Genomic evaluation of litter size variability in Large White pigs

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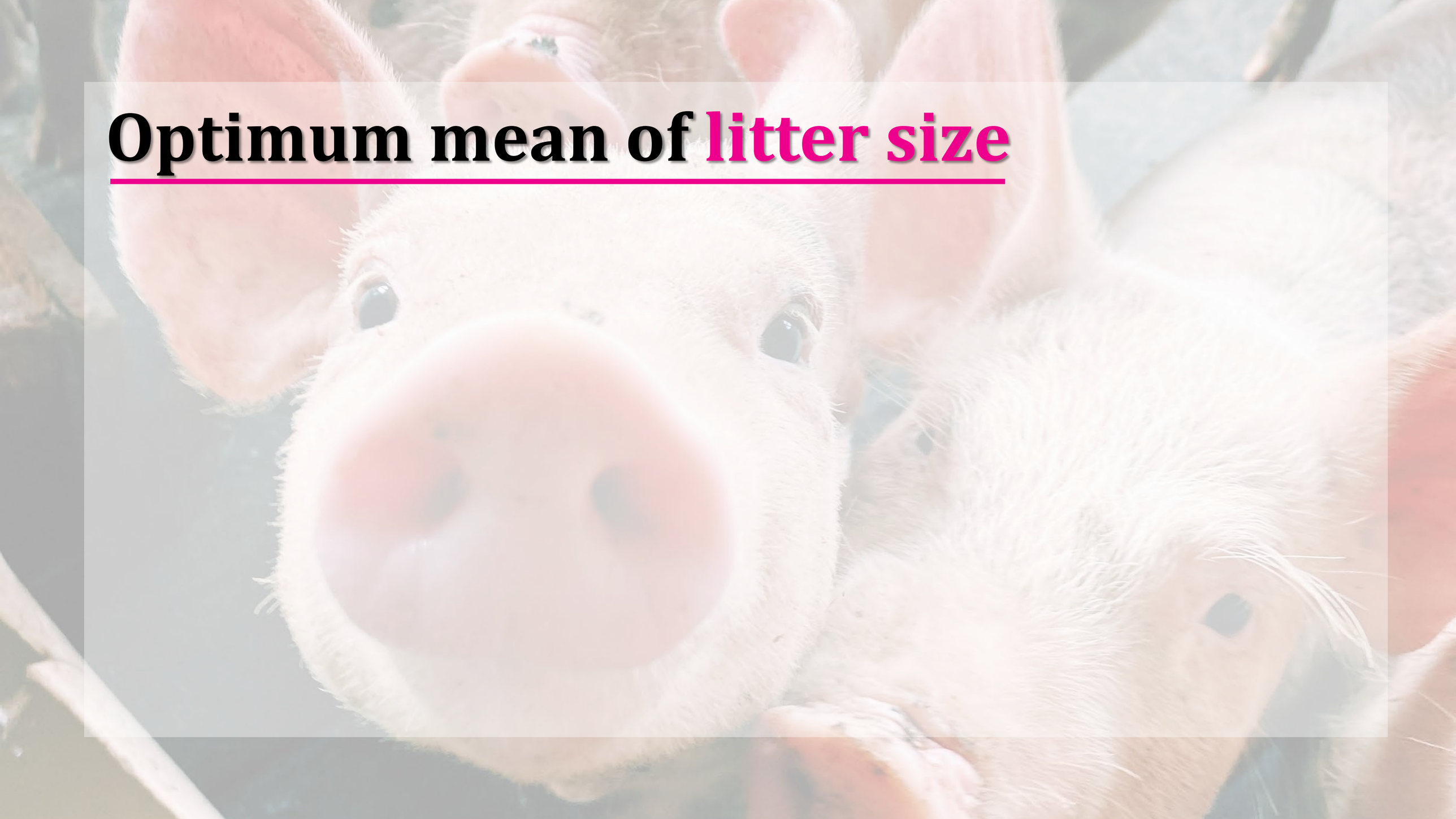
Topigs Norsvin
PROGRESS IN PIGS

THANK YOU!

Why are we focus on variability in litter size?

Optimum mean of litter size



Optimum mean of litter size

LANDRACE

13.7 (± 3.4)

Cieleń et al. (2023)

VS.

