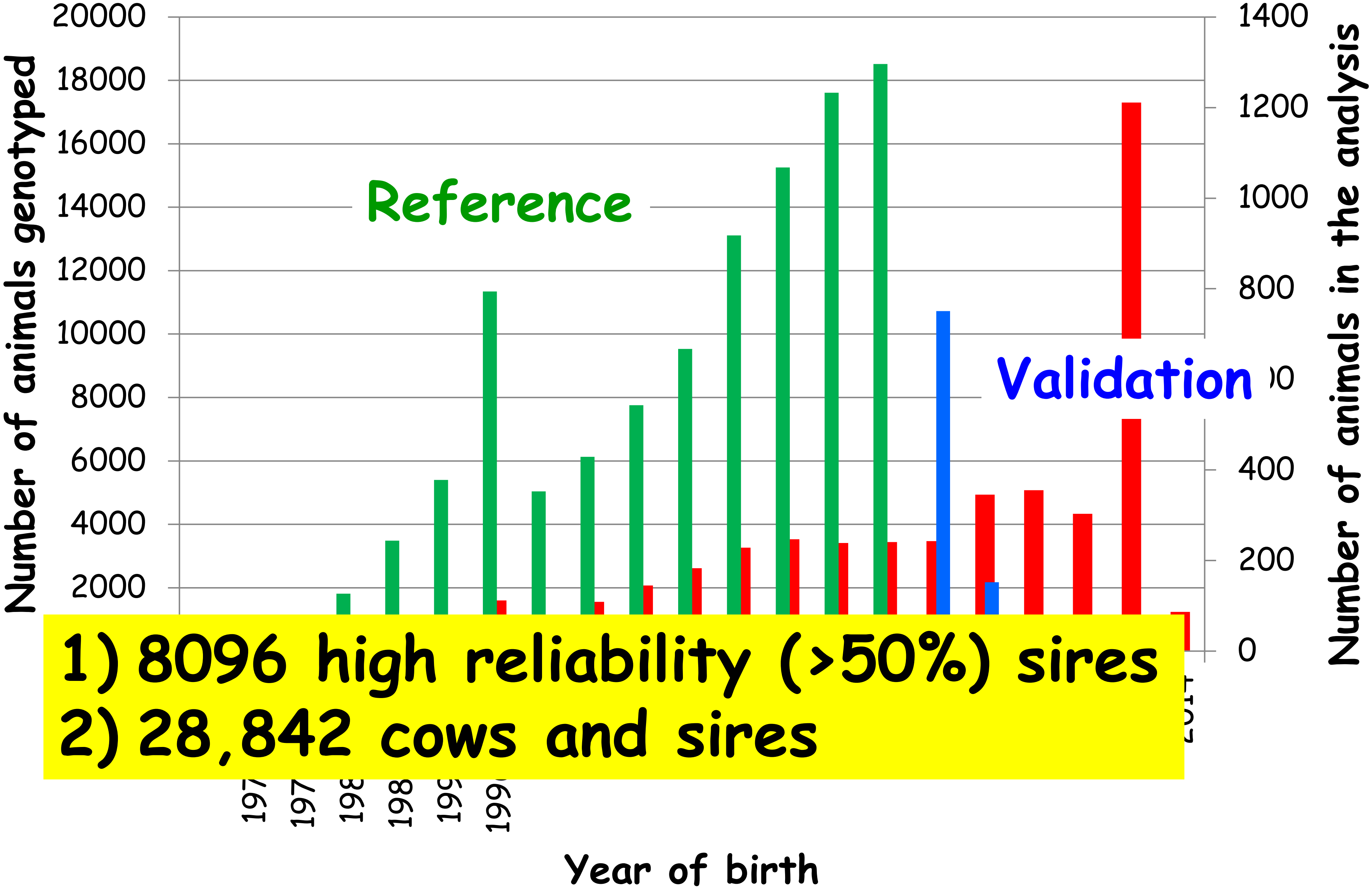
Genomic predictions

Genotyped animals



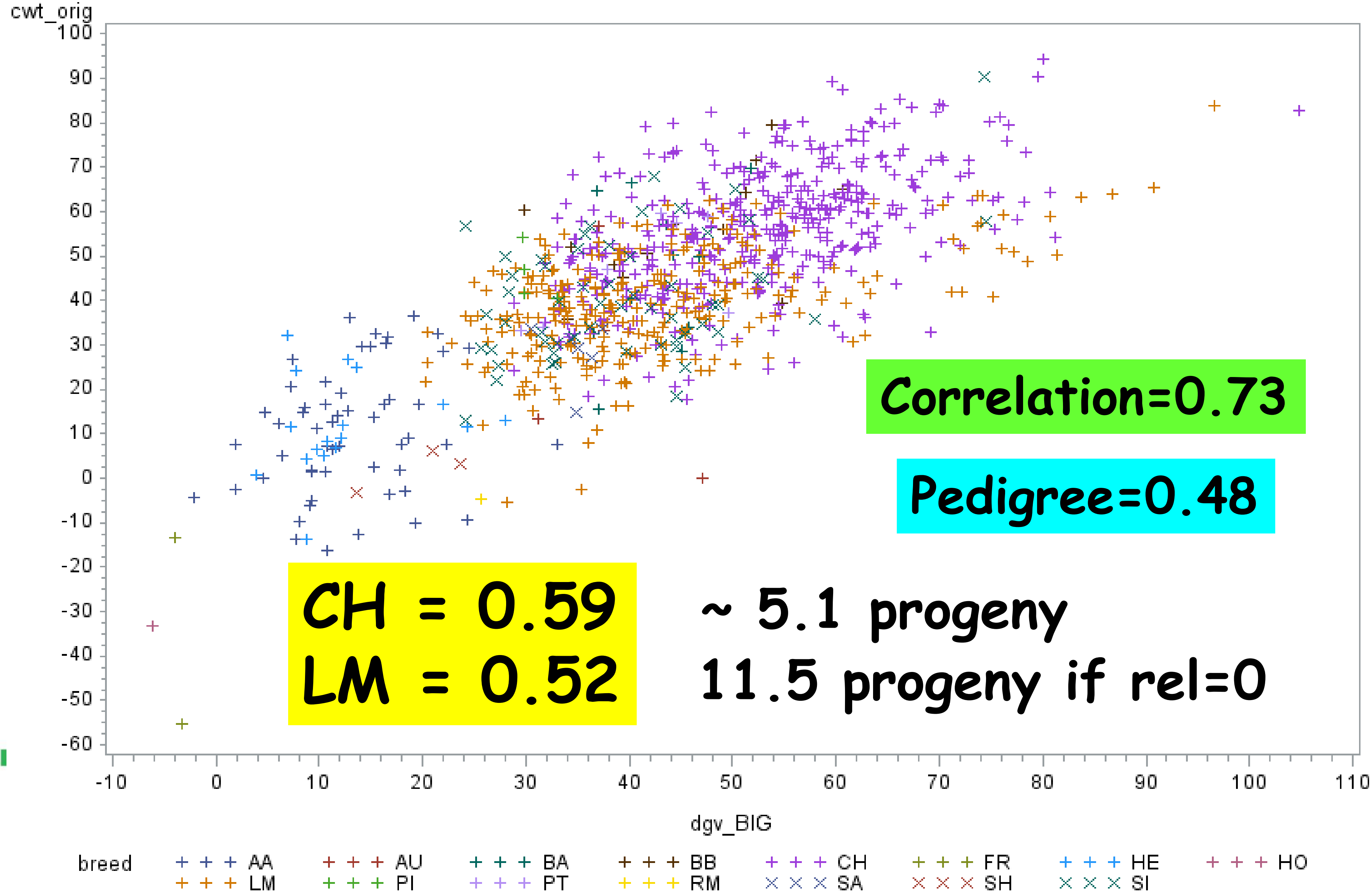
Genotyped animals



1) 8096 high reliability (>50%) sires

2) 28,842 cows and sires

Carcass weight (n=898; >50% rel.)



