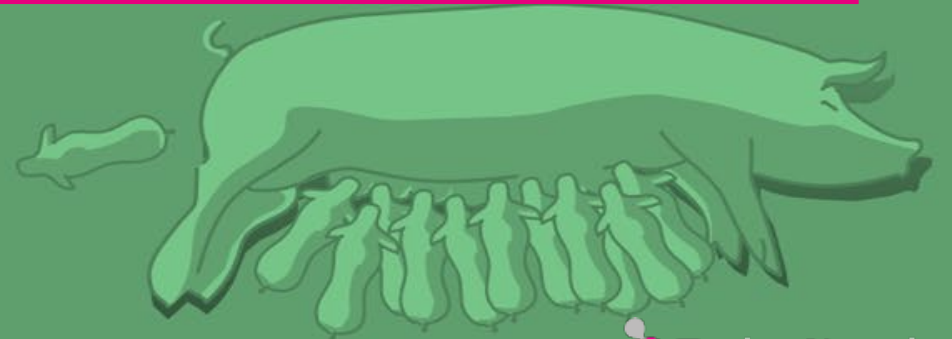




**Topigs Norsvin**

# On the genetics of farrowing duration in pigs

M. S. Lopes, H. S. Wendling, E. Grindflek, E.F. Knol

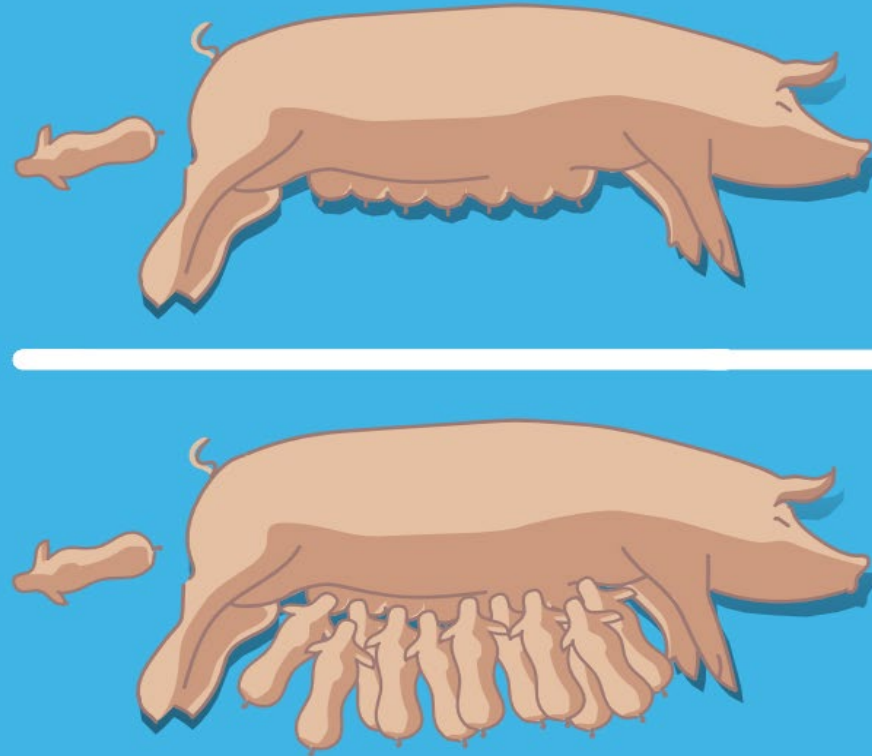


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# Introduction

Definition  
of the trait  
(FRD)



Farrowing  
duration





# Introduction

**Why is it  
important?**

↑ **genetic progress for litter size**  
↑ **farrowing duration (FRD)**

Prolonged FRD can be associated with:

- Higher number of stillbirths
- Impacts the required labor per sow during farrowing
- Impacts colostrum intake of the newborn piglets
- Etc.

# Introduction

Why is it  
challenging?