LARGE WHITE

16.6 (± 3.8)

Cieleń et al. (not published)

Selection to improve litter size

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- Low heritability

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- Negative genetic correlation between direct additive genetic and maternal effect

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- Low heritability
- Negative genetic correlation between direct additive genetic and maternal effect
- Limited size of the nucleus populations

Selection to improve litter size

- Large direct additive genetic variance for litter size

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- Availability of records on many relatives

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- Availability of records on many relatives

Provides possibility for successful improvement of litter size using quantitative and molecular genetics

In this trait is observed a very large variation

$$\text{Litter size} = \text{HYS} + \text{parity} + animal + pe + e$$

Sell-Kubiak et al. (2015)

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Heterogeneity of the residual variance

Sell-Kubiak et al. (2015)

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Heterogeneity of the residual variance

Genetic background

Sell-Kubiak et al. (2015)

In this trait is observed a very large variation

Litter size = HYS + parity + *animal* + *pe* + *e*

Heterogeneity of the residual variance

Genetic background

There is a positive genetic correlation

litter size

its variability

Sell-Kubiak et al. (2015)

Objectives

To confirm previously identified associations and find new ones between pig genomic regions and **litter size variability**

Phenotypic data

- **199,520** litter size record
- **46,901** phenotyped sows
- At least **2** records per sow
- Data collected from **2010** to **2022** from 58 farms (The Netherlands)

Log-transformed variance of residuals

Cieleń et al. (2023)

Log-transformed variance of residuals

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Log-transformed variance of residuals

$$\text{Litter size} = \text{HYS} + \text{parity} + \textit{animal} + \textit{pe} + e$$

Sow	Residual
sow_1	1.981
sow_1	1.988
sow_1	2.592
sow_2	2.108
sow_2	2.773
sow_2	1.671
sow_2	2.278

Cieleń et al. (2023)

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Variance from residual

8.23

Variance from residual

192.12

Cieleń et al. (2023)

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Variance from residual	Log-transformed
8.23	0.32
192.12	0.30

Cieleń et al. (2023)

