UNIVERSITY OF GEORGIA
College of Agricultural & Environmental Sciences

Changes in GEBV in ssGBLUP with inversion by the APY algorithm using different core animals

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APY algorithm and different sets of core animals

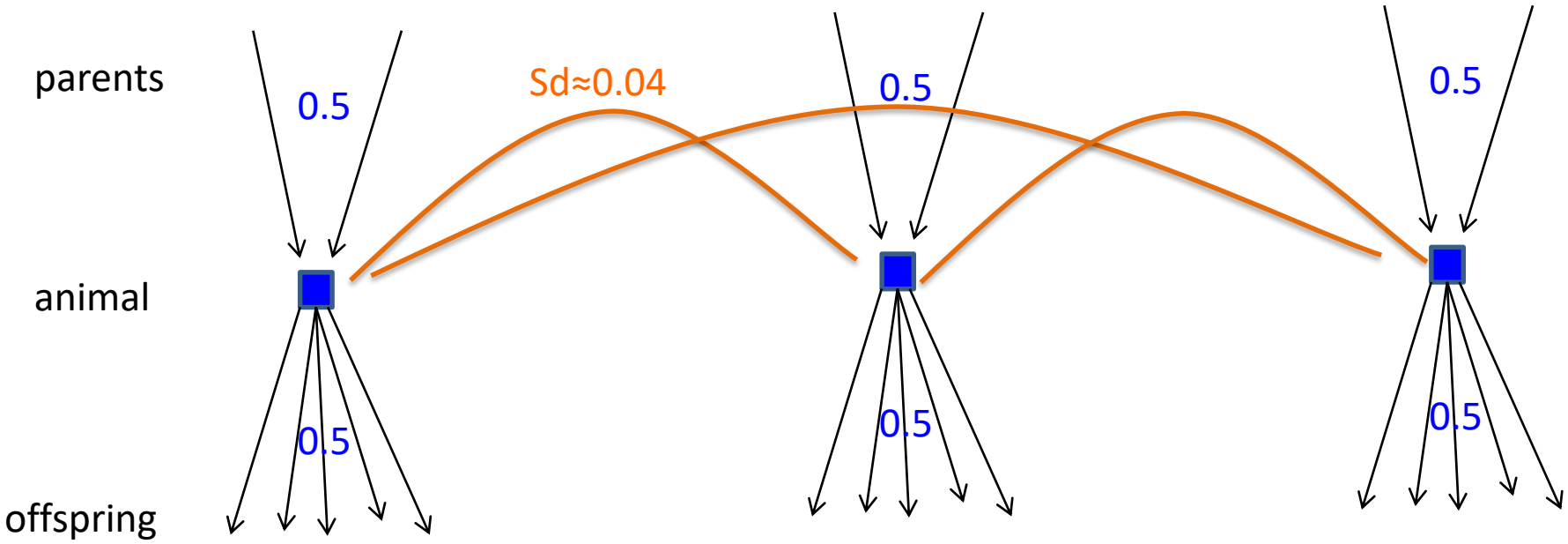
- ssGBLUP used routinely in chicken, pigs and beef
- Inverse of G by APY to reduce costs
  - Up to 2.3 million genotyped animals
- Reports of GEBV changes with different core animals
- Why and how much?

Changes in nongenomic and genomic evaluations

- Little change in BLUP for older animals
  - Fixed effects stable
  - New relationships little affect older animals

- More change in genomic evaluation
  - Each new genotyped animal affects other genotyped animals
  - Details matter

BLUP and genomics



BLUP

$u_i=(u_{sire}+u_{dam})/2+\varphi$

Genomics

$u_i=\mathbf{P}u_{i-1}+\varepsilon$

Genomic evaluations less stable than BLUP

Origin of changes with APY

Genomic relationship matrix – information + noise

$$\mathbf{u}_n = \mathbf{P}\mathbf{u}_c + \boldsymbol{\varepsilon}$$

$$\sigma_a^2 \qquad \eta\sigma_a^2 \qquad (1-\eta)\sigma_a^2$$

0.98 0.02

$$\mathbf{var}(\boldsymbol{\varepsilon}_i) = \boldsymbol{g}_{ii} - \boldsymbol{g}_{i,c}\boldsymbol{G}^{cc}\boldsymbol{g}_{c,i}$$

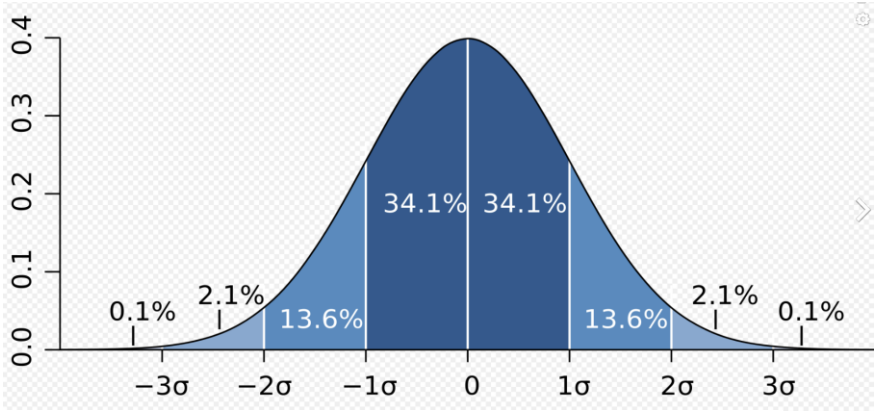
$$\mathbf{sd}(\boldsymbol{\varepsilon}) = \sigma_a \sqrt{(1-\eta)}$$ Main source of noise

Approx. difference between GEBV with 2 random cores:

$$\mathbf{sd}(\boldsymbol{\varepsilon}_1 - \boldsymbol{\varepsilon}_2) \approx 1.4\, \sigma_a \sqrt{(1-\eta)}$$ rel