**Data recording**  
**highly labor demanding**

# The goal

To investigate the genetic background of FRD using a large commercial dataset:

- 1) Estimating genetic parameters for FRD
- 2) Performing a GWAS for FRD

# Materials and methods

## Data

- ✓ Data collection: 2022-2024
- ✓ Large White sows in Brazil
- ✓ 5358 sows
- ✓ 18180 parities

## Genetic parameters

### Fixed effects

- Population average
- Farrowing room
- Litter line (purebred or crossbred)
- Total number born (class)
- Year-week at birth
- Parity number of the sow
- Average birth weight of the piglets
- Day of the week

### Random effects

- Direct genetic effect
- Permanent effect
- Error

# Materials and methods

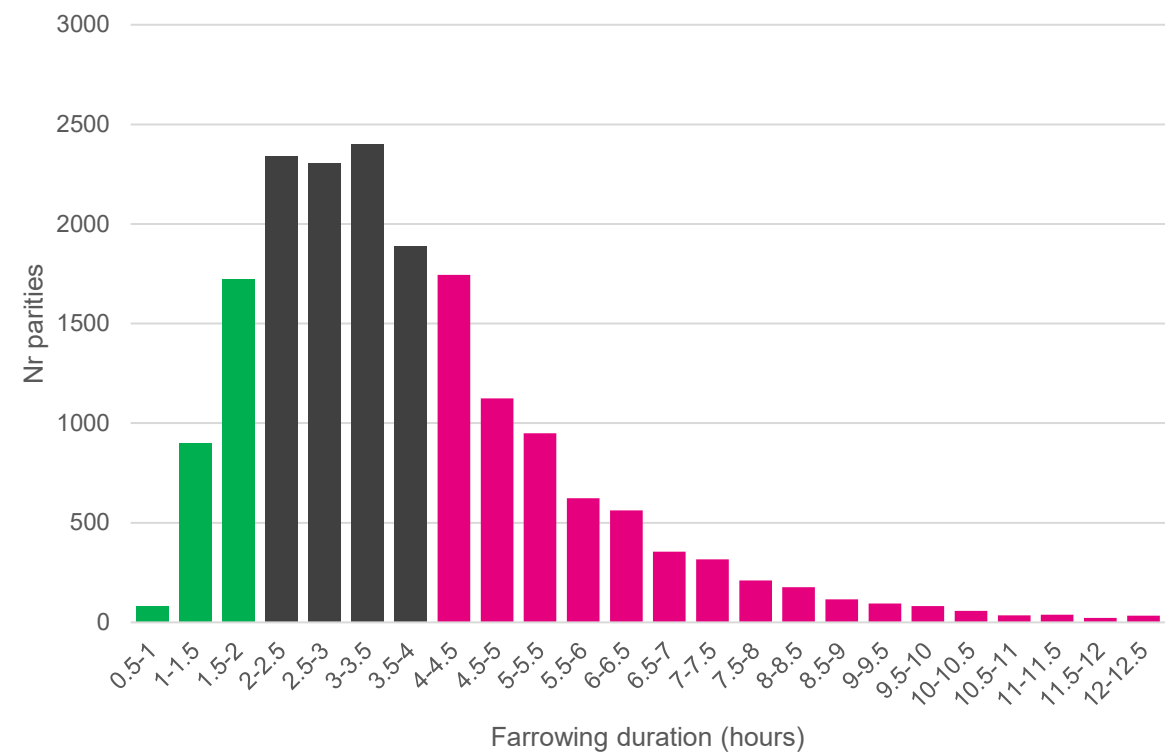
## GWAS

- ✓ Imputed 50K (Illumina 50K and custom 25K)
- ✓ EBVs of the sows (gen. parameters)
- ✓ Single-SNP - GCTA

## pCADD scores

- ✓ High porcine combined annotation dependent-depletion (pCADD) scores
- ✓ WGS variants
- ✓ Derks et al. (2021) | Genomics 113(4):2229-2239