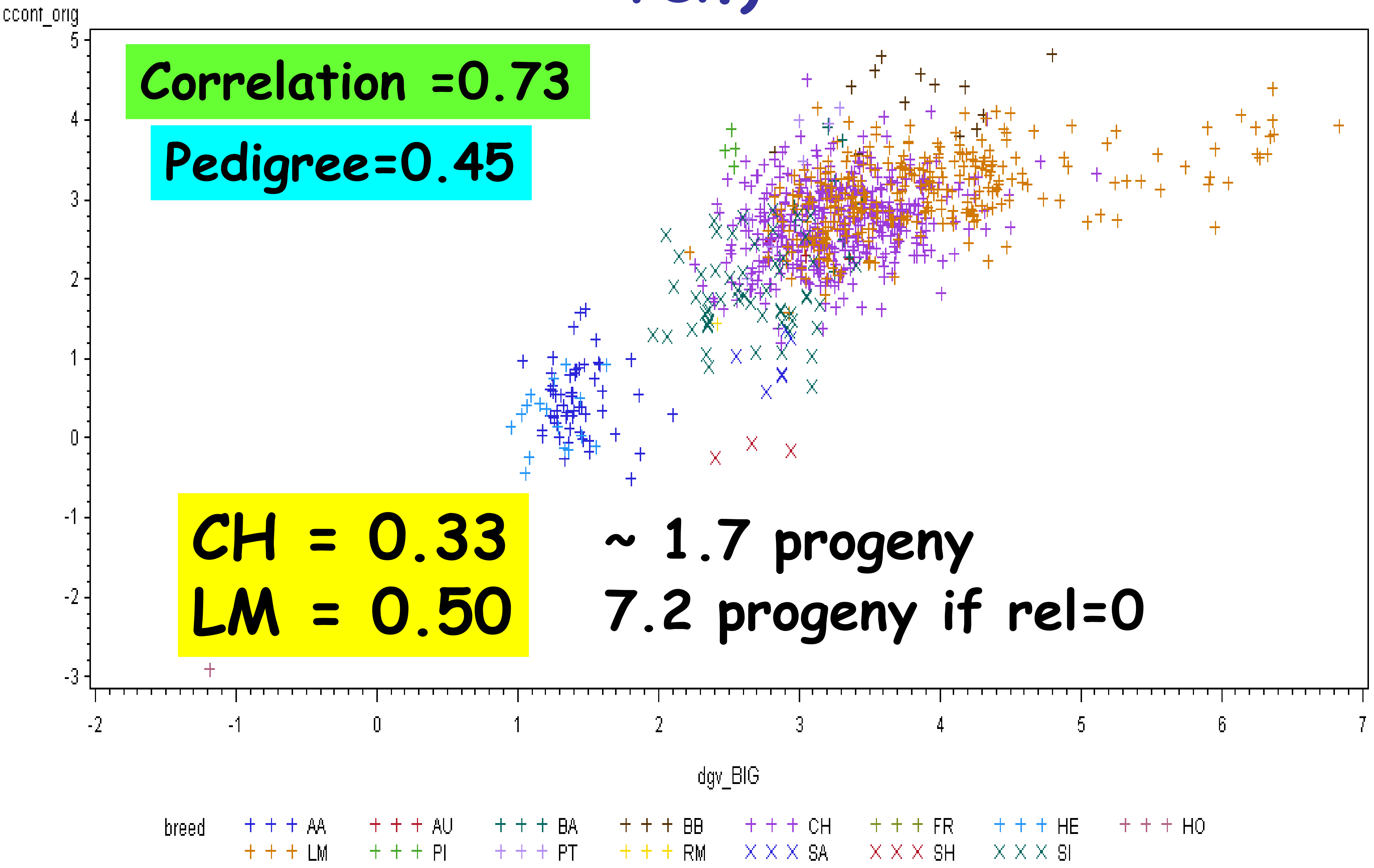
Correlation=0.73

Pedigree=0.48

CH = 0.59
LM = 0.52

~ 5.1 progeny
11.5 progeny if rel=0

Carc conformation (n=898; >50% rel.)