Outliers in normal distribution

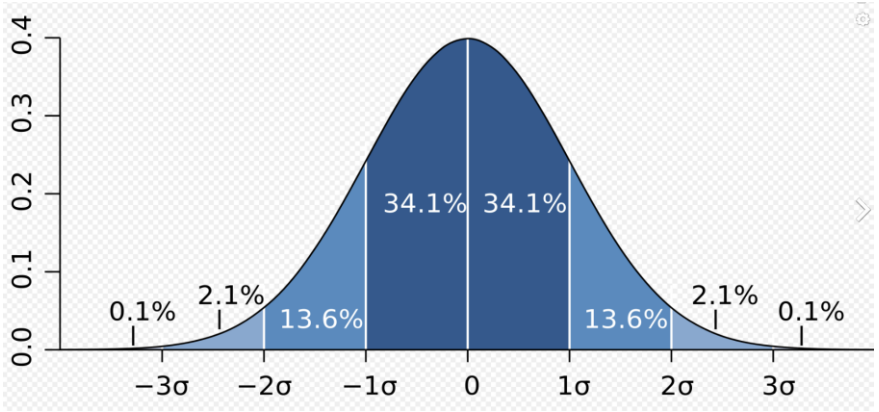
$$\boldsymbol{\varepsilon_1} - \boldsymbol{\varepsilon_2} \sim 1.4\, rel\, N(0,0.02)\sigma_a^2$$



Samples	Avg| N(0, 1) |
All	0.8
Top 1 in 100	2.9
Top 1 in 10,000	4.1
Top 1 in million	5.0

Outliers in normal distribution

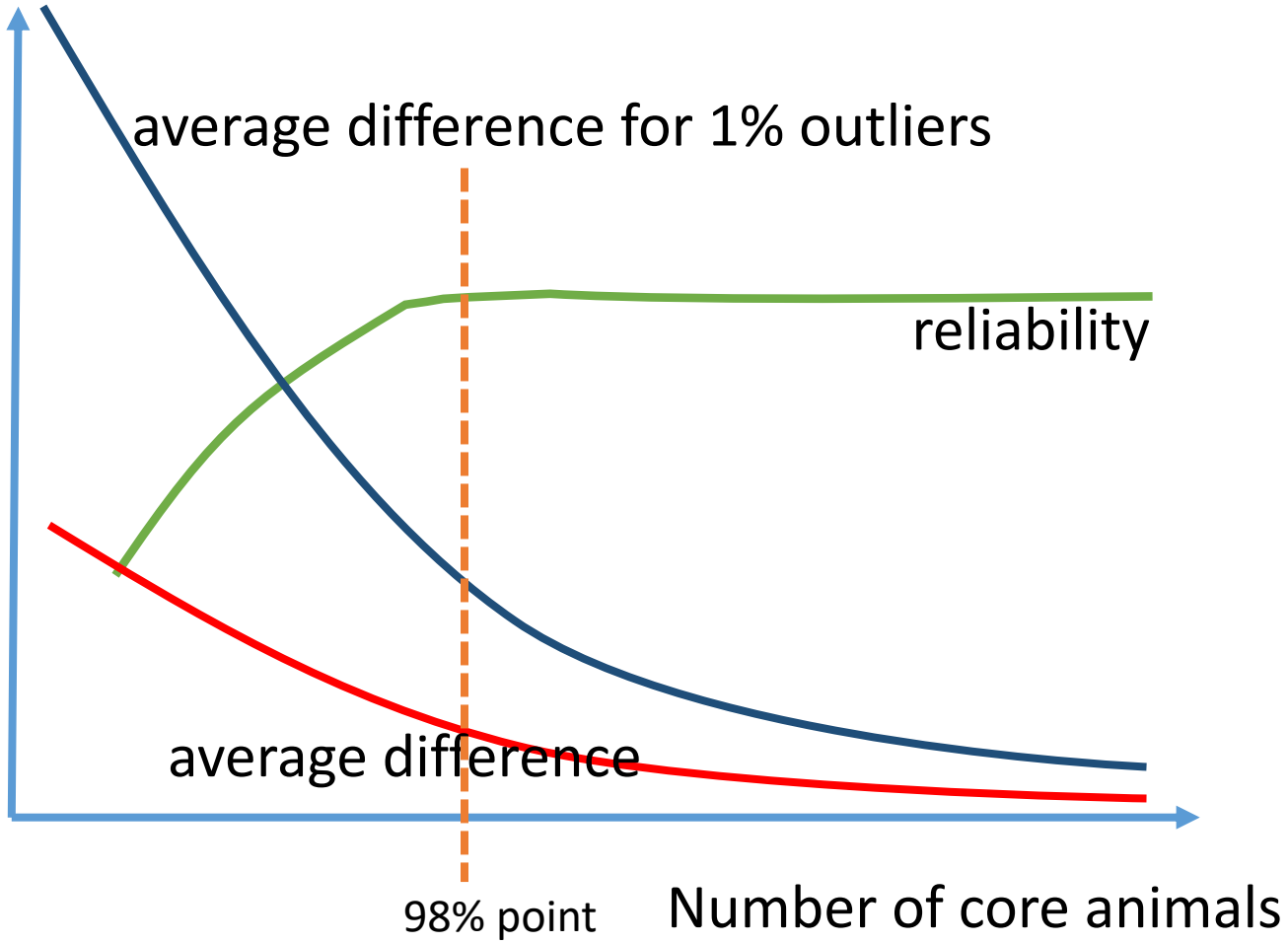
$$\boldsymbol{\varepsilon_1} - \boldsymbol{\varepsilon_2} \sim 1.4\, rel\, N(0,0.02)\sigma_a^2$$