Log-transformed variance of residuals

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192.12	0.30

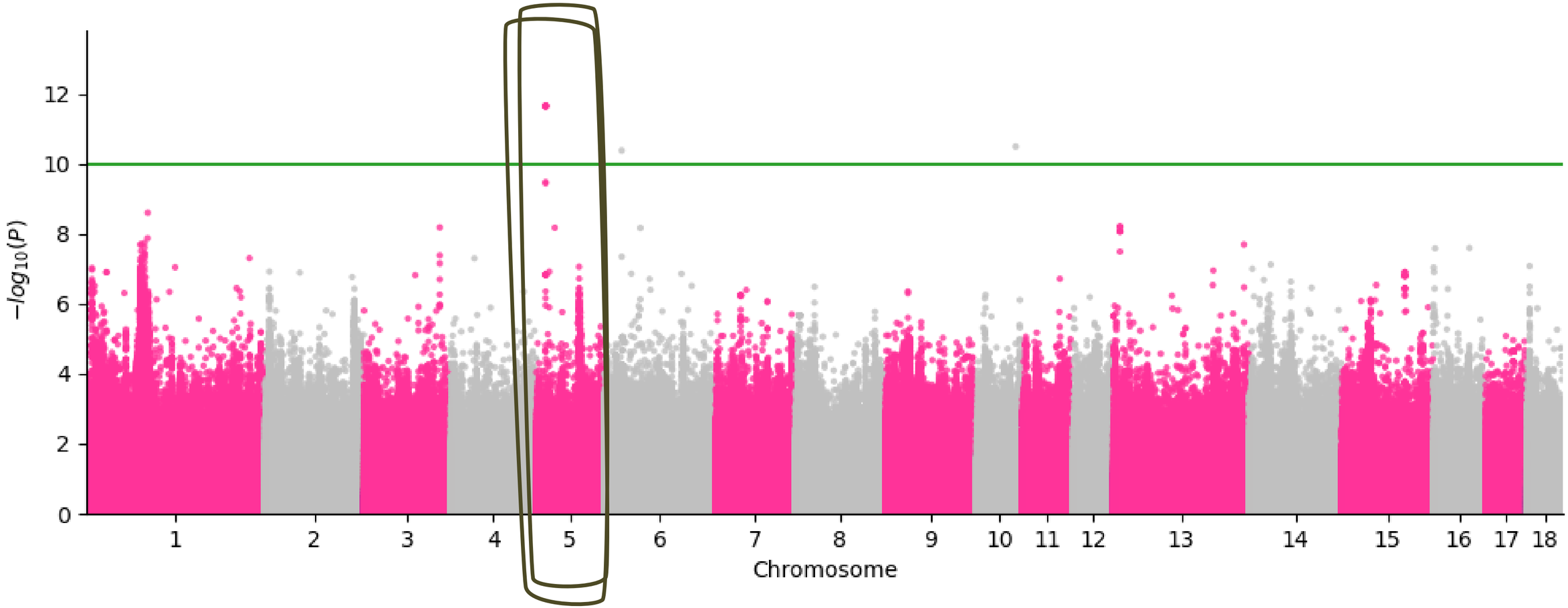
Variability phenotype = LnVarTNB

Cieleń et al. (2023)

Genotypic data and GWAS

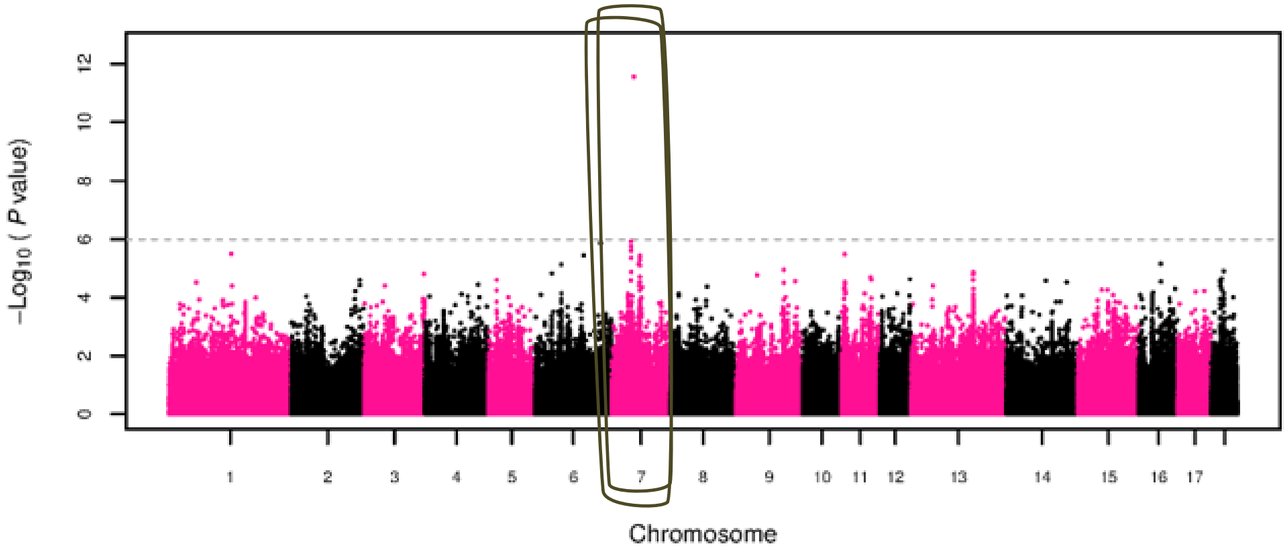
- 46,901 genotyped sows
- Genotype or imputed to full sequence
- 27,035,402 SNPs remained for the analysis
- GCTA software