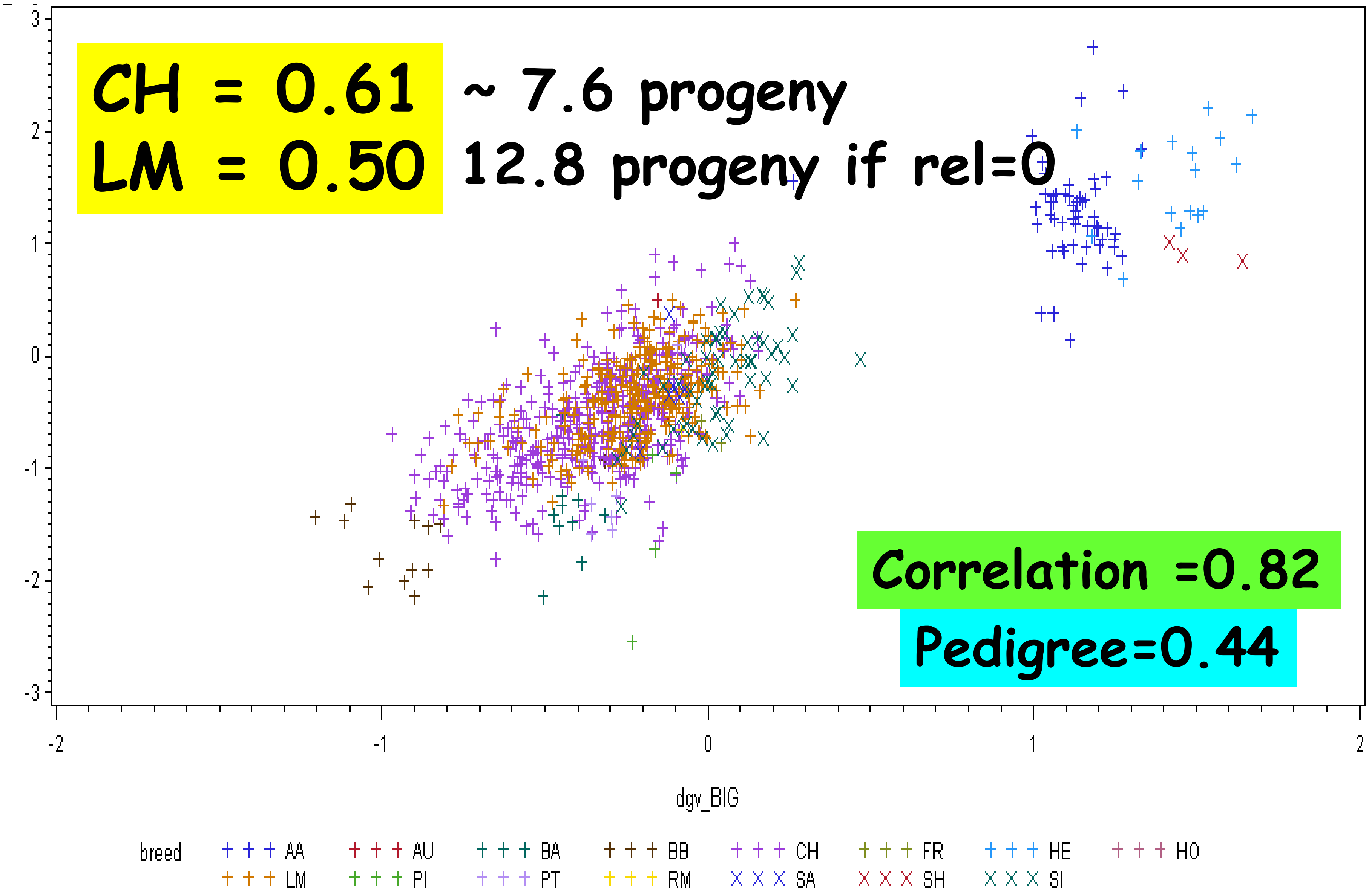
Correlation =0.73

Pedigree=0.45

CH = 0.33
LM = 0.50

~ 1.7 progeny
7.2 progeny if rel=0

Carcass fat (n=898; >50% rel.)