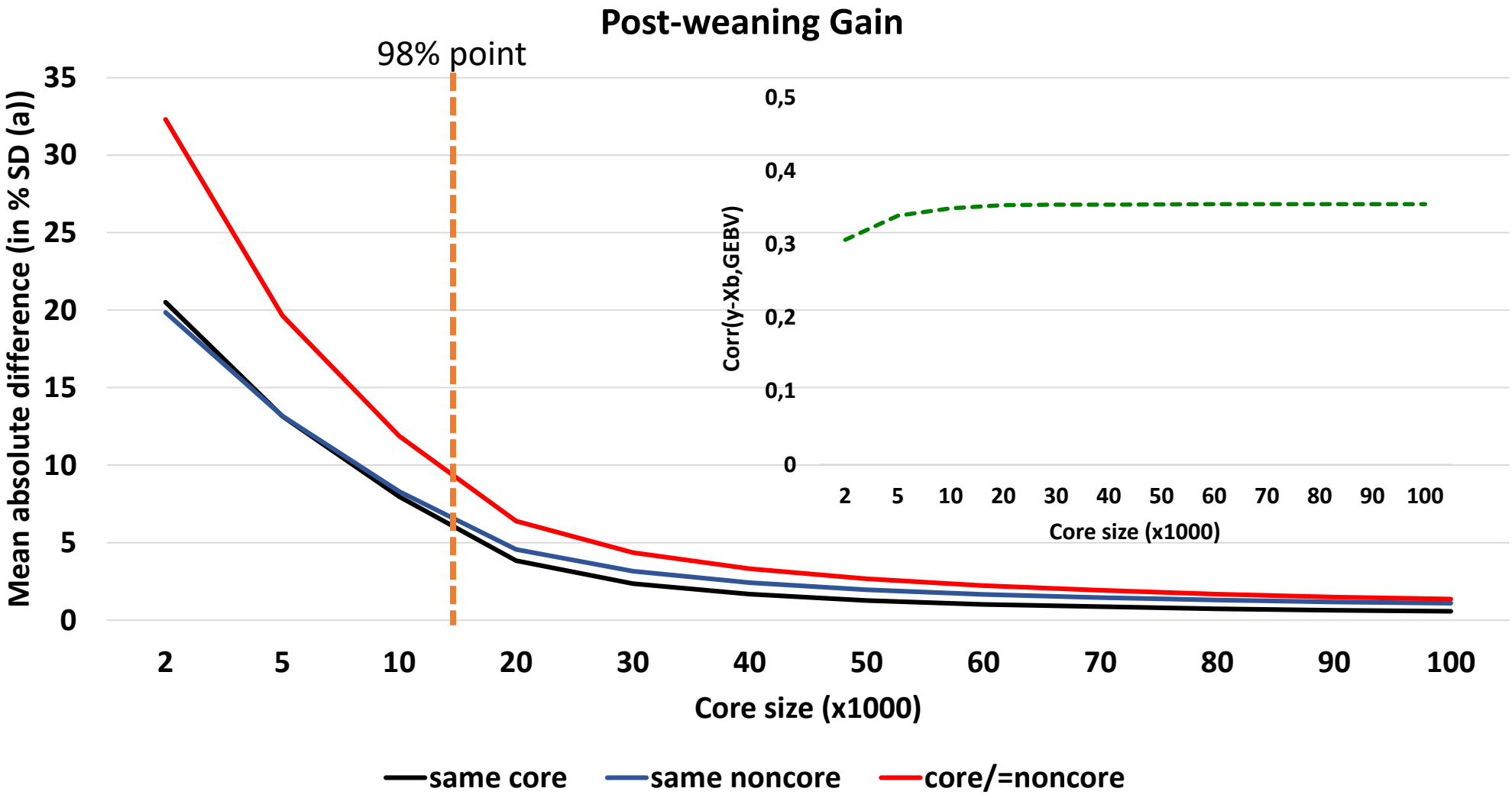
Samples	Avg| N(0, 1) |	Avg(| $\boldsymbol{\varepsilon_1} - \boldsymbol{\varepsilon_2}$ |
All	0.8	0.09
Top 1 in 100	2.9	0.35
Top 1 in 10,000	4.1	0.49
Top 1 in million	5.0	0.60