GWAS results - LnVarTNB

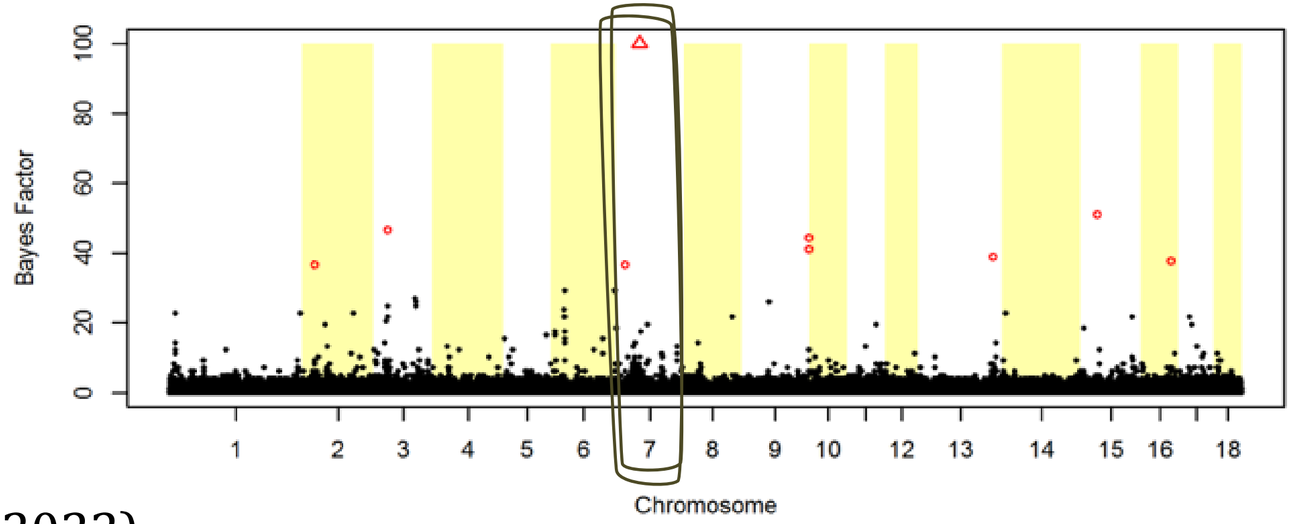


GWAS - previous results

2022



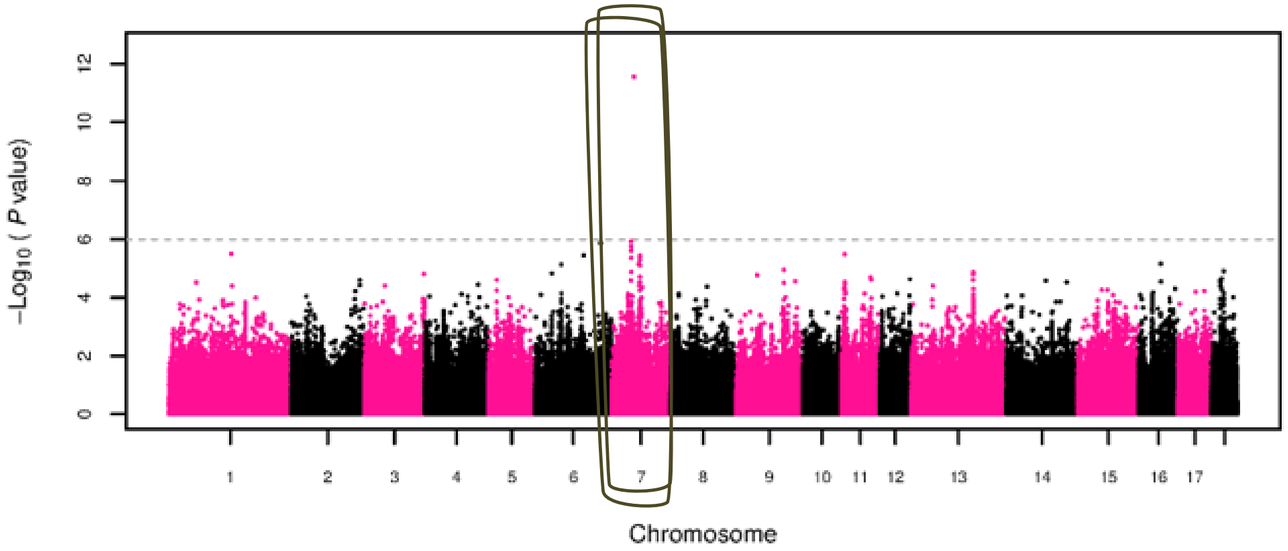
2015



Sell-Kubiak et al. (2015, 2022)

