

# Genomic analysis of reproductive traits in health challenged commercial sow herds

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# Introduction

- ❖ Reproductive efficiency is key to profitability in the swine industry
- ❖ Reproductive traits are lowly heritable and difficult to select for
- ❖ Selection for performance during health challenge difficult
  - Disease traits not expressed in nucleus due to high health status
- ❖ Genomic information can improve selection accuracy

# Objectives

- ❖ Estimate genetic parameters
- ❖ Identify associated genomic regions
- ❖ Perform genomic prediction for reproductive traits

# Gilt Acclimation Project



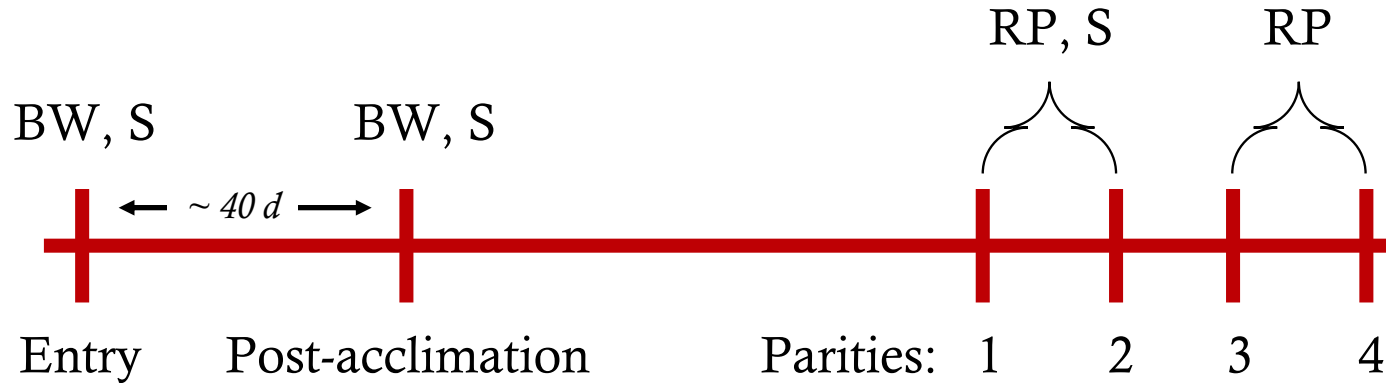
Breeding Companies,  $n \equiv 7$

Multiplier herds  $\rightarrow$  2 to 3/breeding co.;  $n \equiv 17$

Commercial herds  $\rightarrow$  2 to 4/multiplier;  $n = 23$

- Crossbred replacement gilts from high health multipliers
  - Introduced into commercial farms with a history of health challenge
  - Followed standard acclimation and gilt rearing procedures

# Gilt Acclimation Project



## Serology data:

- 1) PRRS
- 2) PCV2
- 3) Influenza (SIV)
- 4) MH (*Mycoplasma hyopneumoniae*)
- 5-13) *Actinobacillus pleuropneumoniae* (app):  
1, 2, 3, 5, 7, 10, 12, and 13

BW: Body Weight

S: Serum

RP: Reproductive Performance

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# Data

- 🕒 7,635 farrowing events from 2,604 sows with 1 to 4 parities
- 🕒 Animals were genotyped using one of three versions of the Illumina PorcineSNP BeadChip
  - 42,145 SNPs in common between versions
  - 38,191 SNPs used after quality control
- 🕒 Genomic relationship estimated using SNPs (VanRaden, 2008)

# Traits Recorded

- Total number of piglets born (TB)
- Number of piglets born alive (NBA)
- Number of stillborn piglets (SB)
- Number of mummified piglets (MUM)
- Number of piglets born dead (NBD)
- Number of piglets weaned (NW)

# Traits Analyzed

- ❖ Lifetime performance
  - Sum performance of parities
- ❖ Average performance
  - Average performance of parities