# Summary of data

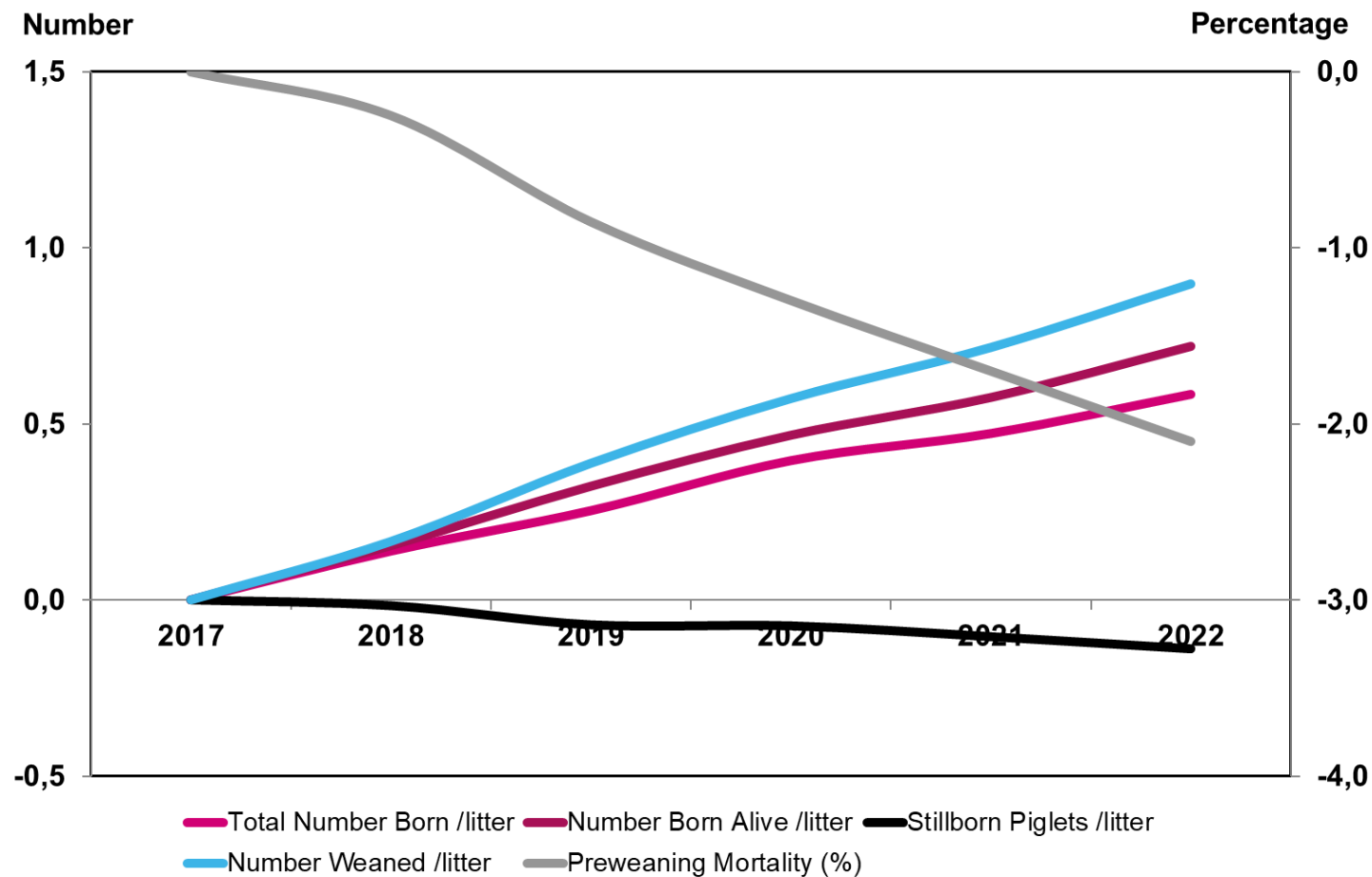


|                   |       |       |       |
|-------------------|-------|-------|-------|
| FRD               | <2h   | 2-4h  | >4h   |
| % of total        | 0.15  | 0.49  | 0.36  |
| Total number born | 13.53 | 15.00 | 15.96 |
| Nr. stillborns    | 0.73  | 0.90  | 1.14  |
| % of stillborns   | 0.05  | 0.06  | 0.07  |