GWAS - previous results

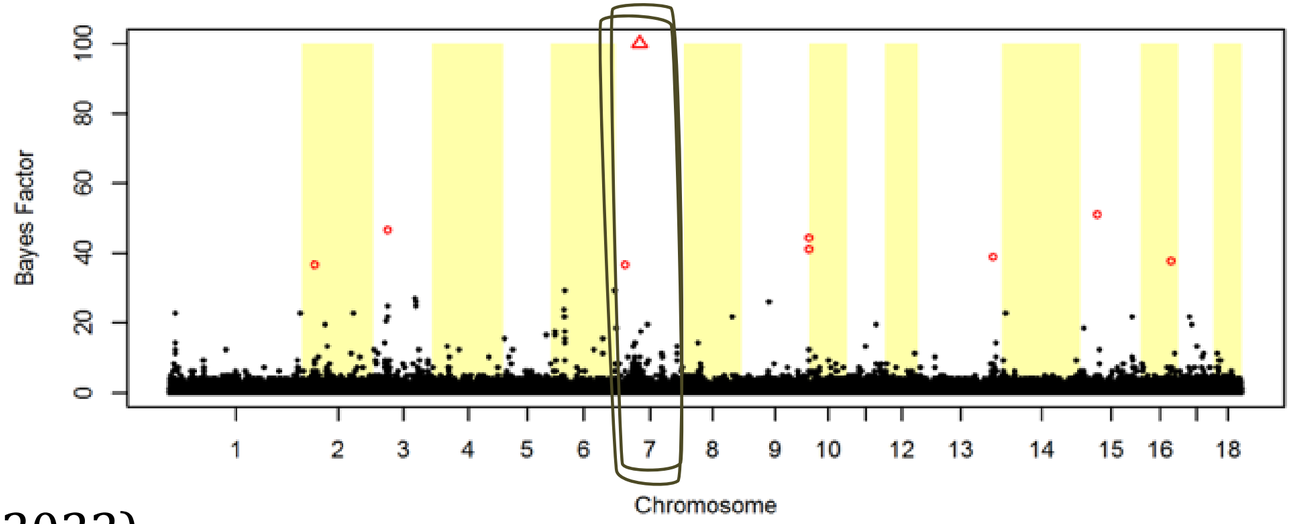
2022



Method/software:
Single-SNP GWAS in GCTA

Phenotyped animals:
~60,000 sows (Degressed EBVs)

2015



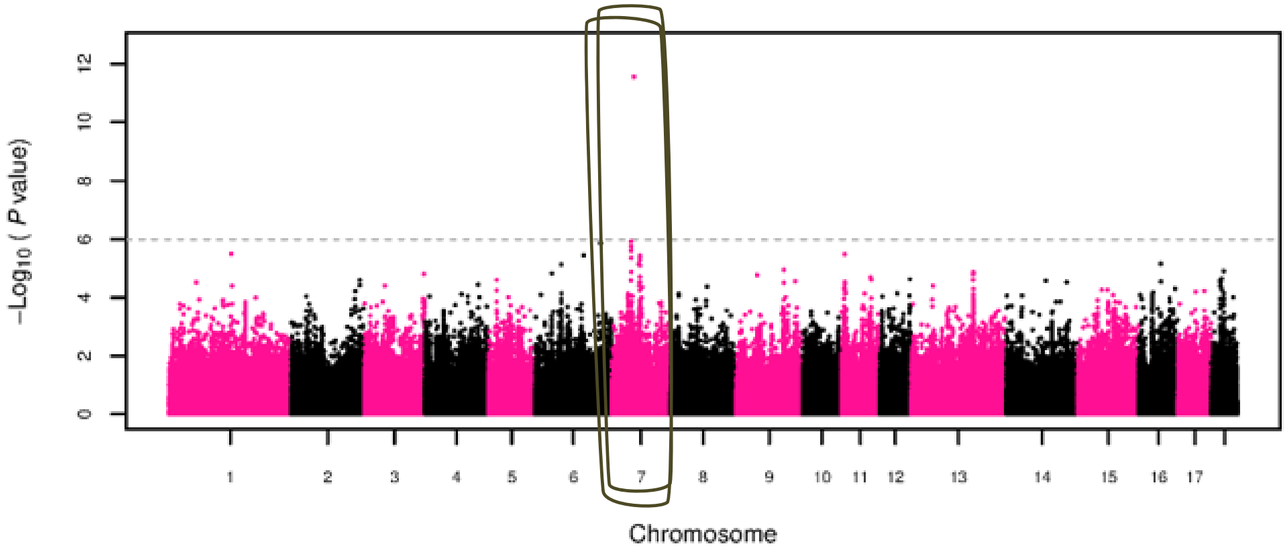
Method/software:
Multiple-SNP GWAS in Bayz