# Adjustment of Average Performance

- ❖ Pre-adjusted phenotype fitted for
- ❖ Model:  $y_{ijkl} = \mu + CG_i + PAR_j + YM_k + u_{ijkl} + pe_{ijkl} + e_{ijkl}$ 
  - CG: fixed effect of contemporary group
  - PAR: fixed effect of parity
  - YM: fixed effect of year-month
  - u: breeding value
  - pe: permanent environmental effect
  - Covariate of net number of fosters used for NW



# Genetic Parameters

## ▣ Lifetime performance

- Model:  $y_{ijk} = \mu + CG_i + u_{ijk} + e_{ijk}$ 
  - CG: fixed effect of contemporary group
  - u: breeding value
  - Covariate of net number of fosters used for NW

## ▣ Average performance

- Pre-adjusted phenotype

# Heritabilities

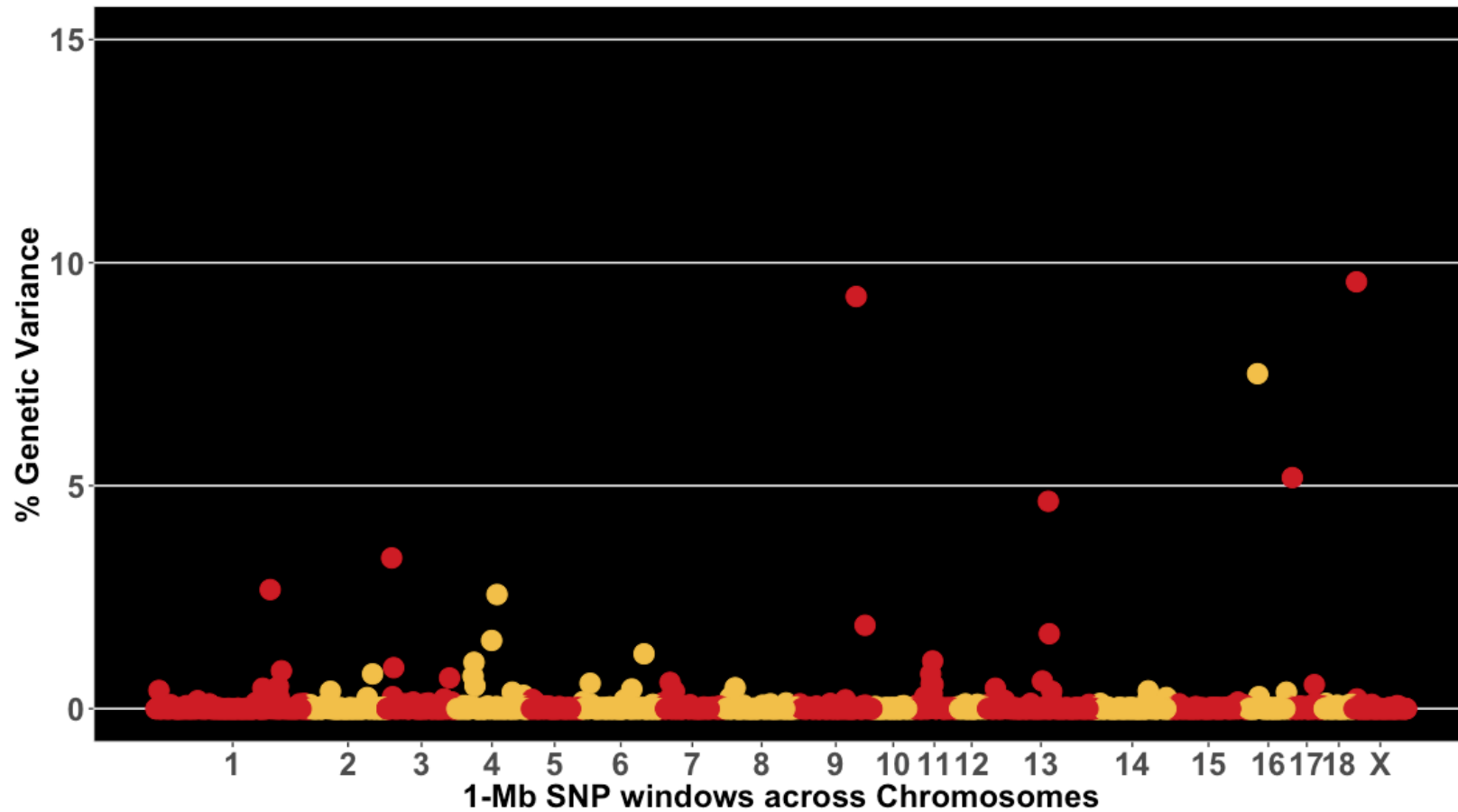
Trait <sup>1</sup>	TB	NBA	SB	MUM	NBD	NW
<b>Average</b>	0.18 (0.03)	0.11 (0.03)	0.16 (0.03)	0.01 (0.02)	0.16 (0.03)	0.03 (0.02)
<b>Lifetime</b>	0.12 (0.04)	0.10 (0.03)	0.17 (0.04)	0.03 (0.03)	0.17 (0.04)	0.02 (0.03)