Rel=0.6

Theoretical reliability and average differences

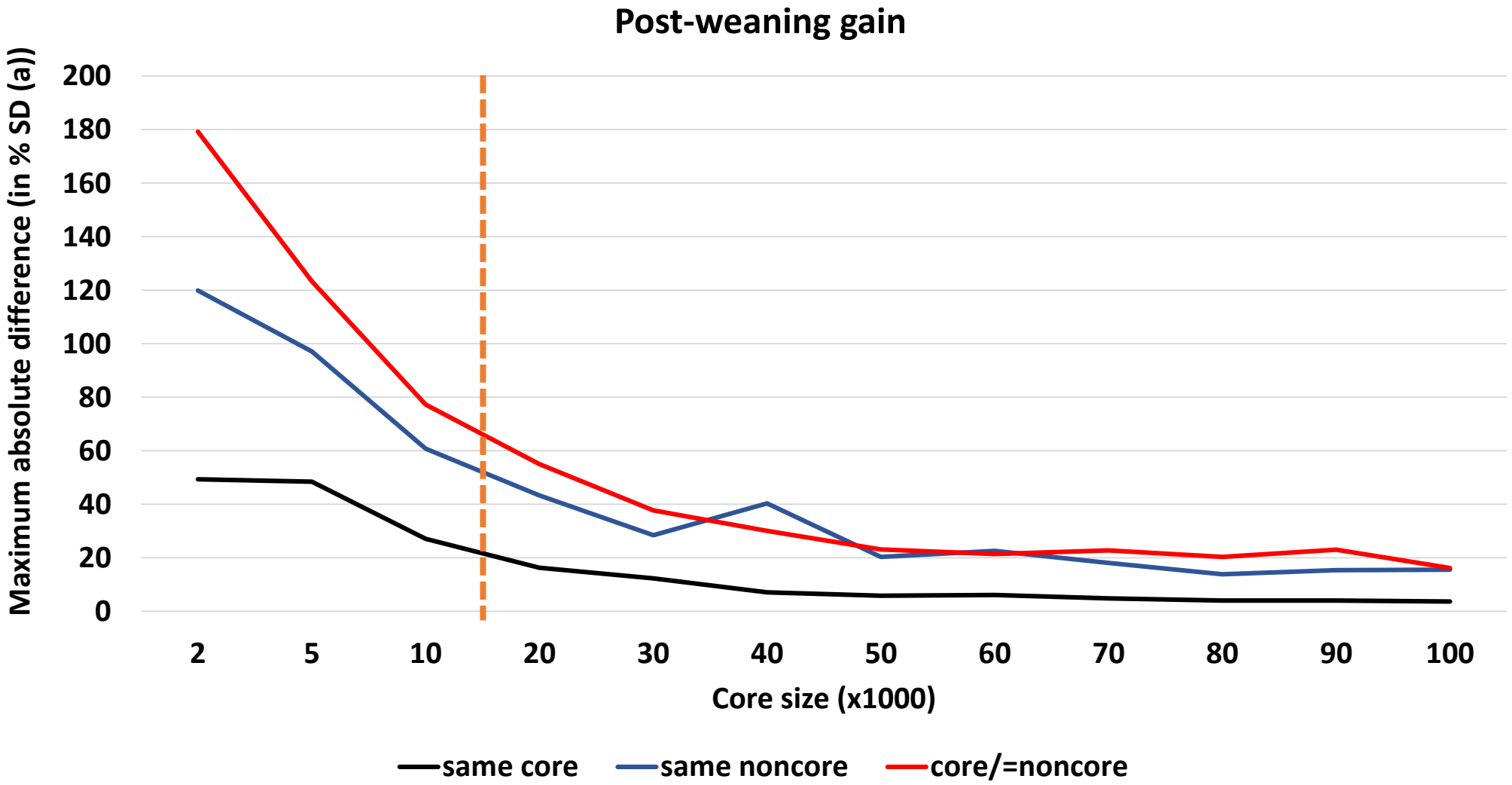


Mean change for Angus



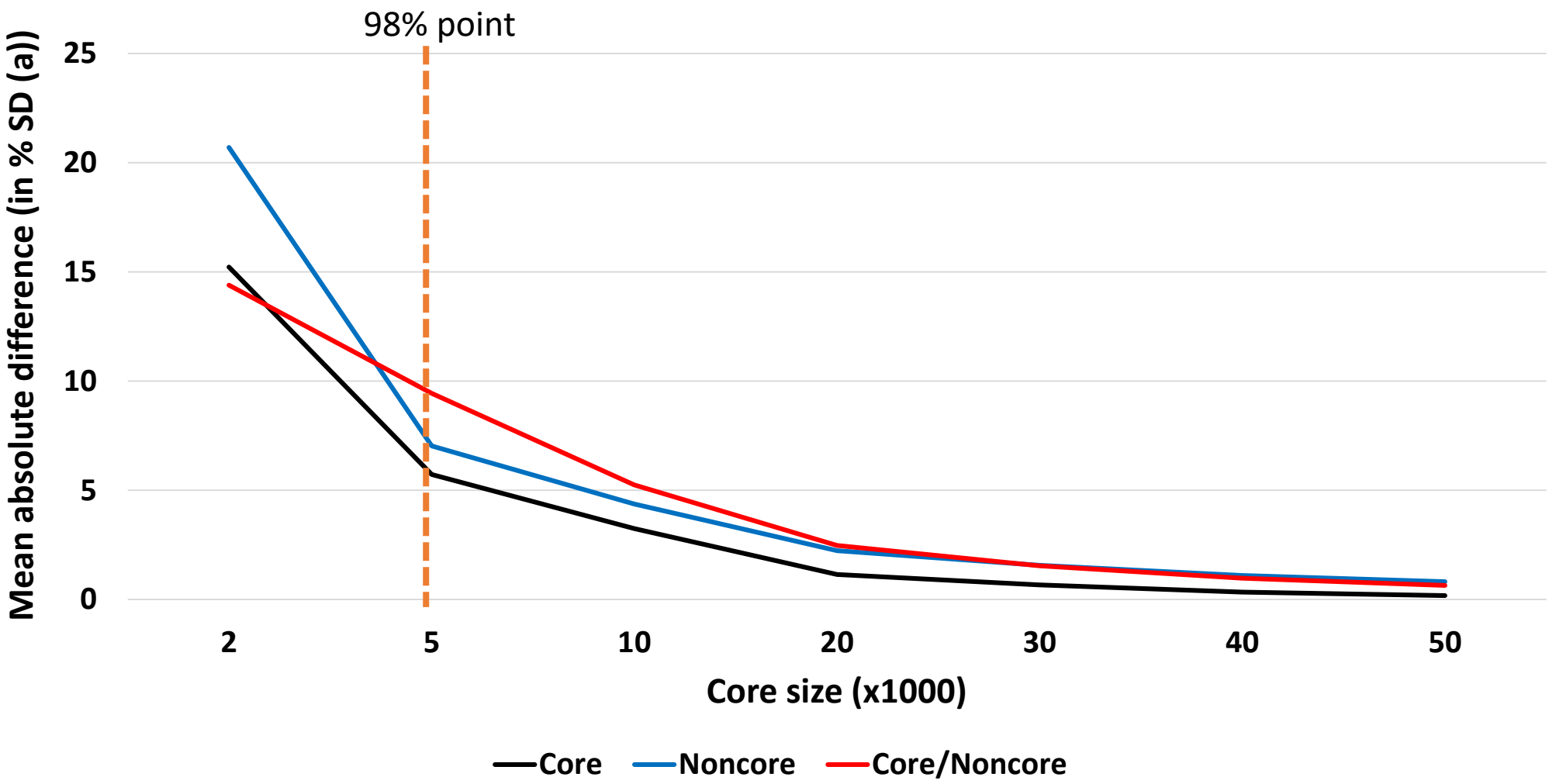
Maximum change for Angus

SD (a) = 27

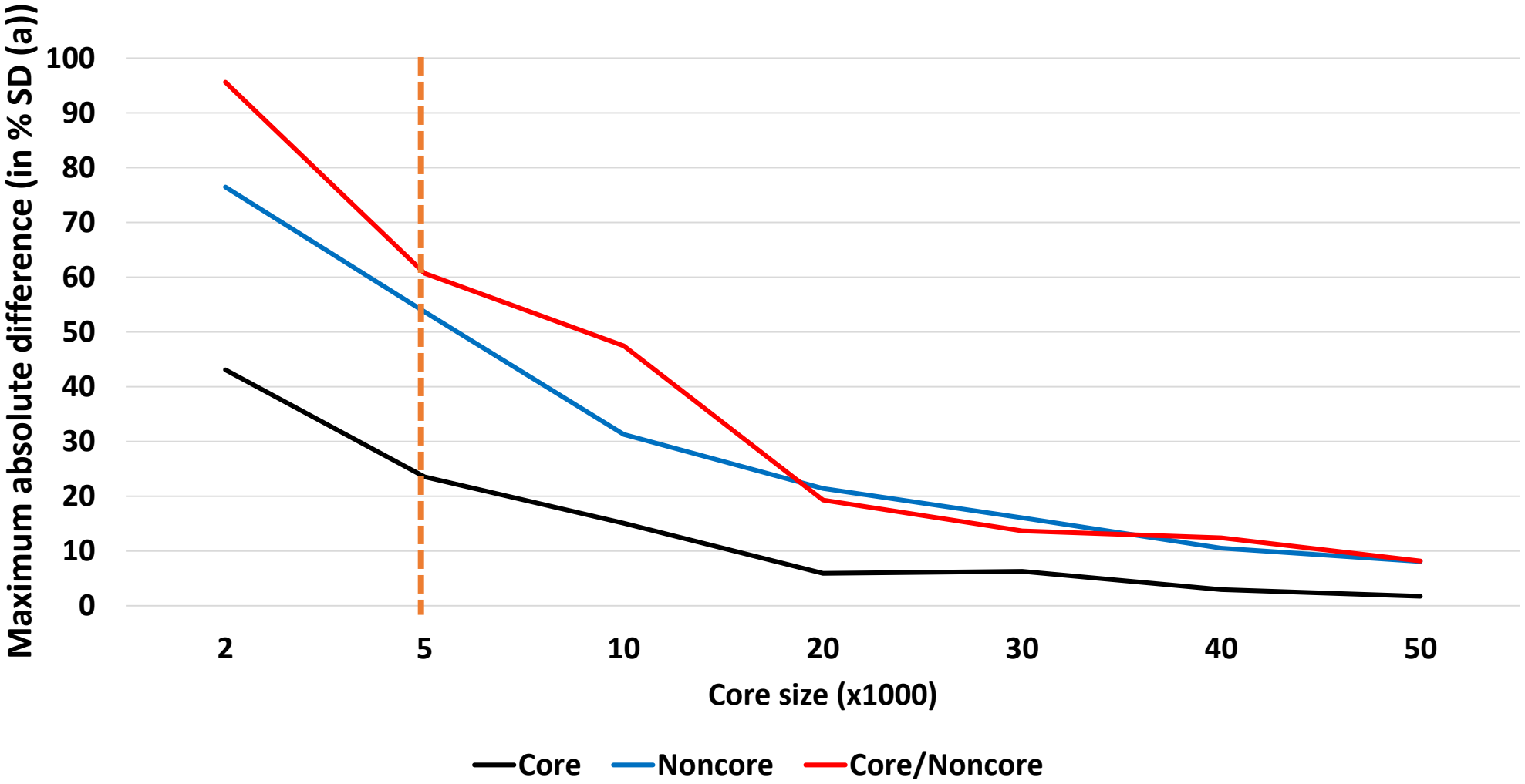


Mean change for Pigs

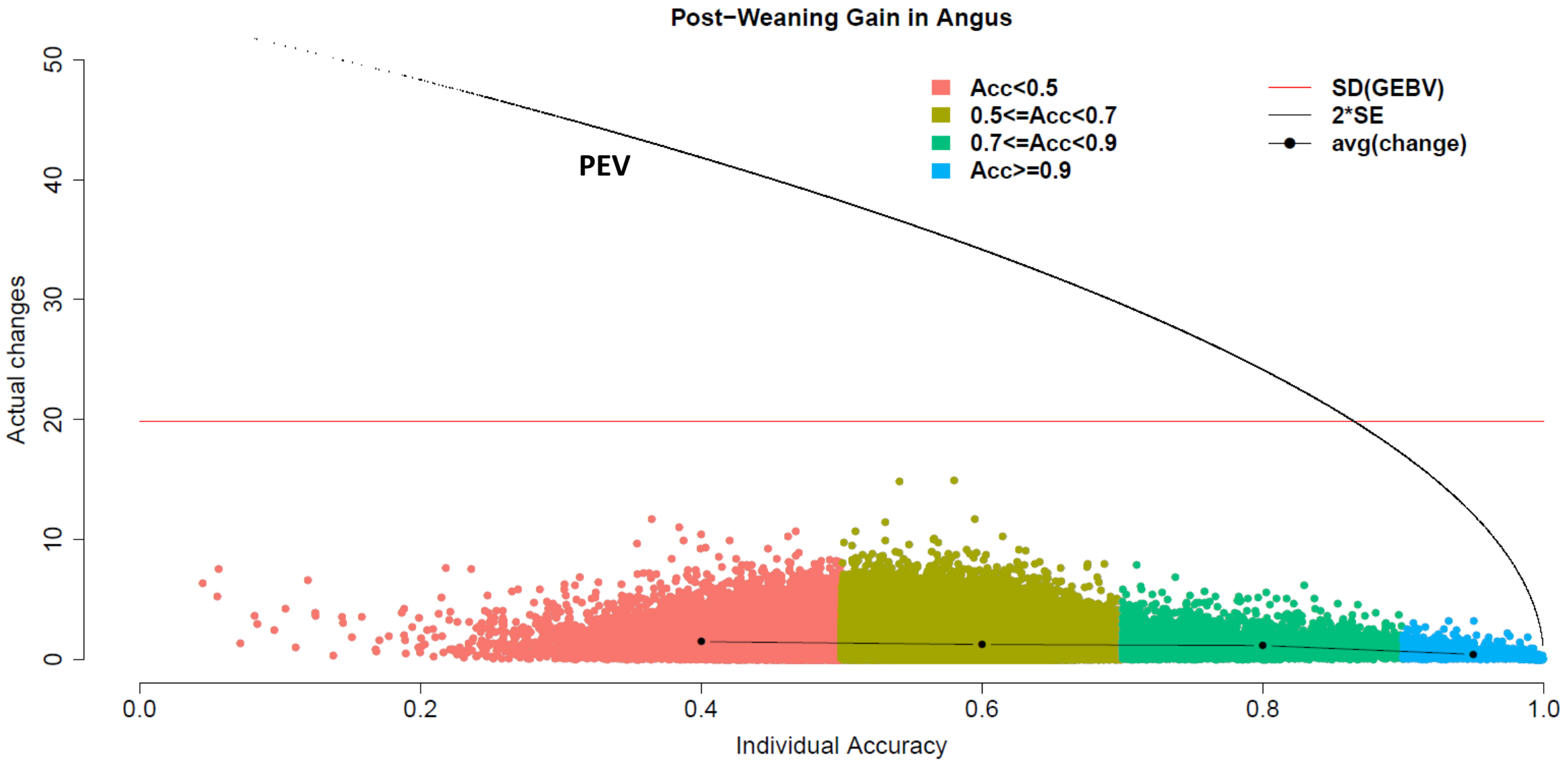
SD (a) = 39



Maximum change for Pigs



Which animals change most?



How to minimize changes due to APY?

- Increase number of core animals
- Treat important animals as core