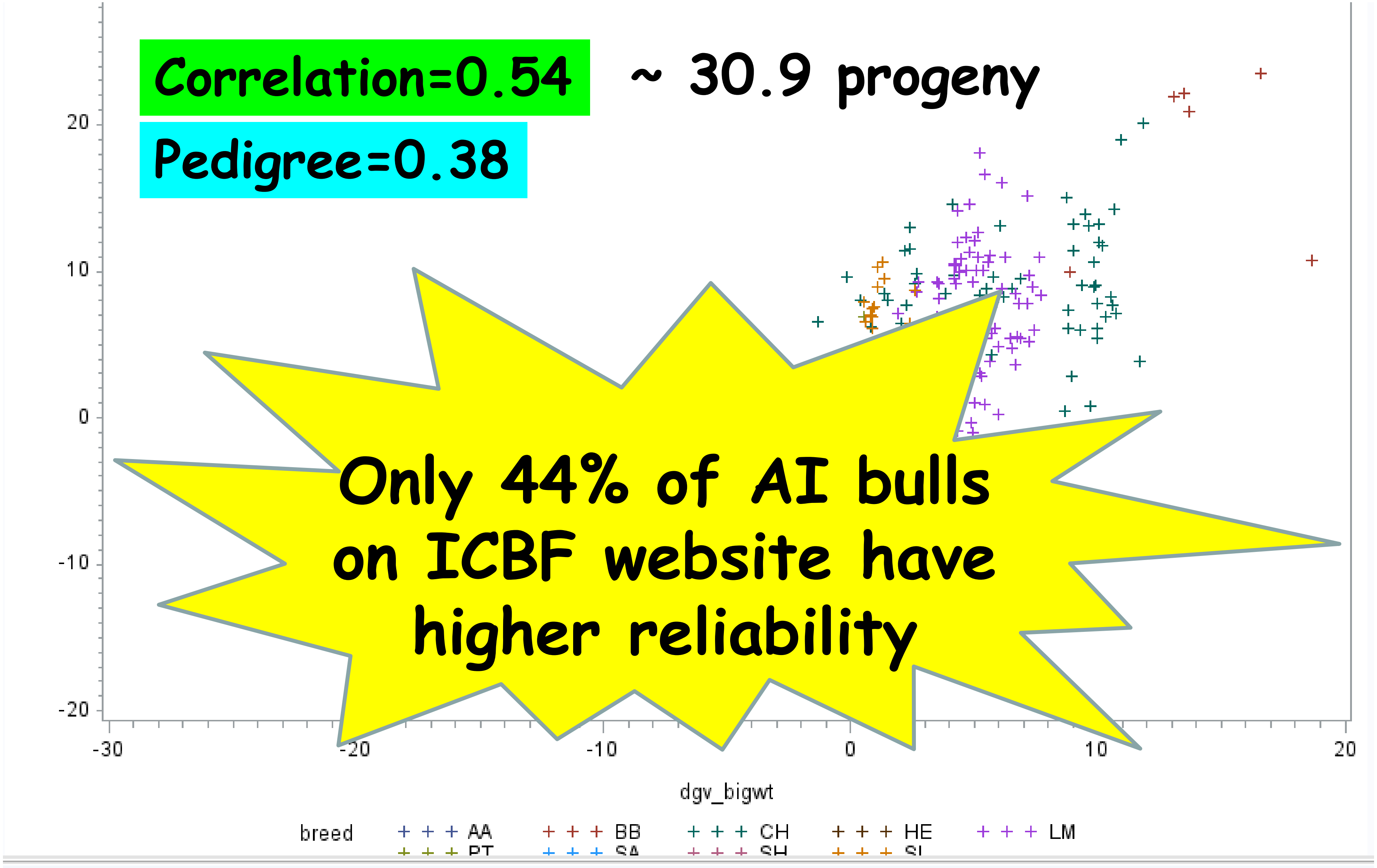
CH = 0.61 ~ 7.6 progeny

LM = 0.50 12.8 progeny if rel=0

Correlation =0.82

Pedigree=0.44

Calving interval (n=227; >50% rel.)