# Genetic trends

**TN70**  
(Large White x Landrace)

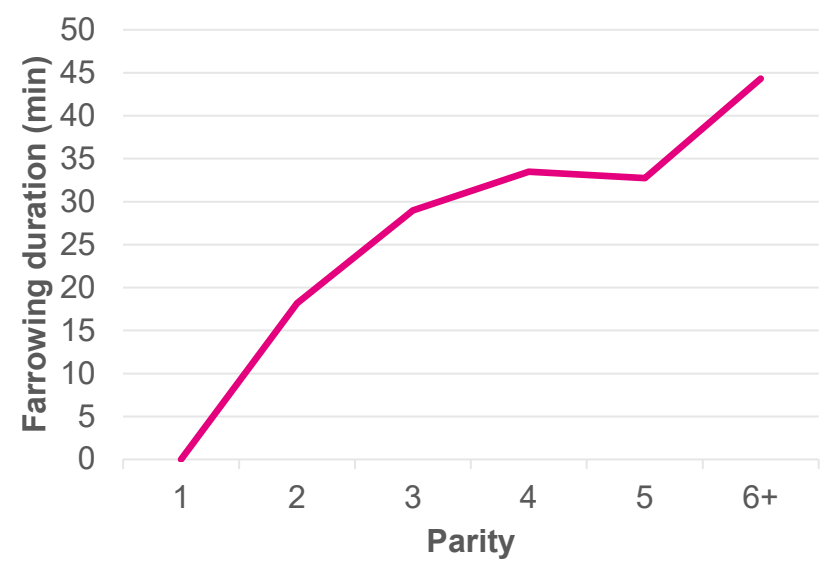
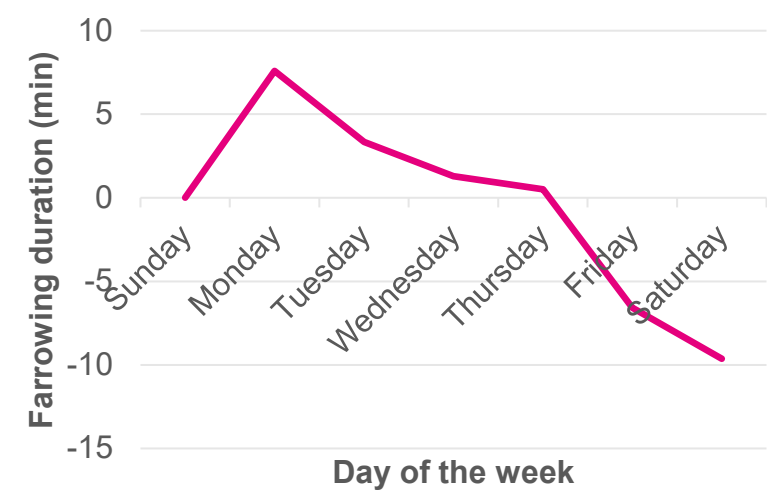
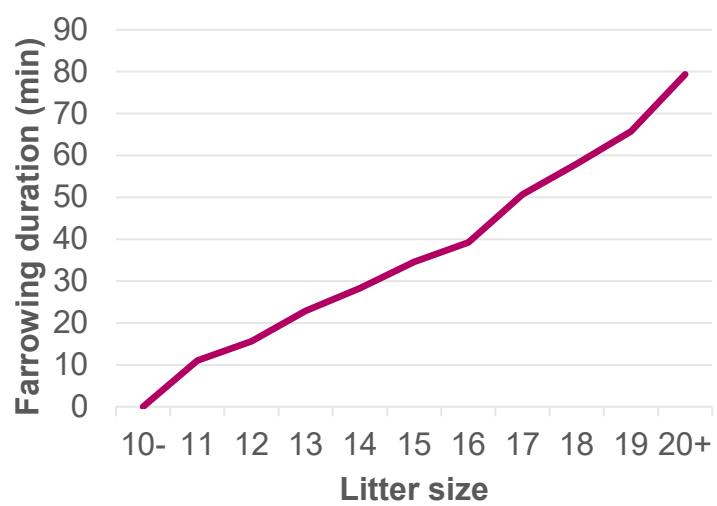


