Faculty of Agricultural and Nutritional Science

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Institute of Animal Breeding and Husbandry

Bayerische Landesanstalt für Landwirtschaft

Genomic selection in German Landrace

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Session 29

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Motivation

Genomic Selection

Successfully implemented in cattle but not yet in pig breeding

Objective

- Investigate the potential for an application of genomic selection in the breeding program for German Landrace in Bavaria
- Focus on fertility traits
- Calibration- and validation samples including boars and sows

Data

- 1,982 animals were genotyped

- Traits analyzed were number of piglets born alive (NBA) and lean meat percentage (LMP)

- After editing of data, 1,868 pigs (314 boars, 1,554 sows) remained in the analysis

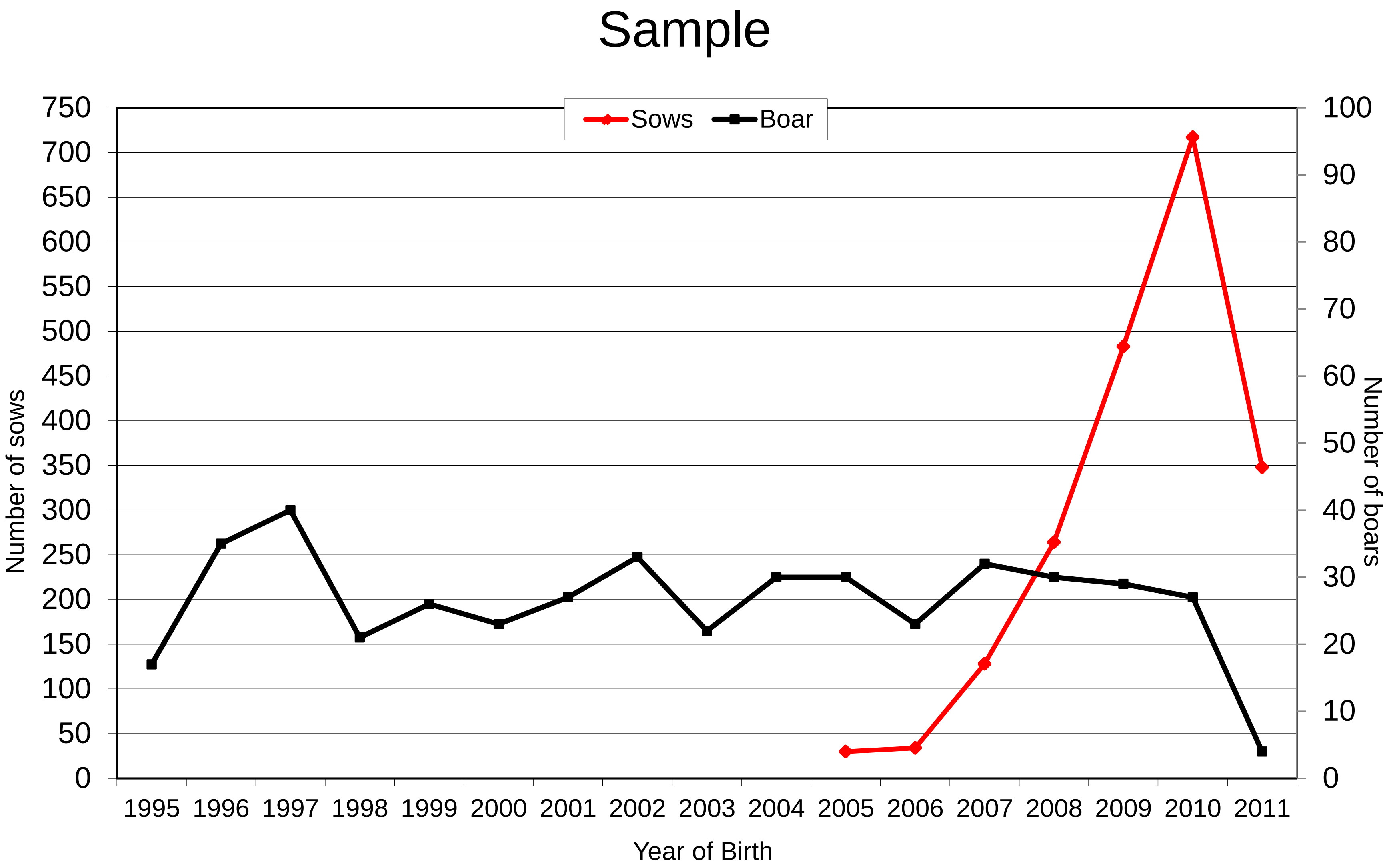
- Genotyping was done by Tierzuchtforschung e.V. using SNP60-Illumina Bead-Chips