<sup>1</sup>TB, total born; NBA, number born alive; SB, stillborn; MUM, mummified; NBD, number born dead; NW, number weaned

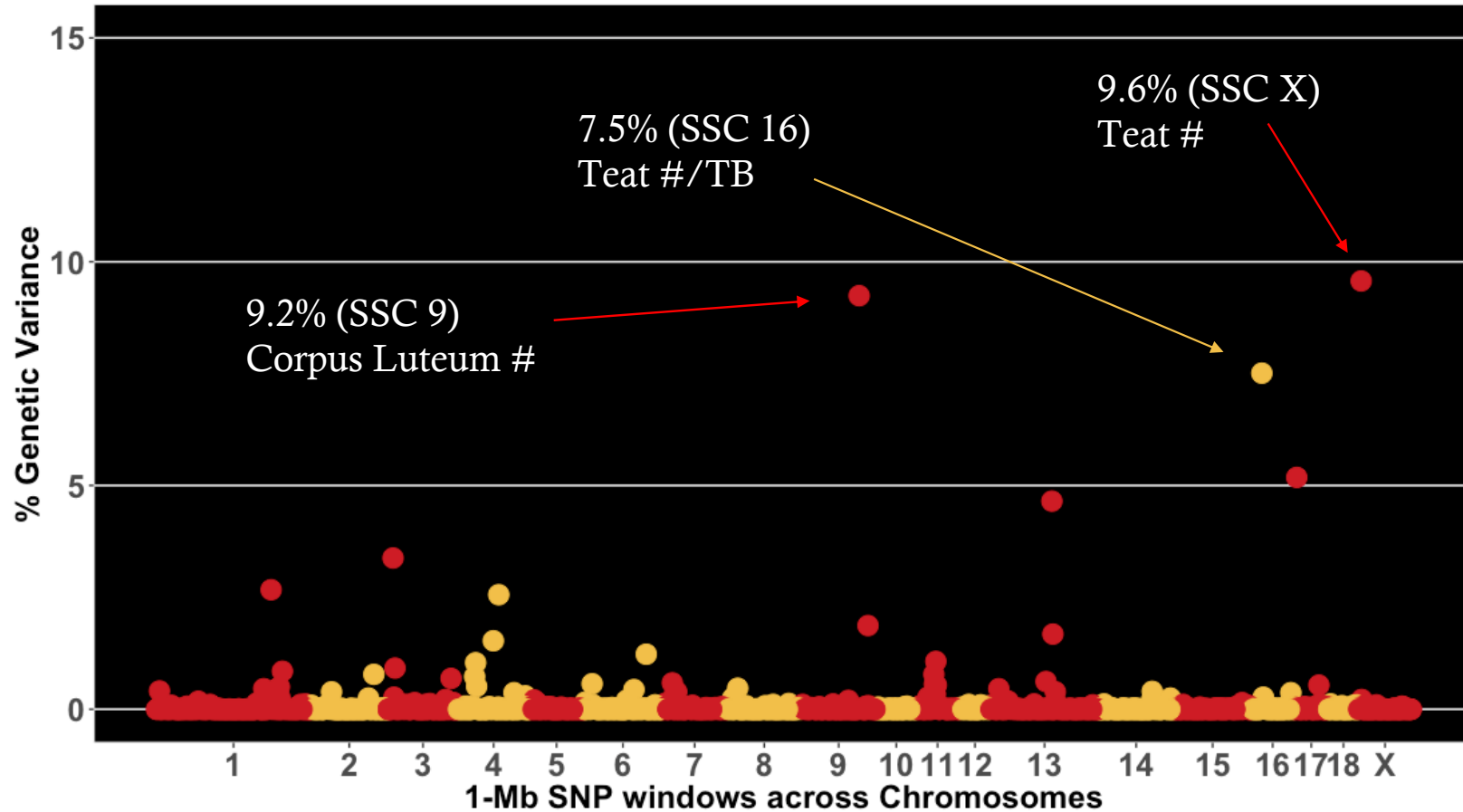
# Genome-Wide Association Study (GWAS)