# 1) Genetic parameters

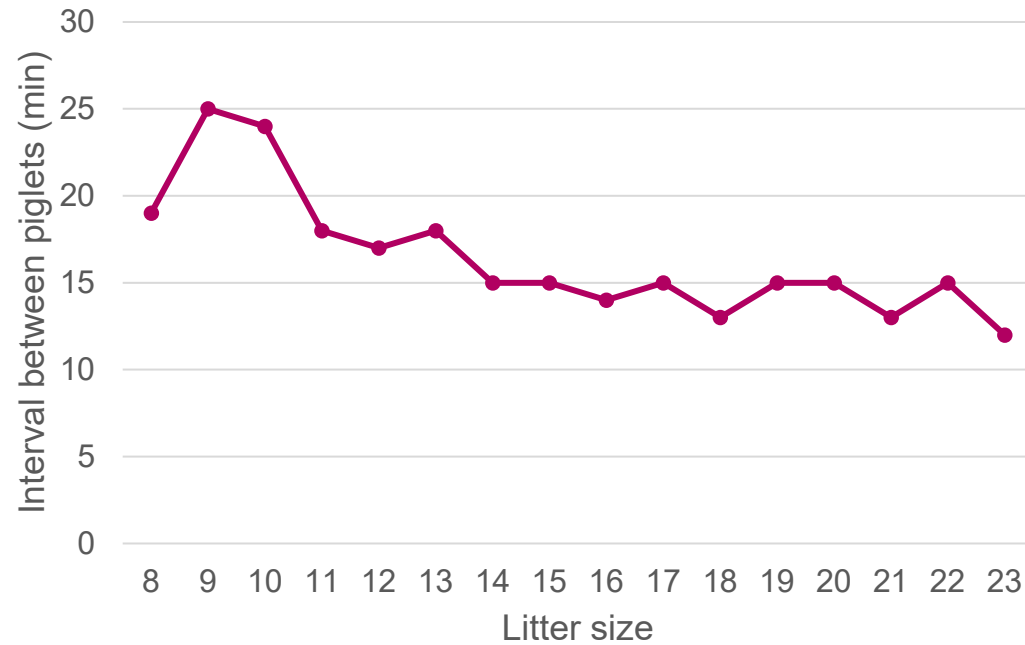
| Effect                              | P value                                   |
|-------------------------------------|-------------------------------------------|
| Farrowing room                      | 0.90                                      |
| Litter line (purebred or crossbred) | 0.05                                      |
| Total number born (class)           | <b><math>9.91 \times 10^{-107}</math></b> |
| Year-week at birth                  | <b><math>7.27 \times 10^{-23}</math></b>  |
| Parity number of the sow            | <b><math>1.77 \times 10^{-34}</math></b>  |
| Average birth weight of the piglets | 0.27                                      |
| Day of the week                     | <b><math>2.11 \times 10^{-5}</math></b>   |

| Parameter           | Value (minutes)                   |
|---------------------|-----------------------------------|
| Additive            | $771 \pm 112$                     |
| Permanent effect    | $341 \pm 103$                     |
| Residual            | $10,391 \pm 126$                  |
|                     |                                   |
| <b>Heritability</b> | <b><math>0.07 \pm 0.01</math></b> |