Data

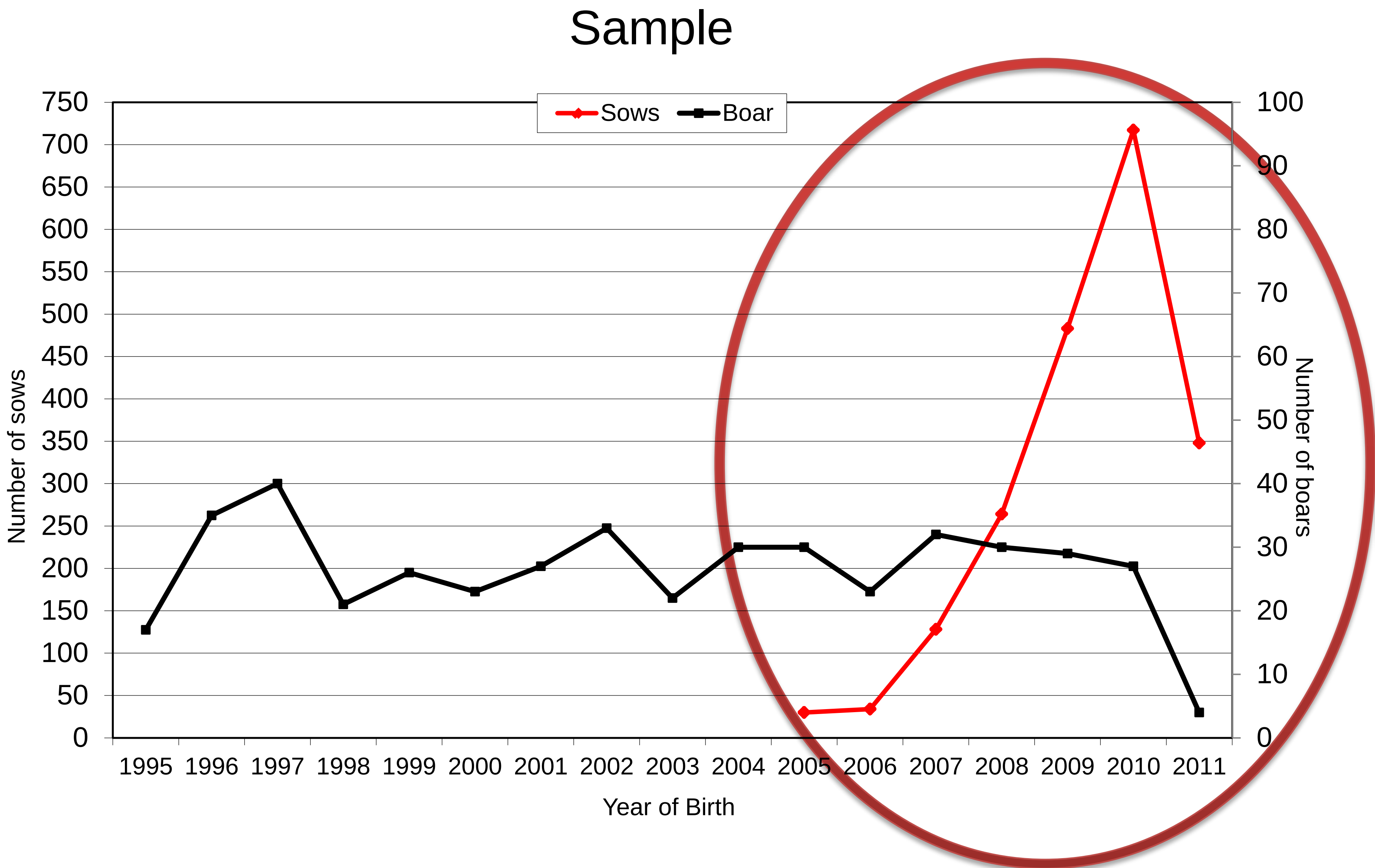
- Boar samples stored since 1995
  - Living and slaughtered boars
  - Stored by GeneControl GmbH

- Sow samples stored since 2006
  - Mainly from living animals
  - From nucleus and 13 downstream multiplier farms

Data


Sample
Sows
Boar
Number of sows
750
700
650
600
550
500
450
400
350
300
250
200
150
100
50
0
Number of boars
100
90
80
70
60
50
40
30
20
10
0
1995
1996
1997
1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
Year of Birth

Data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Sows
Boar
Number of sows
750
700
650
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450
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250
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100
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90
80
70
60
50
40
30
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10
0
1995
1996
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1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
Year of Birth

Data

Characterization of genotyped animals

	Boars		Sows	
	mean	min/max	mean	min/max
Progeny on station	49.1	2 / 454	2.9	1 / 15
NBA of daugthers	55.0	1 / 420	3.5	1 / 25
Number of litters	-	-	4.7	1 / 12