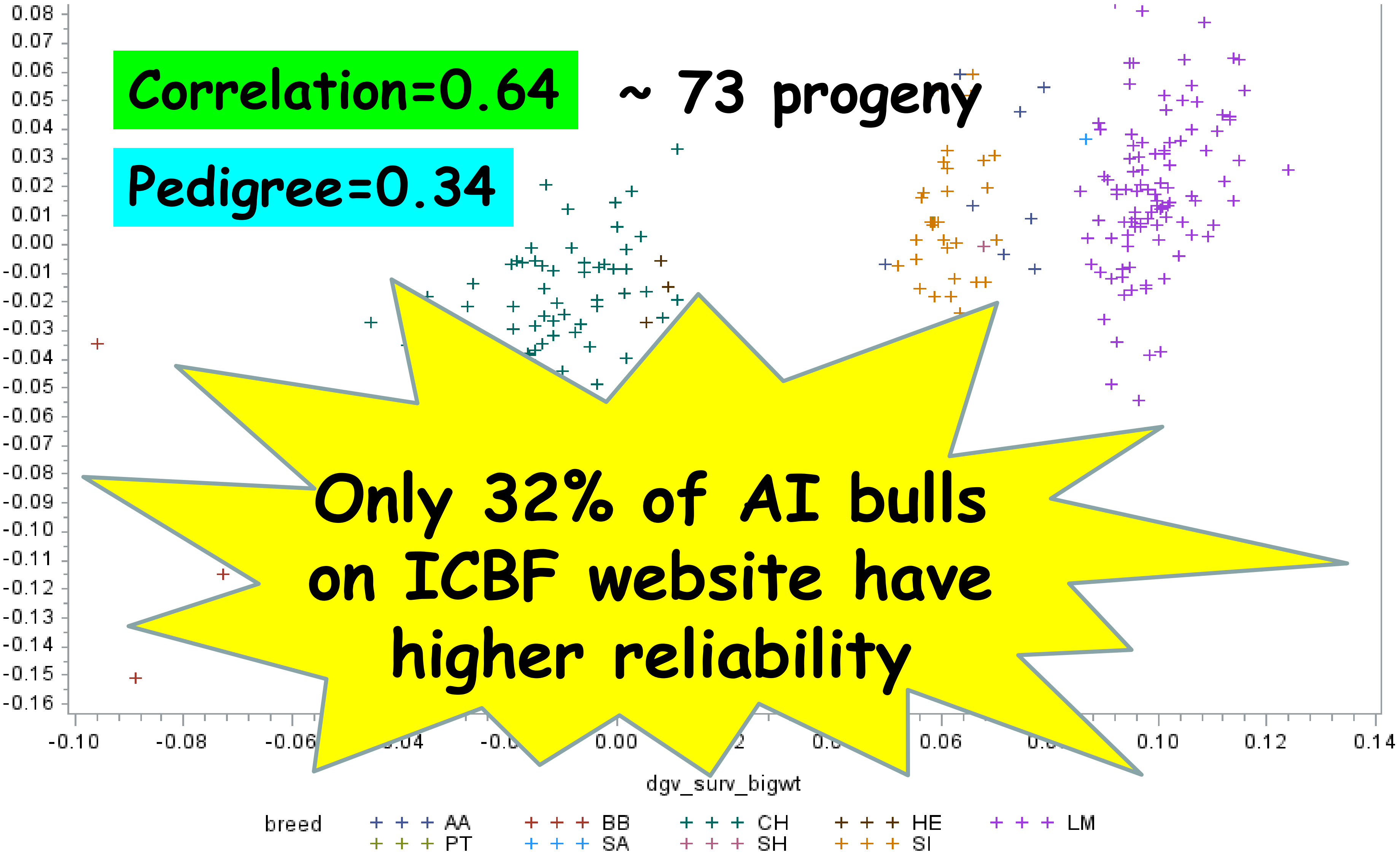
Correlation=0.54

Pedigree=0.38

~ 30.9 progeny

Only 44% of AI bulls on ICBF website have higher reliability

Survival (n=227; >50% rel.)