# 1) Genetic parameters

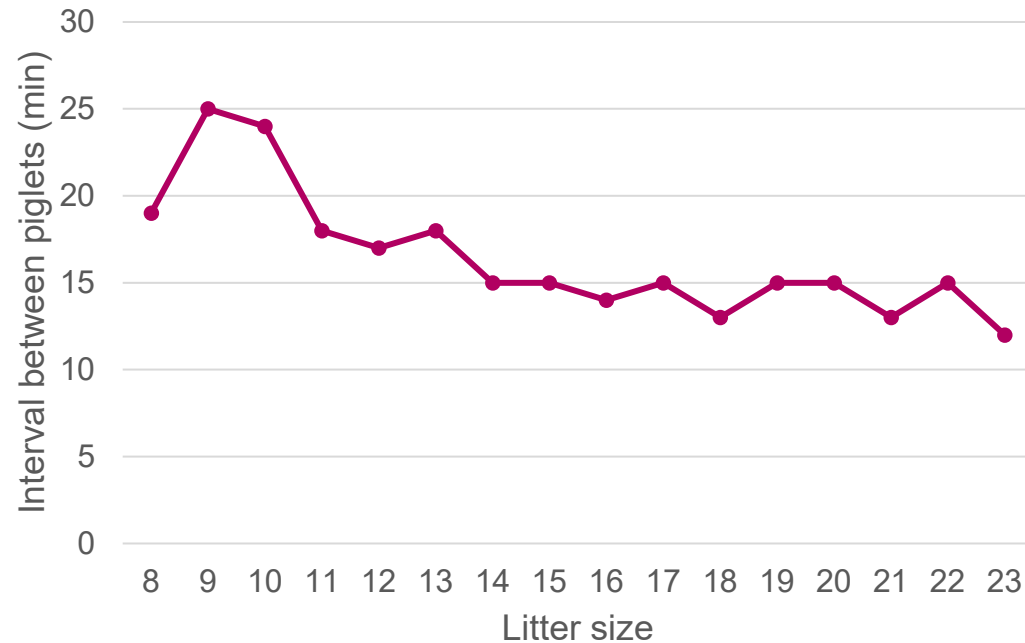


# Birth interval between consecutive piglets

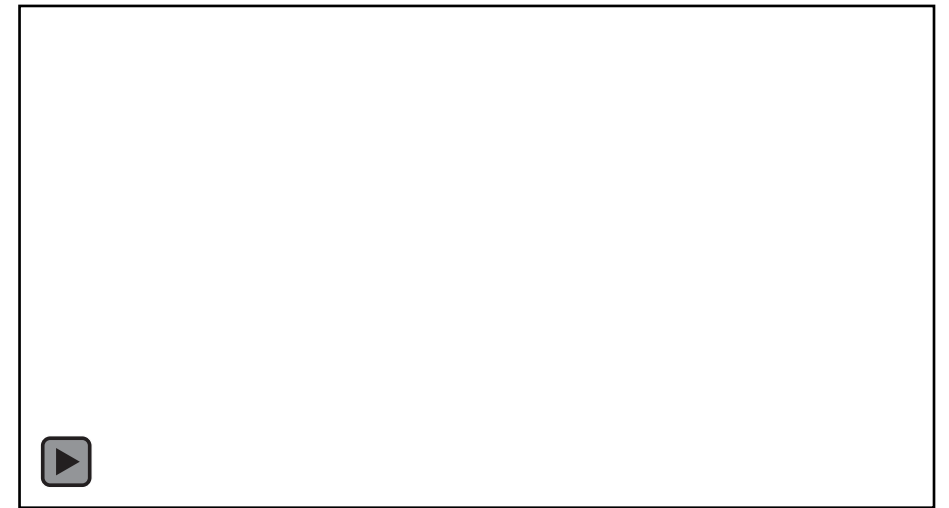


700 litters with individual time at birth recording for accurate interval between piglets