NBA : Number of piglets born alive

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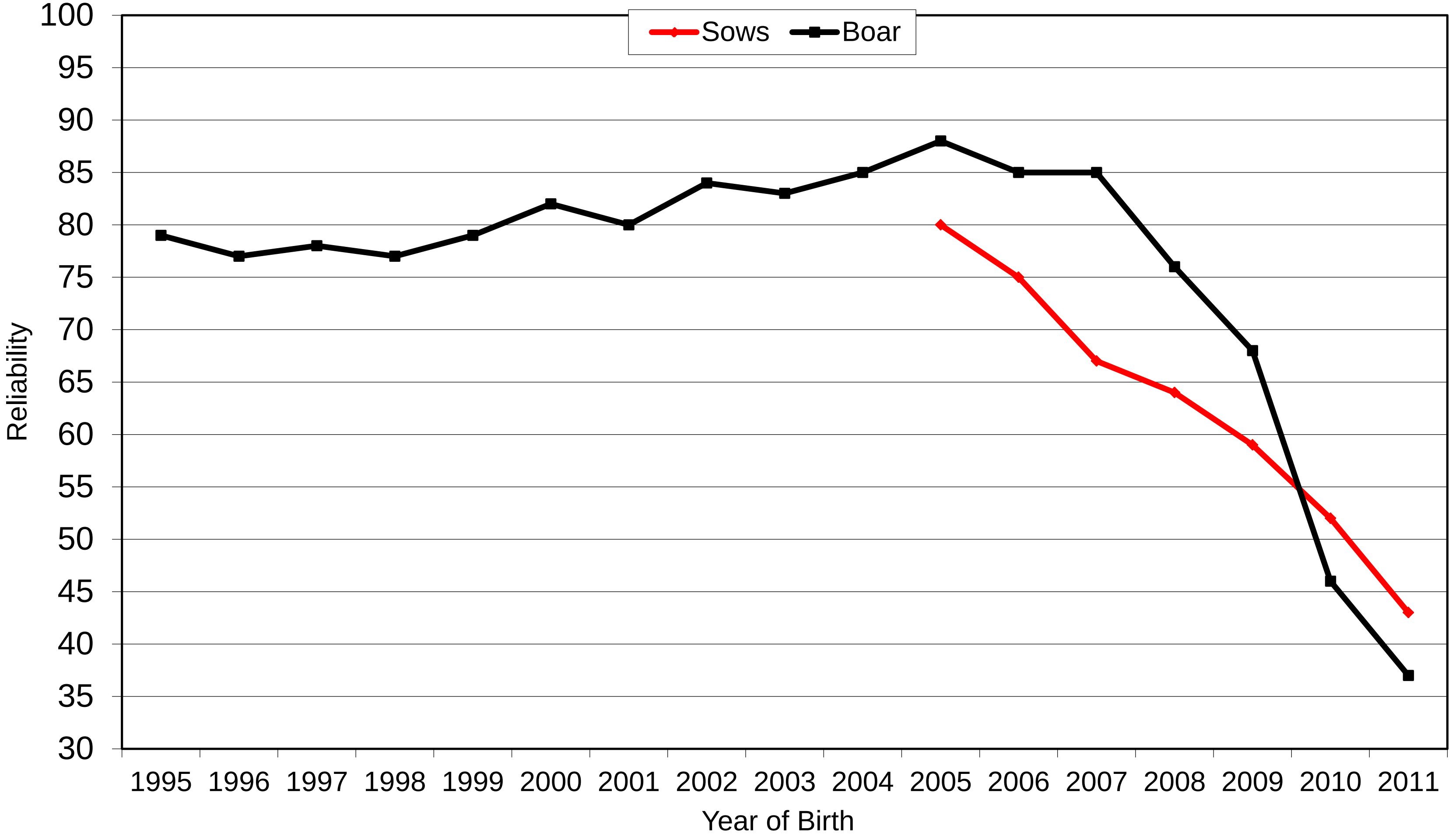
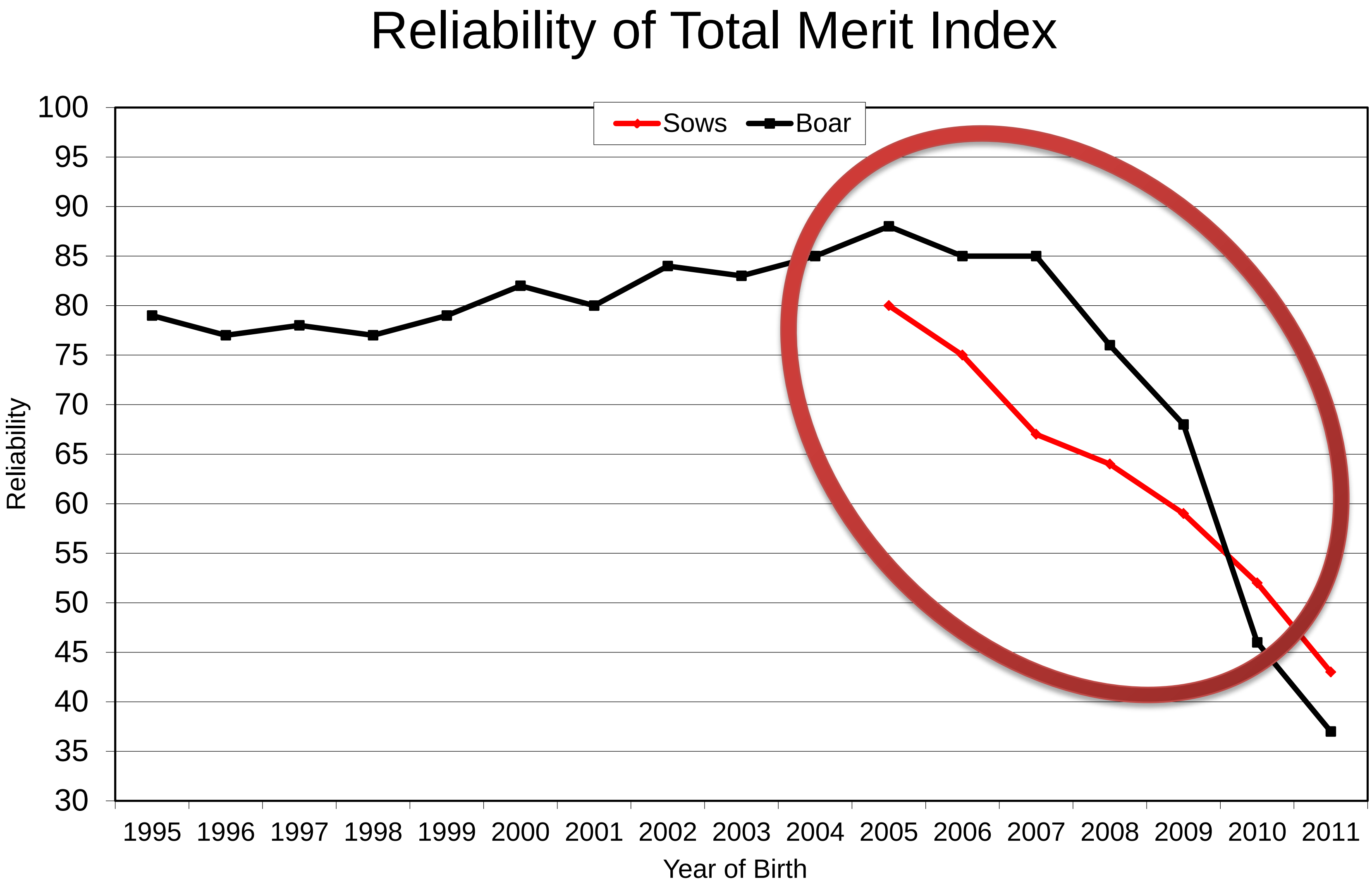
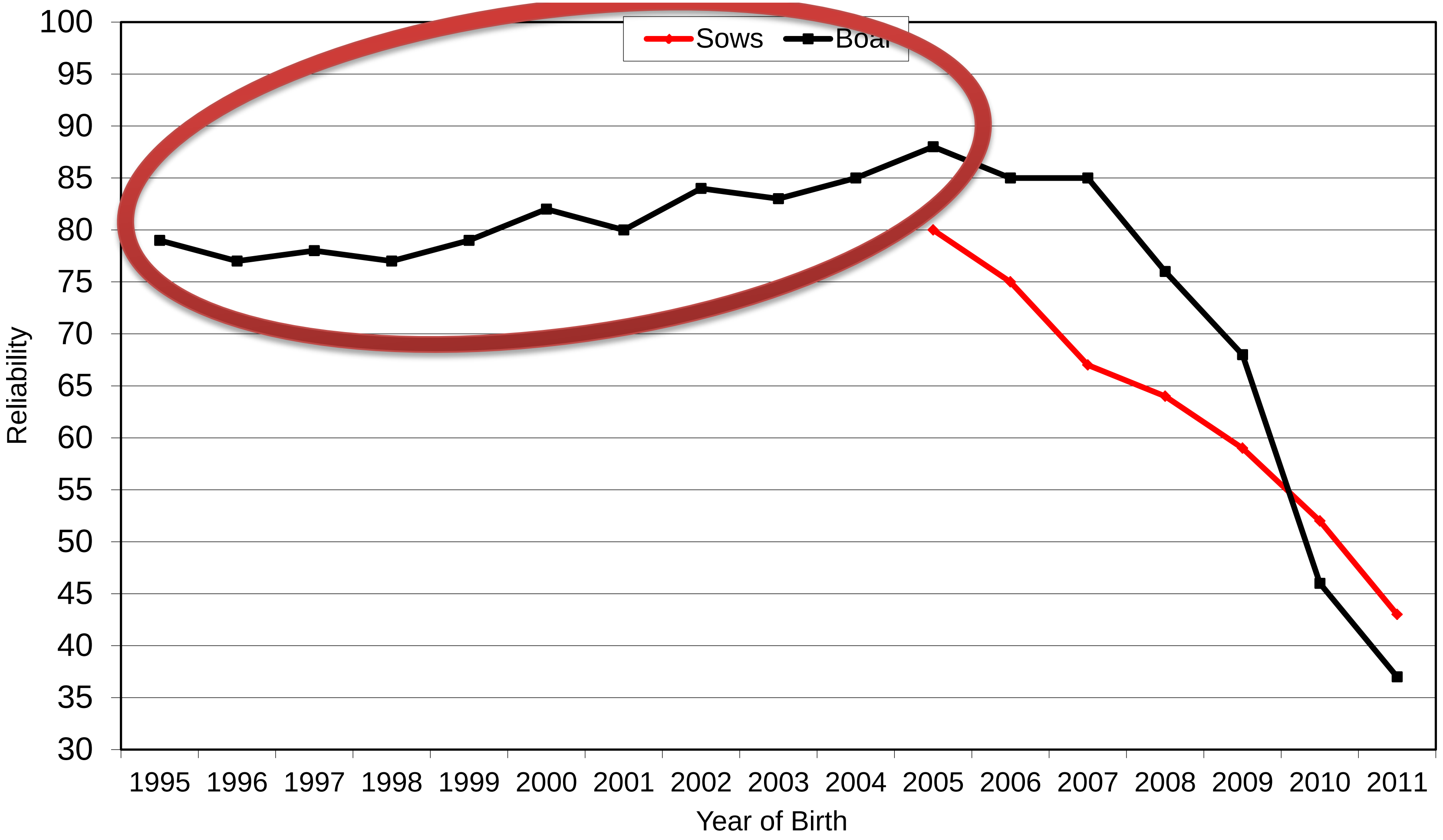