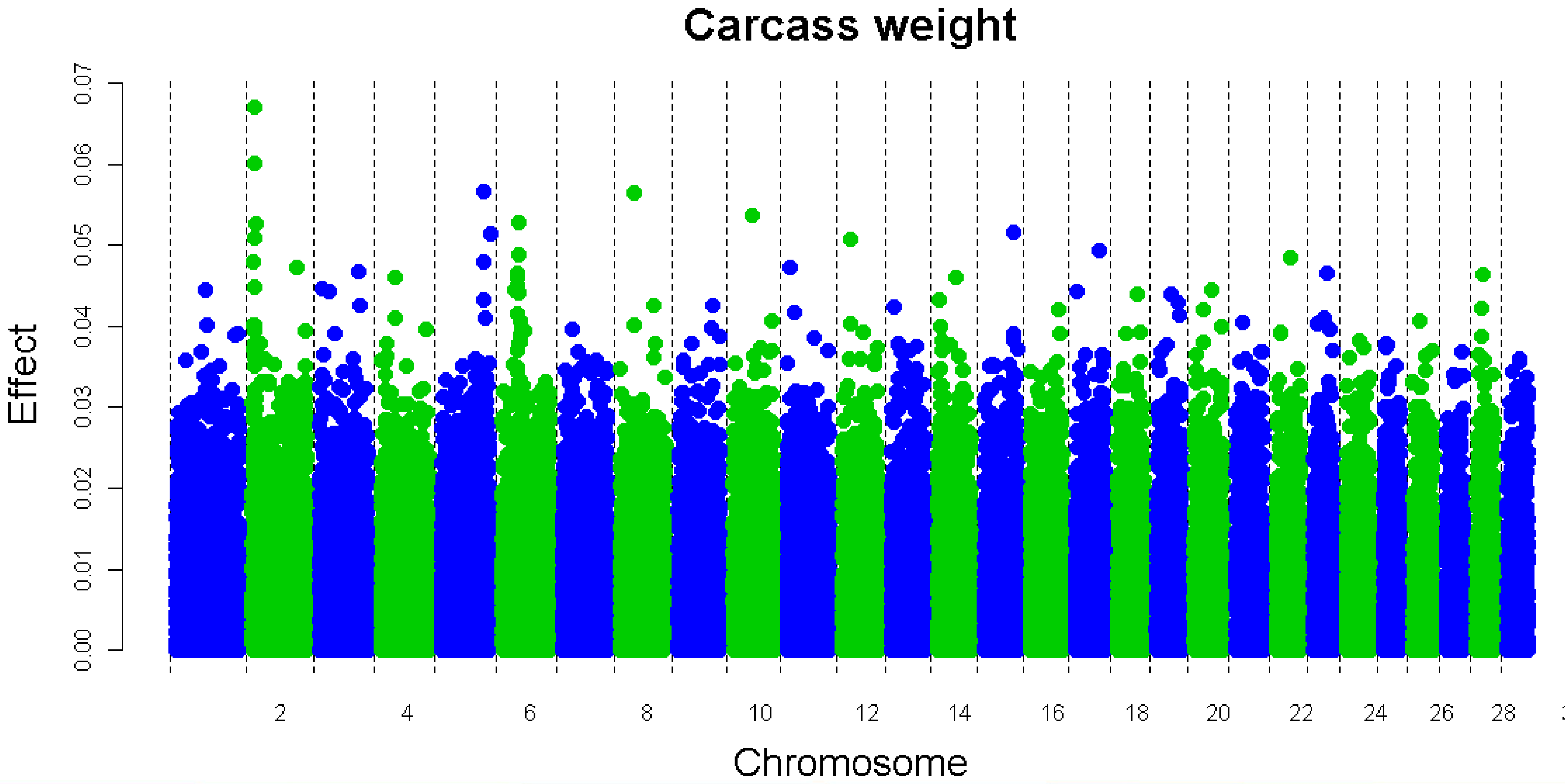
Correlation=0.64

Pedigree=0.34

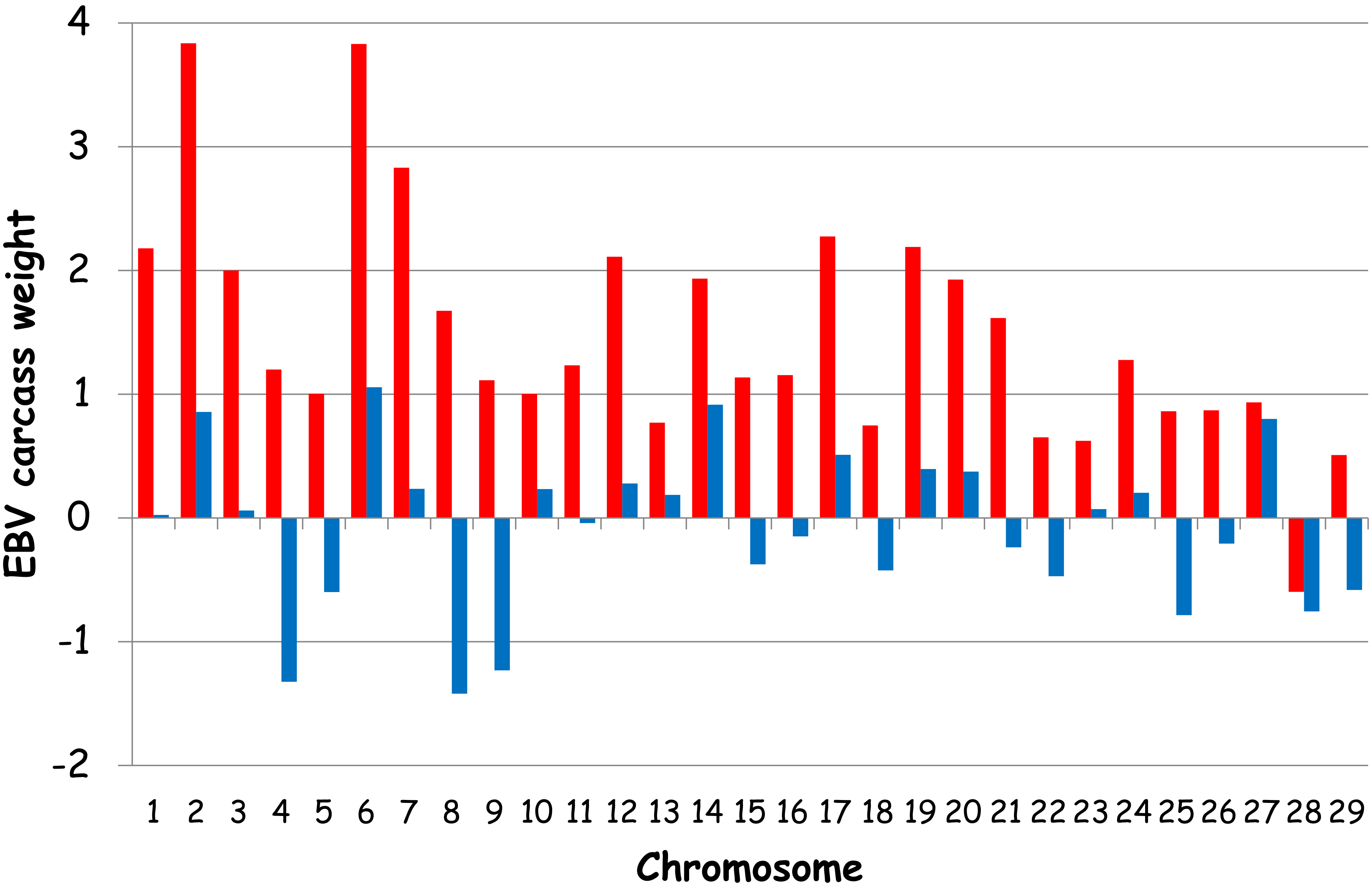
~ 73 progeny

Only 32% of AI bulls on ICBF website have higher reliability

Where's the genes???



CF52 v EOB - chromosomal values



Conclusions

- Put genomics in your vocabulary
- Genomic selection providing greater accuracy of selection
- Scientific advisory committee had some good suggestions
  - Accuracy comparable with internationally
  - Accuracy comparable with dairy in 2009
  - Sufficiently accurate to implement
- Possible implementation in mid-2015

Acknowledgements

- Research Stimulus Fund
  - MultiGS 11/S/112
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  - RSF-06-0328
- Industry