- ❖ Final analysis with Bayes-B
  - $\pi = 0.995$
- ❖ Fixed effects same as genetic parameters
- ❖ SNP effects fit as random
- ❖ GenSel used for analysis

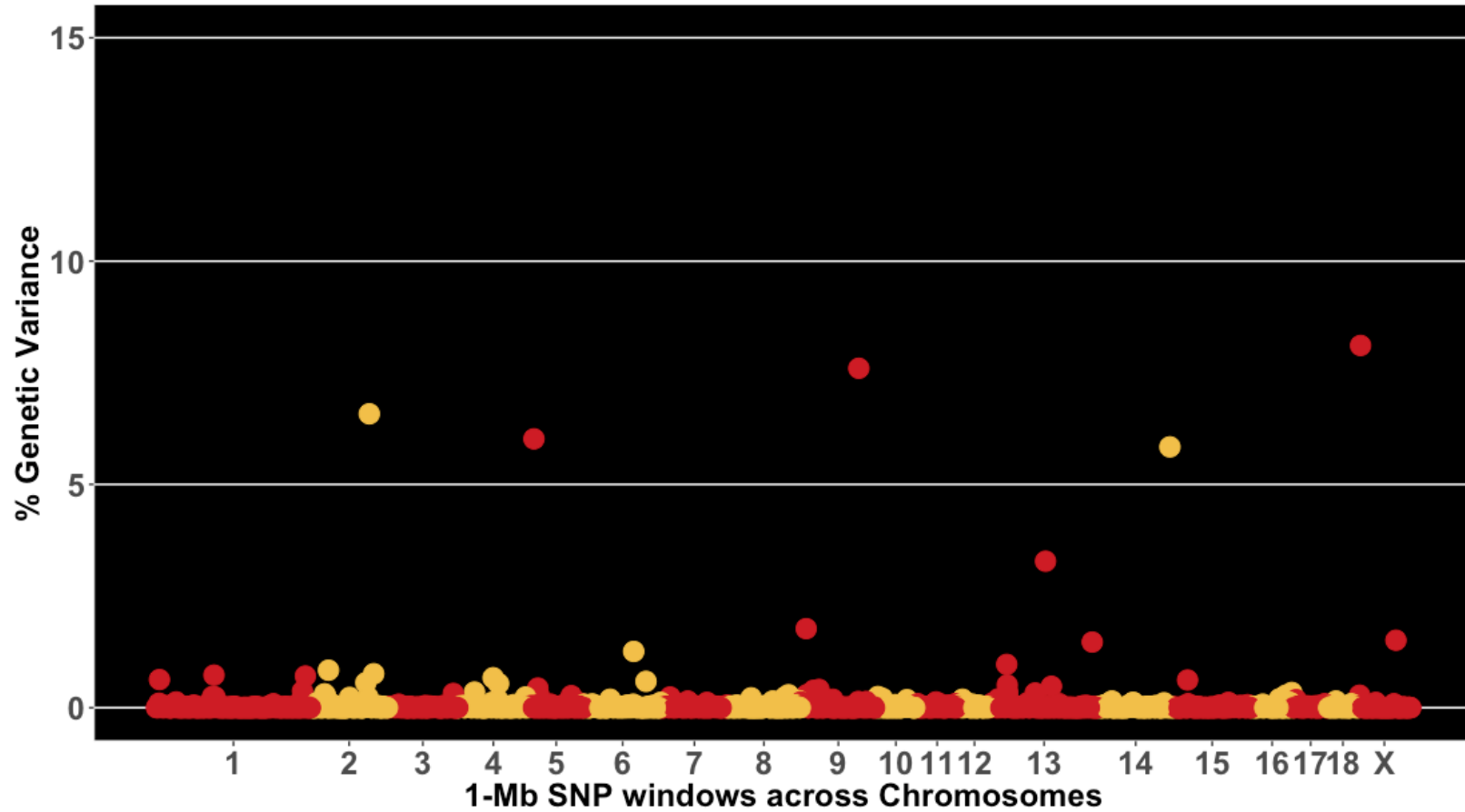
# Number Stillborn – Average Performance