Reliability of Total Merit Index

Data


Reliability of Total Merit Index
Sows
Boar
100
95
90
85
80
75
70
65
60
55
50
45
40
35
30
Reliability
1995
1996
1997
1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
Year of Birth

Data



Reliability of Total Merit Index

Data

- Traits
  - number of piglets born alive (NBA; $h^2 = 0.24$)
  - lean meat percentage (LMP; $h^2 = 0.60$)

→ NBA is the mean average of the breeding value of first litters (NBA 1) and the breeding value of second and higher litters (NBA 2+)

→ Phenotypic data from herdbook farms and piglet-producers

→ LMP data was recorded on progeny test station in Schwarzenau and Grub

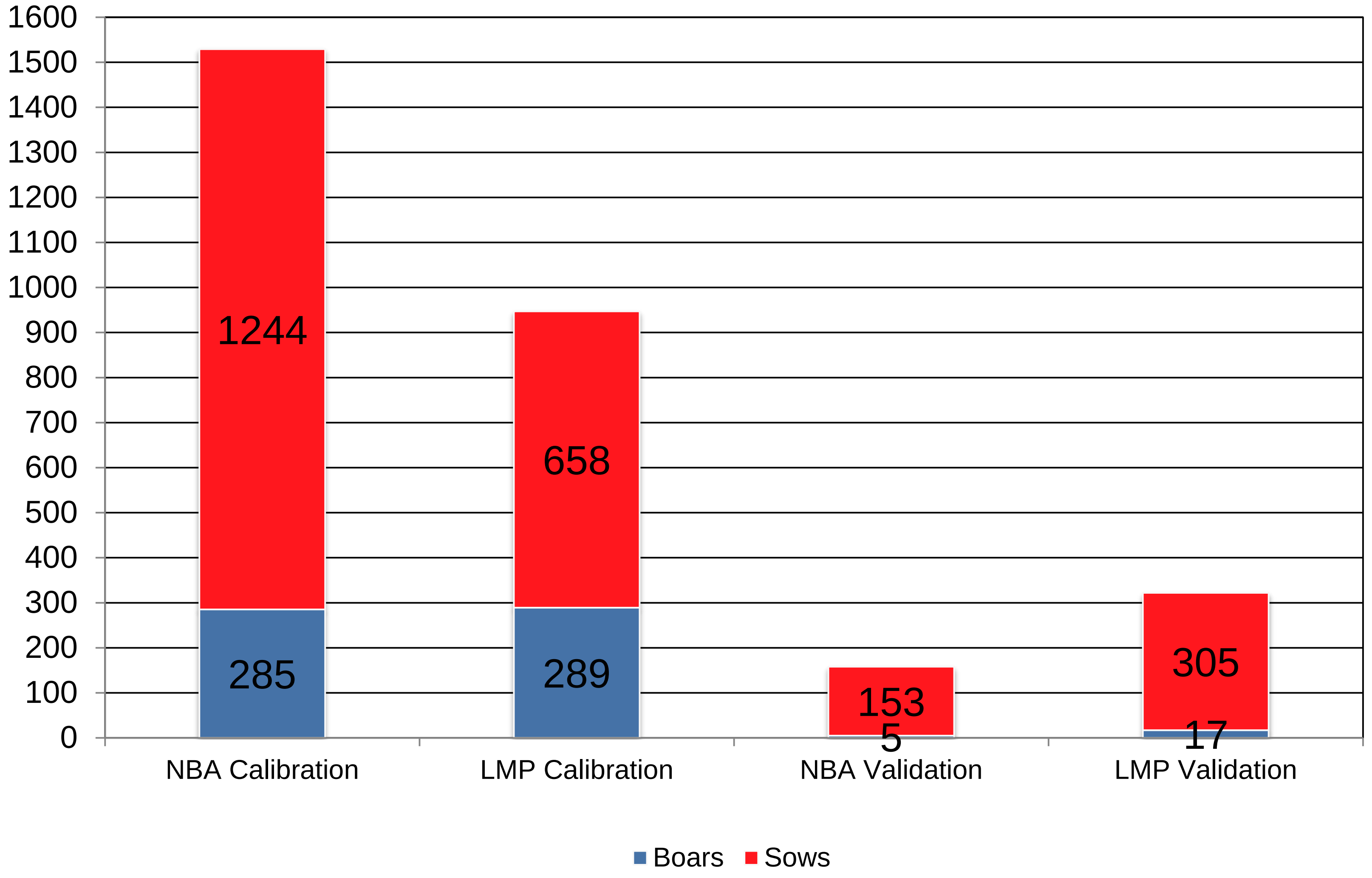
Method

- Validation via forward-prediction according to Interbull validation-test (Mäntysaari et al., 2011)

- Two different data-sets:
  - Reduced run: all animals since 2011 without own performance
  - Complete run: all available phenotypic information