- Keep core animals same for some period (e.g., 1 year)
- Use indirect prediction
- Use groups of bulls

Average change for outliers

$$GEBV = rel * BV + rel(1 - rel)N(0, \sigma_a^2)$$

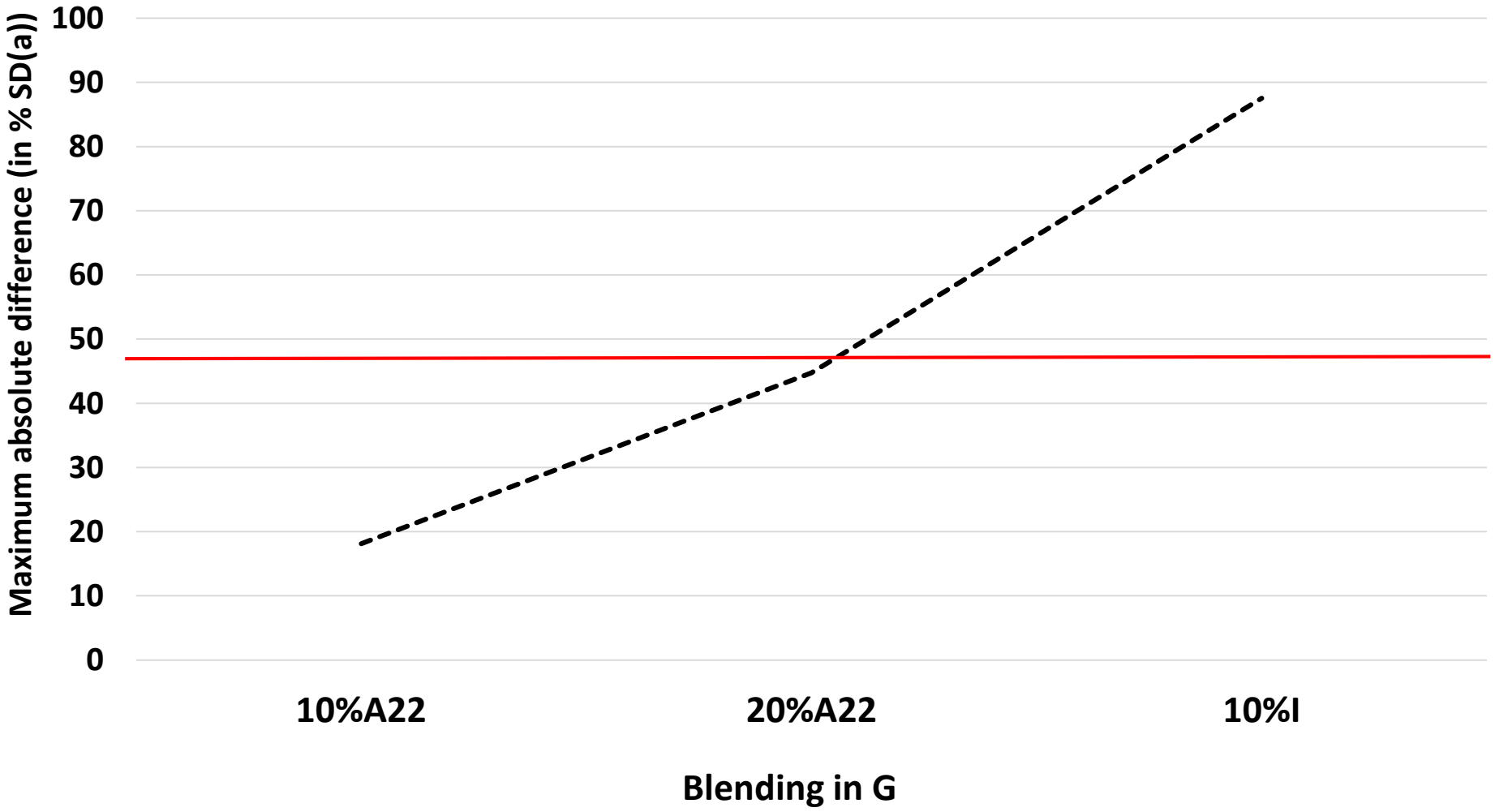
Reliability	Average deviation in additive SD			
	All	1 in 100	1 in 10,000	1 in million
0.80	0.40	1.04	1.56	1.96

Average change for outliers

$$GEBV = rel * BV + rel(1 - rel)N(0, \sigma_a^2)$$

Reliability	Average deviation in additive SD			
	All	1 in 100	1 in 10,000	1 in million
0.80	0.40	1.04	1.56	1.96
0.99	0.1	0.26	0.39	0.49

Changes in GEBV with different blending relative to 0.05 A_{22}



Pigs

All GEBV correlated >0.99

Conclusions

- More fluctuations in genomic evaluations than in BLUP
- Fluctuations of GEBV with APY due to choice of core animals
- Little impact on accuracy/reliability with sufficient number of core animals (EIG98 to EIG99)
- Fluctuations in line with reliabilities and normal distribution