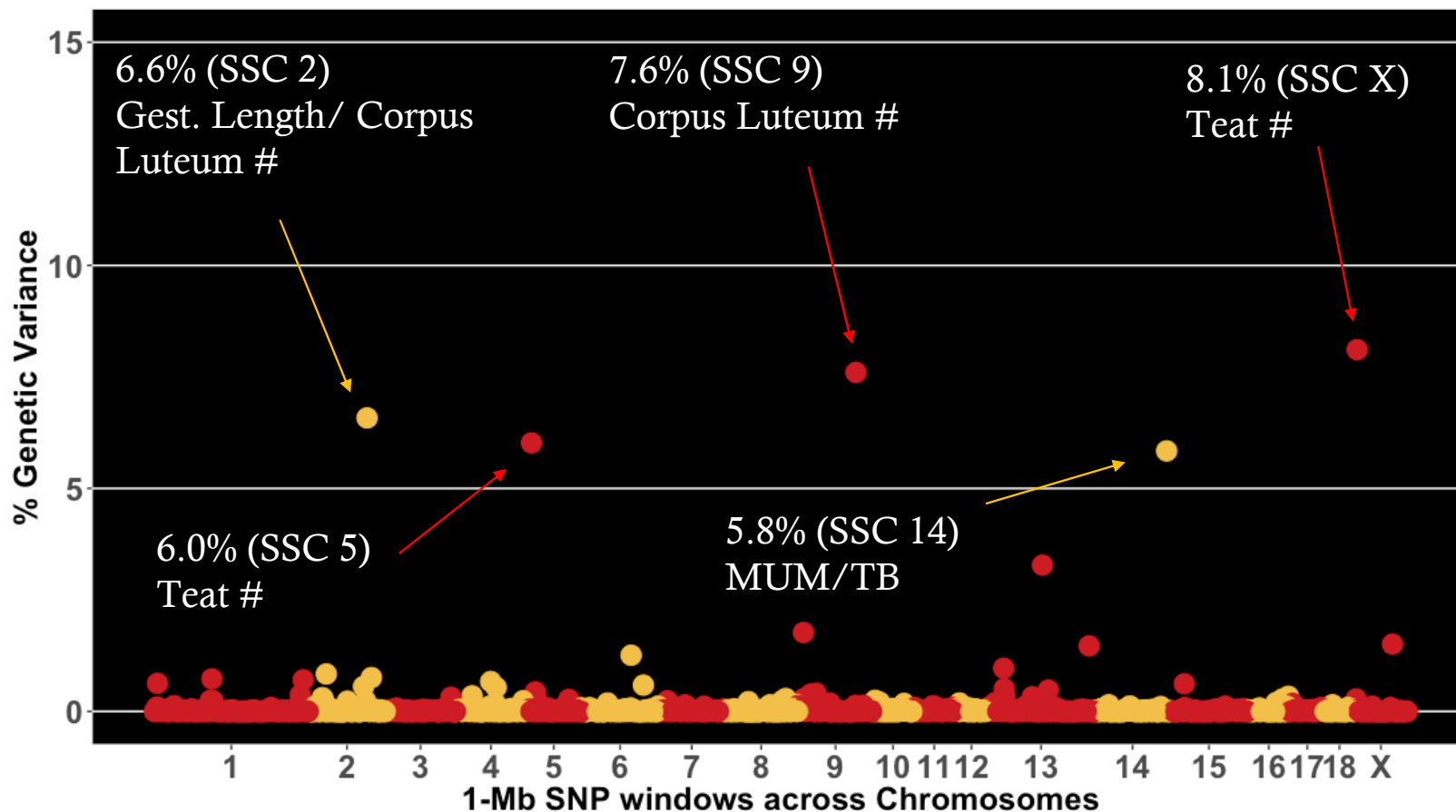
# Number Stillborn – Average Performance