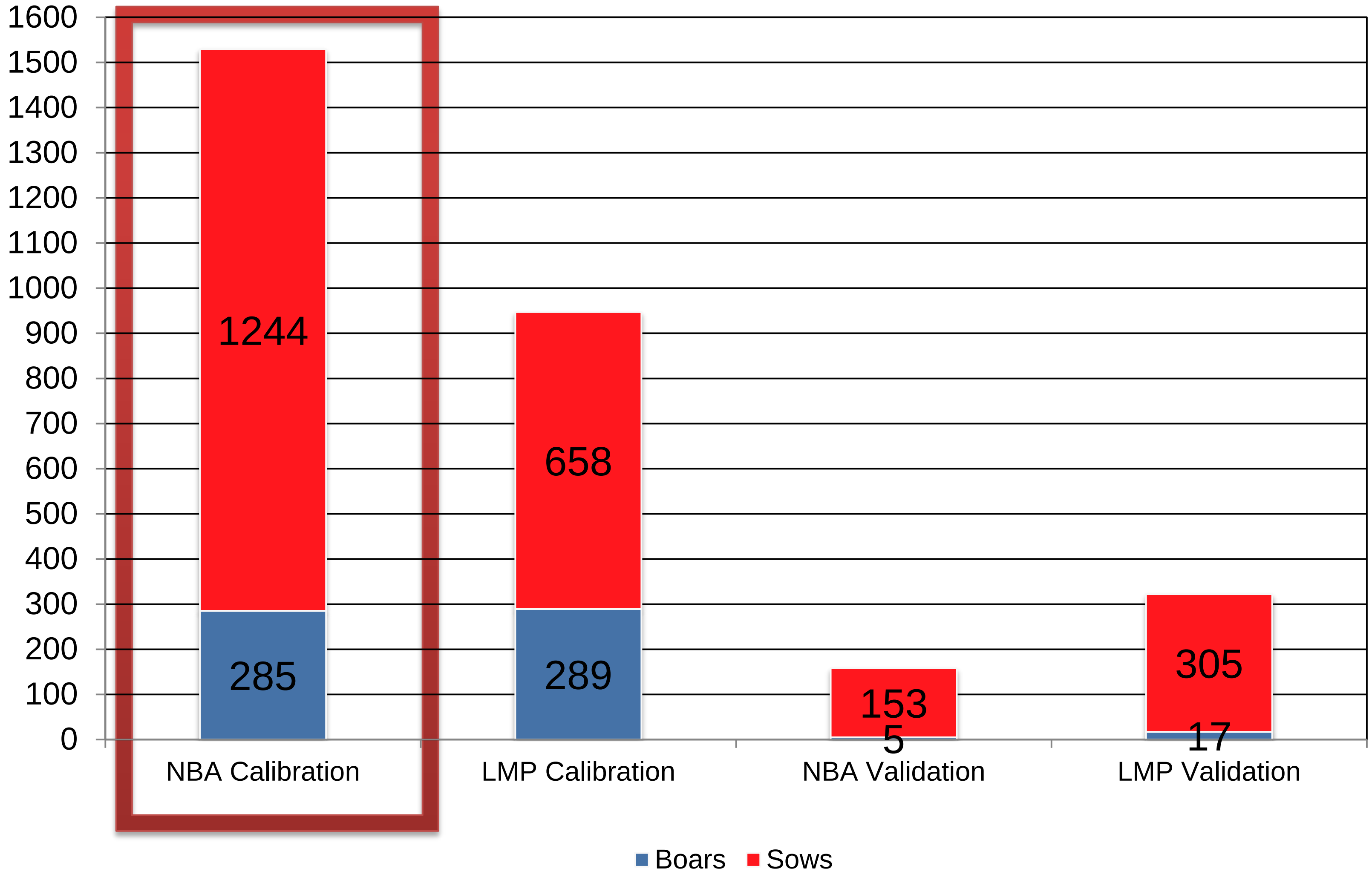
Method

Size of calibration and validation datasets

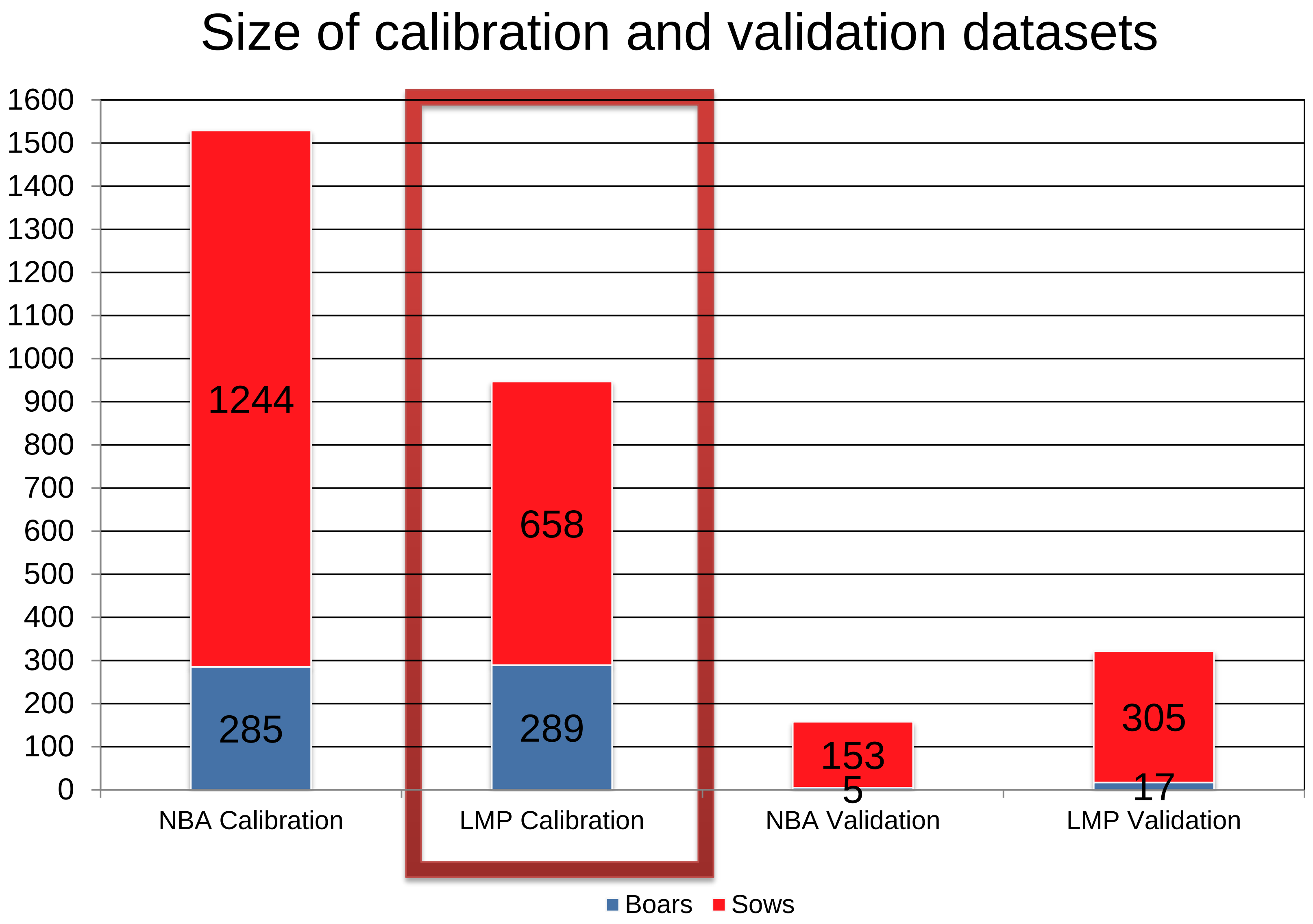


Method

Size of calibration and validation datasets



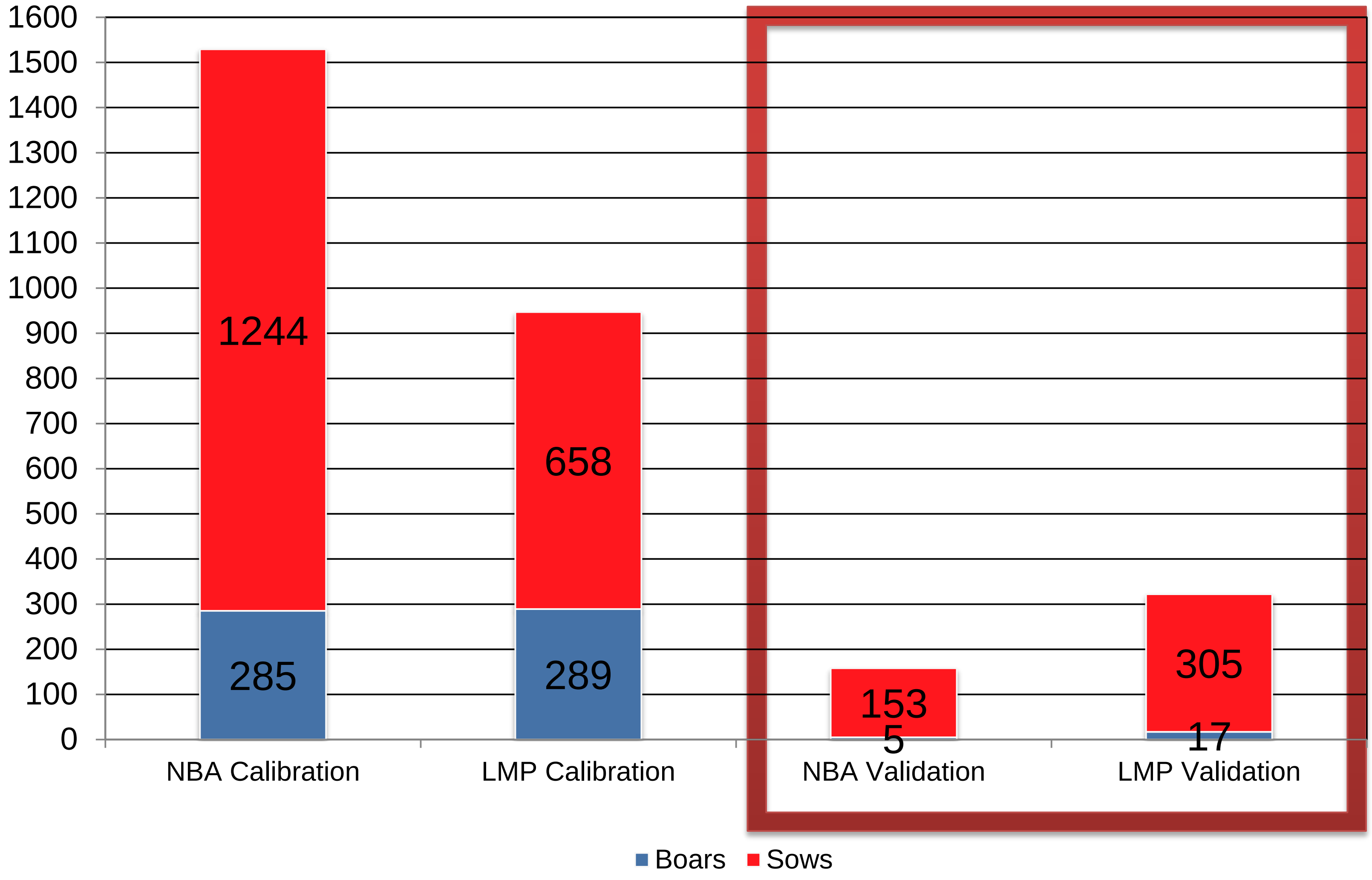
Method



Size of calibration and validation datasets
1600
1500
1400
1300
1200
1100
1000
900
800
700
600
500
400
300
200
100
0
1244
285
658
289
153
5
305
17
NBA Calibration
LMP Calibration
NBA Validation
LMP Validation
Boars
Sows

Method

Size of calibration and validation datasets



Method

- Deregressed estimated breeding values were used as response variable (Garrick et al. 2009)
- Direct genomic values (DGV) were calculated using the gBLUP approach (VanRaden 2008)