Phenotyped animals:
~121,000 sows (Degressed EBVs)

Sell-Kubiak et al. (2015, 2022)

GWAS - previous results

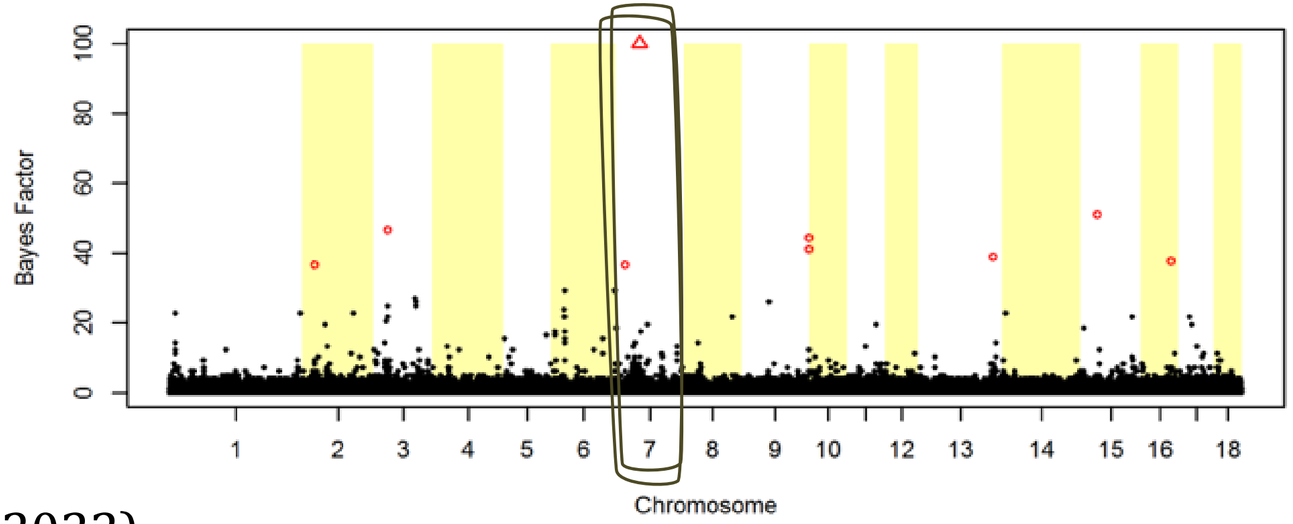
2022



Genotyped animals:
~12,000
Large White pigs

No. SNPs:
526,000

2015



Genotyped animals:
2,067
Large White pigs

No. SNPs:
40,969

Sell-Kubiak et al. (2015, 2022)

Post-GWAS

Based on GWAS results, the location of the significant SNPs was used to search for candidate genes

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Based on GWAS results, the location of the significant SNPs was used to search for candidate genes

- **Focus on chromosome 5**
- **BIOMART from Ensemble**
- **Position of an SNP ±50 Kbp**

Candidate genes on SSC 5 ±50 Kbp

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WNT10B → Important role in early embryonic development and pregnancy maintenance

Tao et al. (2013)

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AKAP3 → **Regulate sperm motility (bovine, human, mouse)**

Xu et al. (2014)

Candidate genes on SSC 5 ±50 Kbp

WNT10B → Important role in early embryonic development and pregnancy maintenance

Tao et al. (2013)

AKAP3 → Regulate sperm motility (bovine, human, mouse)

Xu et al. (2014)

DYRK4 → Plays a role in the female reproductive system

Tao et al. (2017)

Candidate genes on SSC 5 ±50 Kbp

PARP11

→ **Functional relevance for nuclear envelope stability and nuclear reorganization during spermiogenesis**

Meyer-Ficca et al. (2015)

Candidate genes on SSC 5 ±50 Kbp

PARP11 → Functional relevance for nuclear envelope stability and nuclear reorganization during spermiogenesis