Acknowledgements

Tom Lawlor
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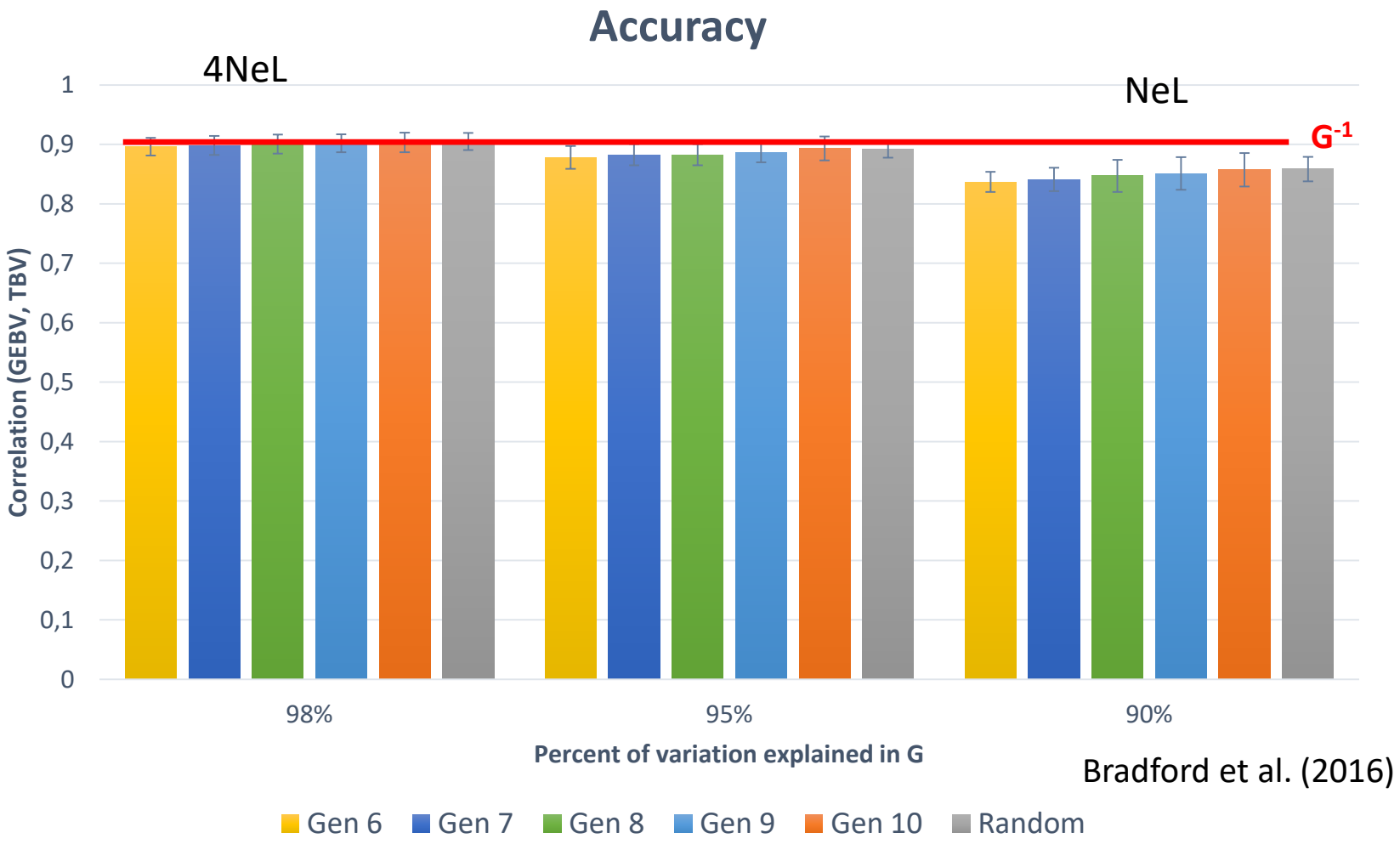
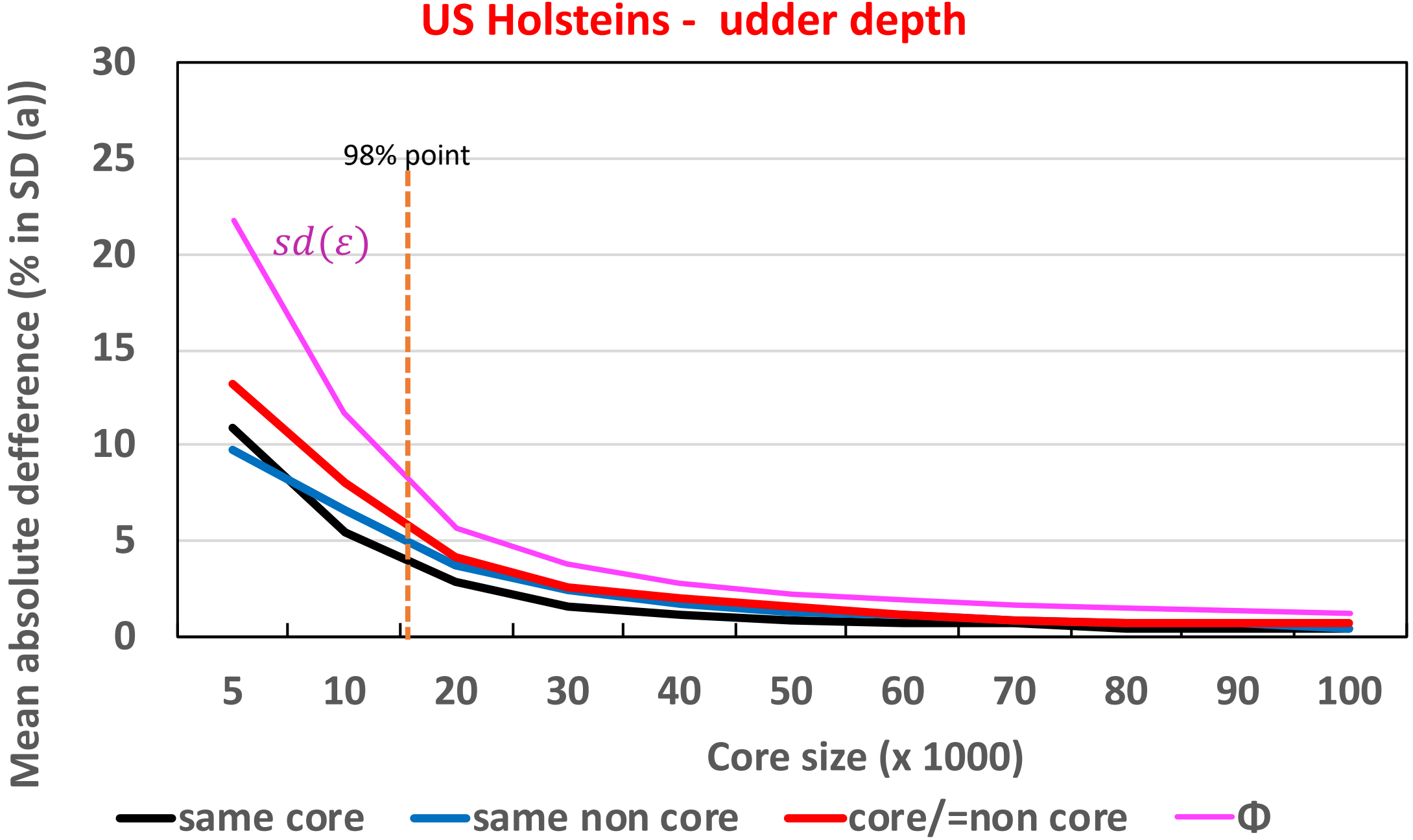
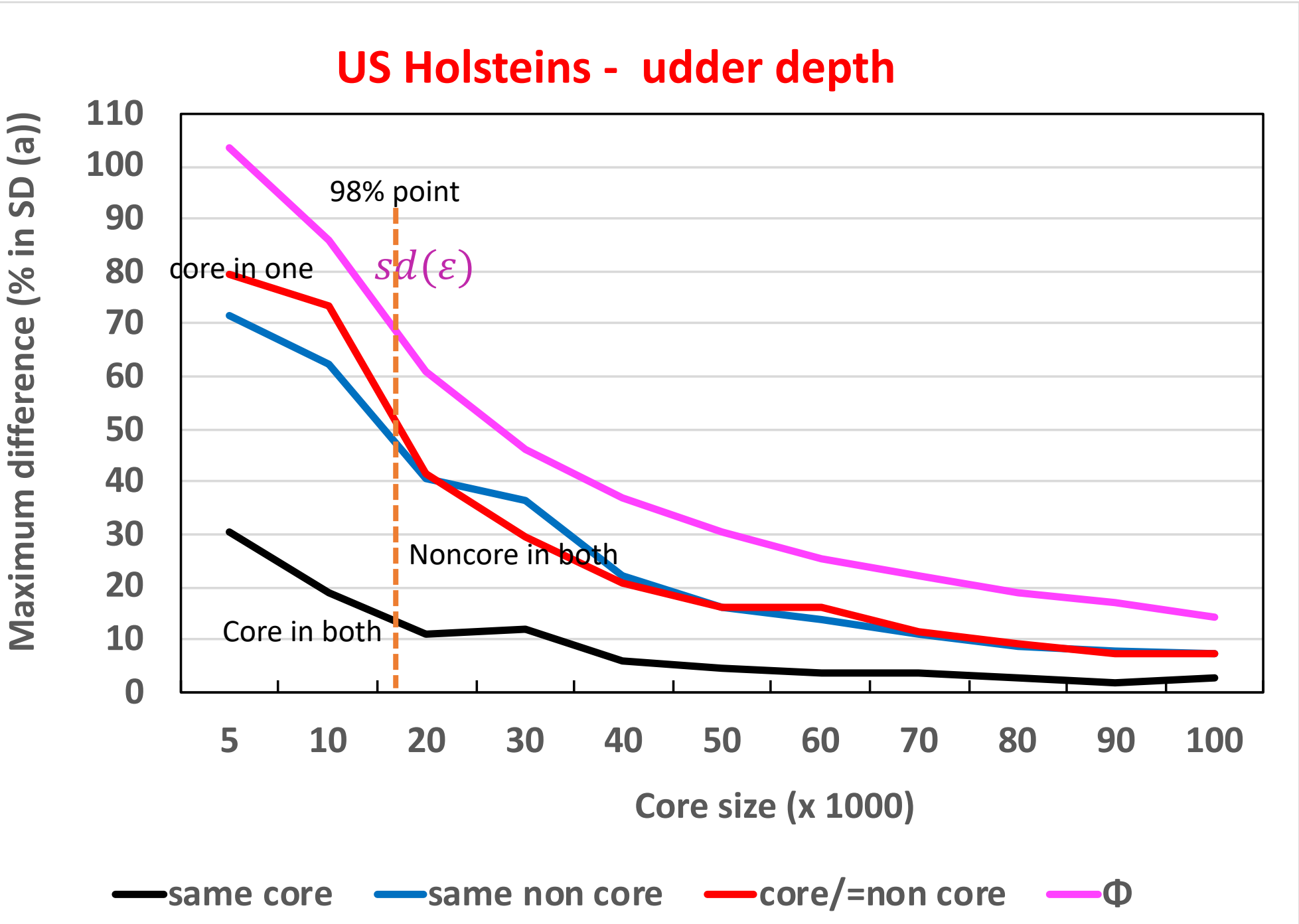
Which core animals in APY?



Bradford et al. (2016)


US Holsteins - udder depth
Mean absolute defference (% in SD (a))
30
25
20
15
10
5
0
98% point
$sd(\varepsilon)$
5
10
20
30
40
50
60
70
80
90
100
Core size (x 1000)
same core
same non core
core/=non core
Φ


US Holsteins - udder depth
Maximum difference (% in SD (a))
110
100
90
80
70
60
50
40
30
20
10
0
98% point
$sd(\varepsilon)$
core in one
Noncore in both
Core in both
5
10
20
30
40
50
60
70
80
90
100
Core size (x 1000)
same core
same non core
core/=non core
Φ