- Genomic breeding values (GEBV) were calculated by blending direct genomic values with conventional parent averages (VanRaden et al., 2009)
- Reliability was corrected for prior selection on PA with ‘realized genomic reliabilties’ according to VanRaden (2008)

Results

Realized genomic reliabilities (R^2)

	PA	DGV	GEBV
NBA	0,38	0,54	0,58
LMP	0,41	0,43	0,44

NBA : Number of piglets born alive
LMP: Lean meat percentage

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Reliability was corrected for prior selection on PA with ‘realized genomic reliabilities’ according to VanRaden (2008)

→ Not on the same scale as reliability of conventional EBVs

Discussion

- Realized reliabilities of GEBV for NBA are higher (0.58) than the parent-average (0.38)

- For LMP, the gain in reliability (0.44) is small from PA (0.41)

- Calibration with boars and sows in one sample is feasible

Outlook

- Genomic selection can be beneficial for maternal traits.
- Genomic selection may also be attractive for traits like boar-taint or intra-muscular-fat
- Realized reliabilities for carcass traits may hardly justify additional costs of Genomic Selection
- Short-term implementation of Genomic Selction is feasible

Thank You!

Project partner:
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Christian-Albrechts-Universität zu Kiel
LKV Bayern
Tierzuchtforschung München e.V.

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