# Birth interval between consecutive piglets

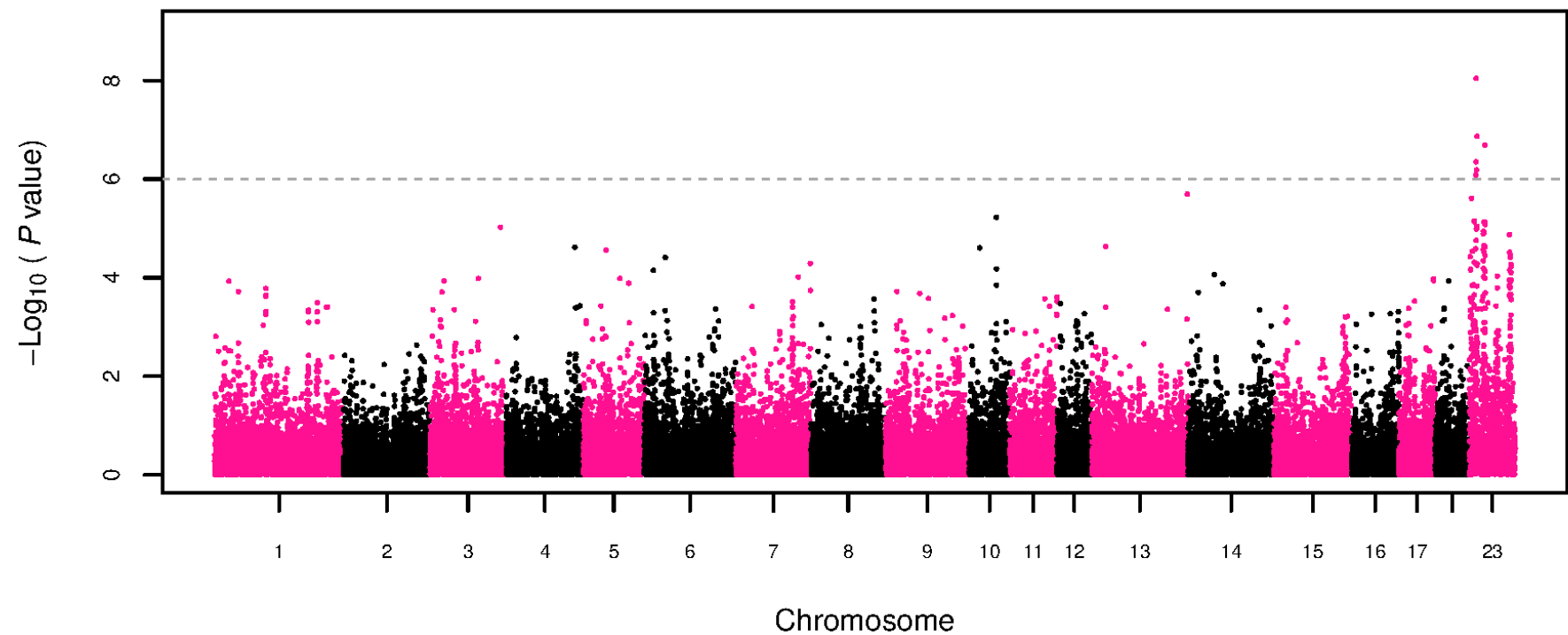


700 litters with individual time at birth recording for accurate interval between piglets



**Especial case**  
41 piglets  
12 minutes between piglets on average

## 2) GWAS for FRD



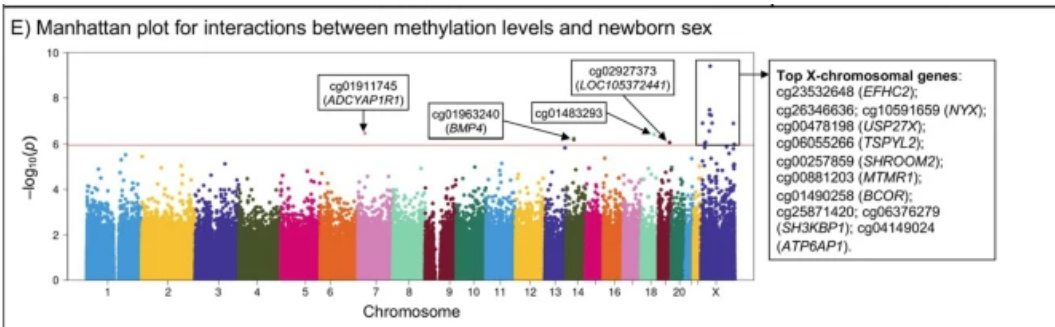
| SNP                | Chr | bp       | MAF  | $\text{Log}_{10}(P)$ | b    | se   | expl_VG |
|--------------------|-----|----------|------|----------------------|------|------|---------|
| WU_10.2_X_16997874 | 23  | 15751195 | 0.24 | 8.04                 | 3.68 | 0.64 | 0.02    |

# Candidate genes

| Gene    | pCADD score |
|---------|-------------|
| SH3KBP1 | 18.58       |
| RPS6KA3 | 17.60       |
| ADGRG2  | 14.44       |

## SH3KBP1

Hu, Jie, et al. "Sex differences in the intergenerational link between maternal and neonatal whole blood DNA methylation: a genome-wide analysis in 2 birth cohorts." *Clinical epigenetics* 15.1 (2023): 51.



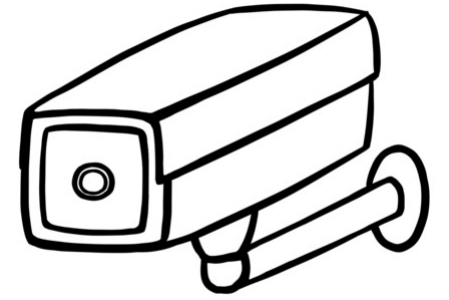
## RPS6KA3

Rogers, R. Curtis, and Fatima E. Abidi. "RPS6KA3-Related intellectual disability." (2018).

## ADGRG2

- Zhang, Dao-Lai, et al. "Gq activity-and  $\beta$ -arrestin-1 scaffolding-mediated ADGRG2/CFTR coupling are required for male fertility." *Elife* 7 (2018): e33432.
- Danielsson, Hanna, et al. "Blood protein profiles related to preterm birth and retinopathy of prematurity." *Pediatric Research* 91.4 (2022): 937-946.
- Gormley, Matthew, et al. "Preeclampsia: novel insights from global RNA profiling of trophoblast subpopulations." *American journal of obstetrics and gynecology* 217.2 (2017): 200-e1.

# Camera technology



**Data recording**  
**labor demanding**  
**accuracy**



# Conclusion

- Although the heritability of FRD was low, this study brings new insights that may contribute to the genetic improvement of this trait.
- We found a genomic region on X chromosome related to FRD. Genes in this region have been reported to influence birth events, but the mechanism related to FRD needs to be further investigated.



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