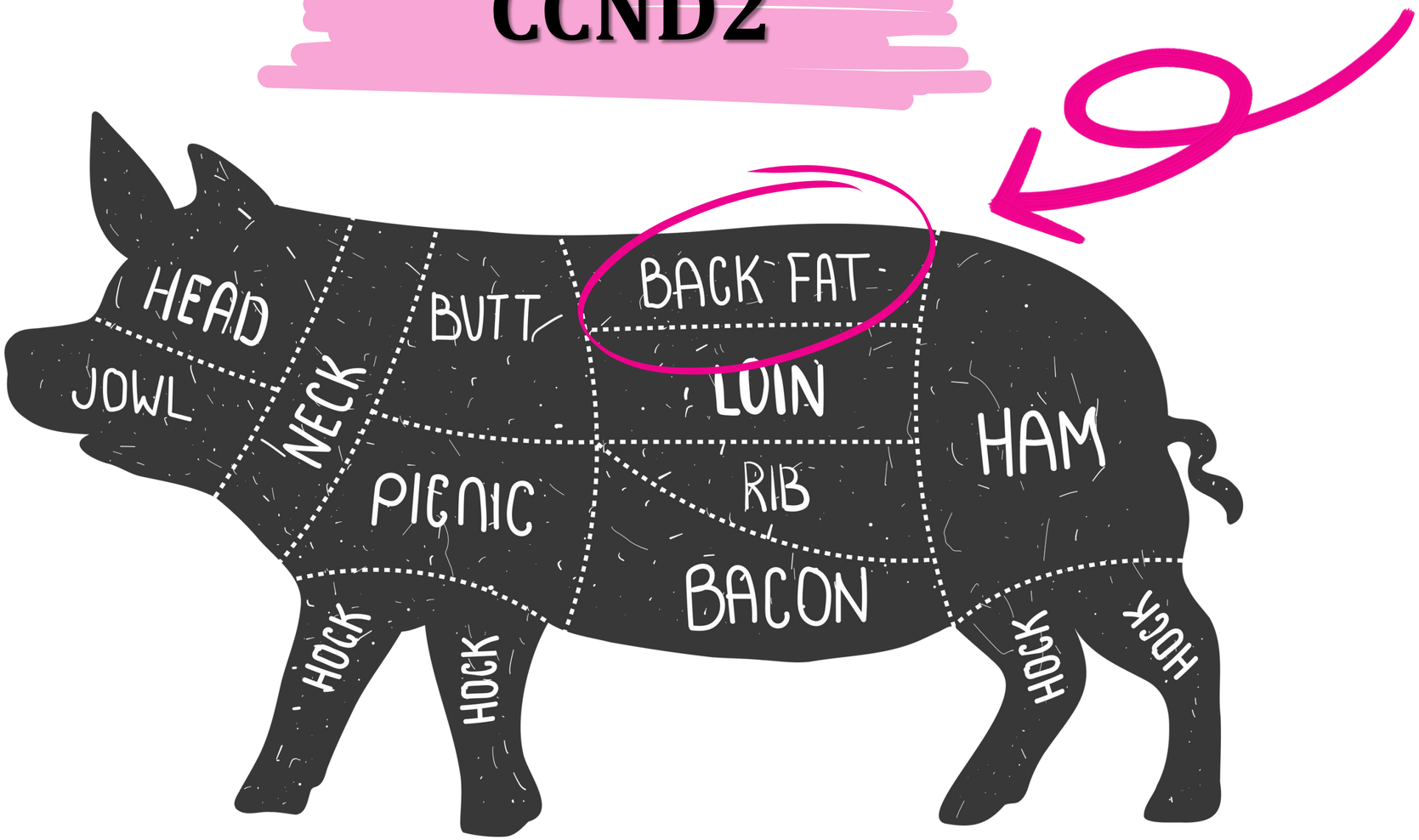
Meyer-Ficca et al. (2015)

CCND2 → Proliferation regulator during folliculogenesis

Wang et al. (2021)

Candidate genes on SSC 5 ±50 Kbp

CCND2



Oliveira et al. (2022)

Conclusions

SSC5 is the new genomic region in pigs associated with **litter size variability**

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Thank you for your attention!

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