# Number Born Dead – Lifetime Performance



# Number Born Dead – Lifetime Performance

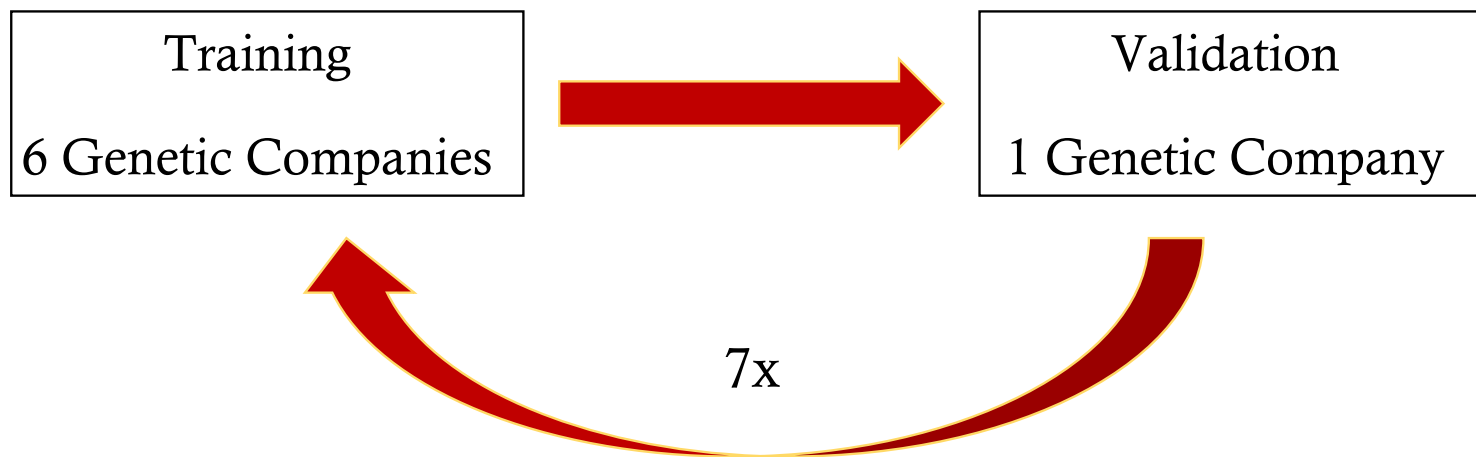


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# Genomic Prediction

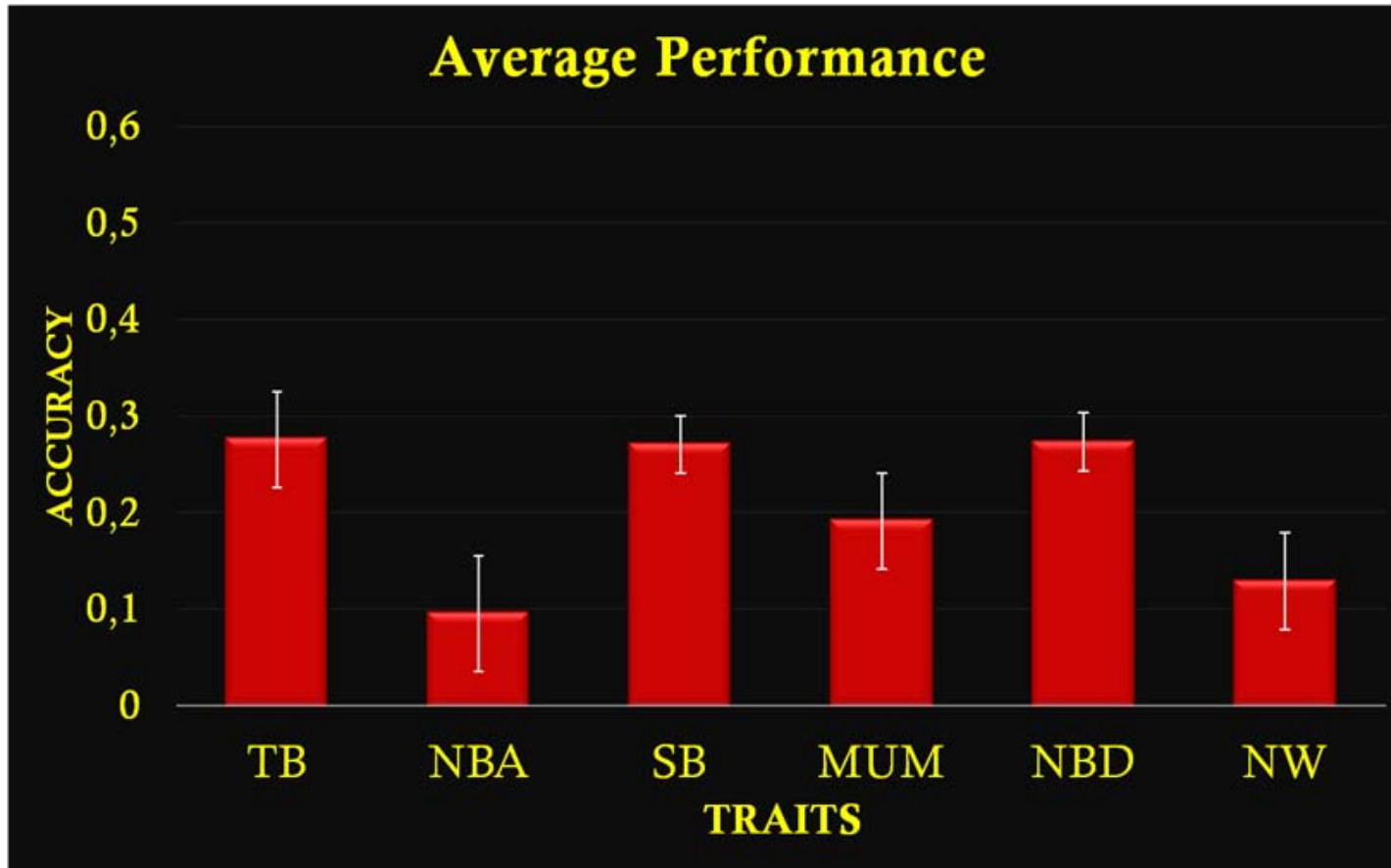


❖ Sevenfold cross-validation

❖ Accuracy = weighted sum of correlation/ $\sqrt{h^2}$



# Accuracy of Genomic Prediction



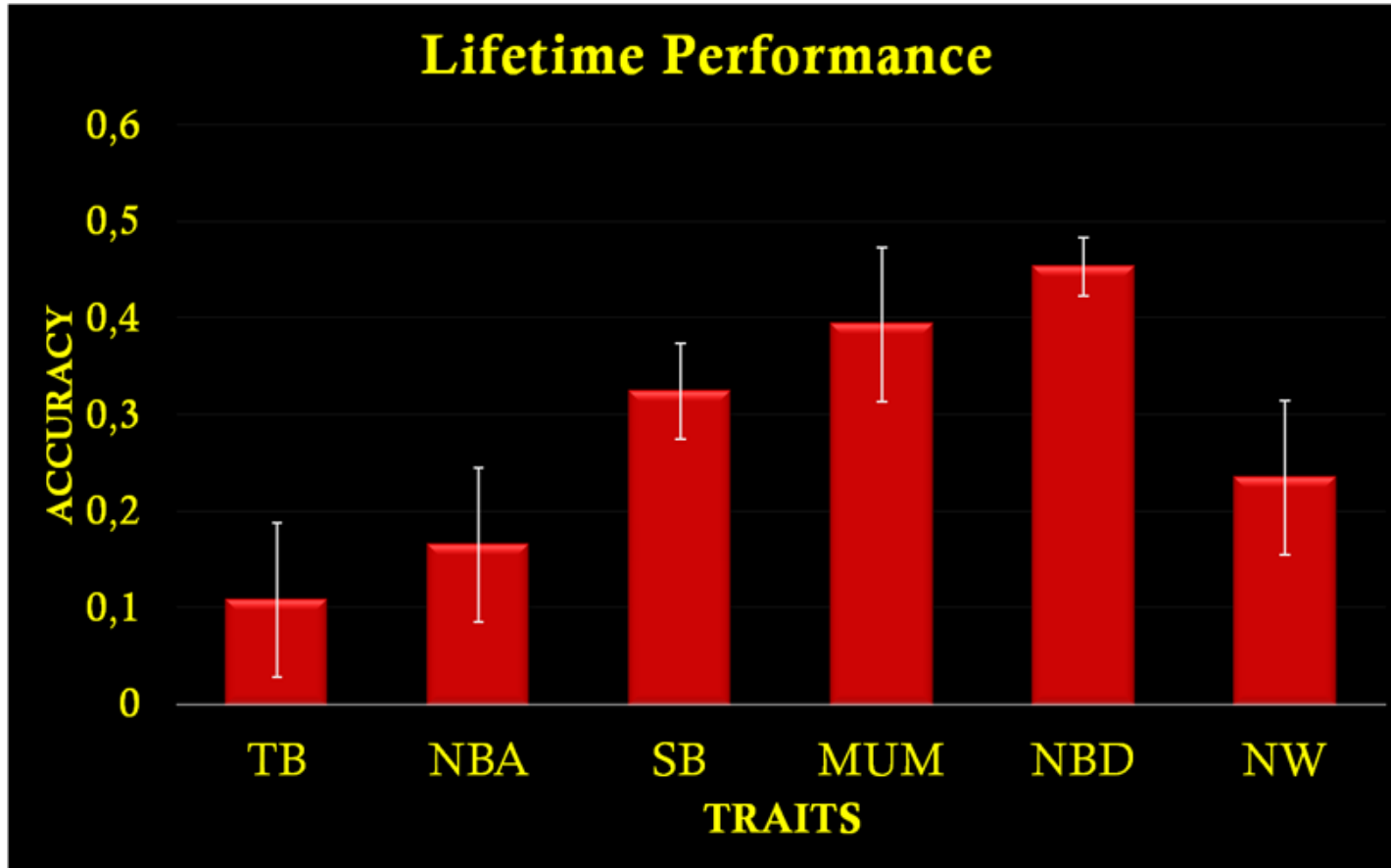
TB, total born; NBA, number born alive; SB, stillborn; MUM, mummified; NBD, number born dead; NW, number weaned

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# Accuracy of Genomic Prediction



TB, total born; NBA, number born alive; SB, stillborn; MUM, mummified; NBD, number born dead; NW, number weaned

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# Conclusions

- ❖ Reproductive data is lowly heritable
  - Similar between average and lifetime performance
- ❖ As for GWAS:
  - Some large QTL (>20% genetic variance)
    - Lifetime Performance: SB and NBD
    - Average Performance: SB and NW

# Conclusions

- ❖ Moderate accuracies overall
  - Highest for lifetime production NBD ( $0.45 \pm 0.03$ )
- ❖ Can still make predictions despite health challenges

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