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CENTER FOR QUANTITATIVE
GENETICS AND GENOMICS

# GWAS using a Bayesian approach for litter size and piglet mortality in Danish pigs

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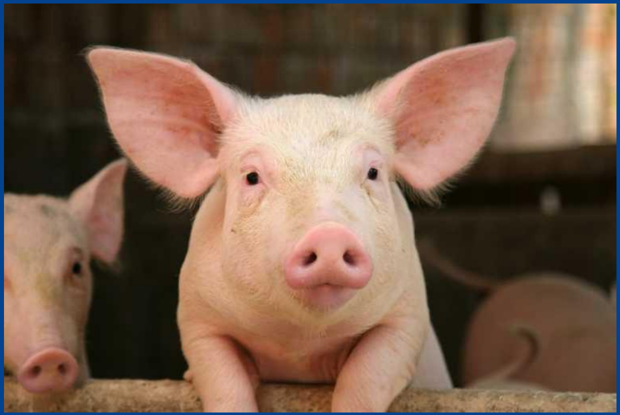

# Outline

- **Introduction**
- **Materials & Methods**
- **Results & Discussion**
- **Conclusions**

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# Litter size & mortality

- Litter size & mortality
  - reproductive traits of major economic importance
- Total number born
  - litter size at weaning ↑ mortality ↑
- Litter size at d 5
  - litter size at weaning ↑ mortality ↓

# Objective

- Identify QTL for the litter size and piglet mortality in Danish Landrace and Yorkshire pigs.
- Propose a novel method based on Bayesian mixture model to detect QTL regions.

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# Data

- Phenotypes
  - TNB: total number of piglets born
  - LS5:  litter size at five days after birth
  - Mort: mortality rate before day 5
- Genotypes
  - Illumina PorcineSNP60 BeadChip

# Size of data

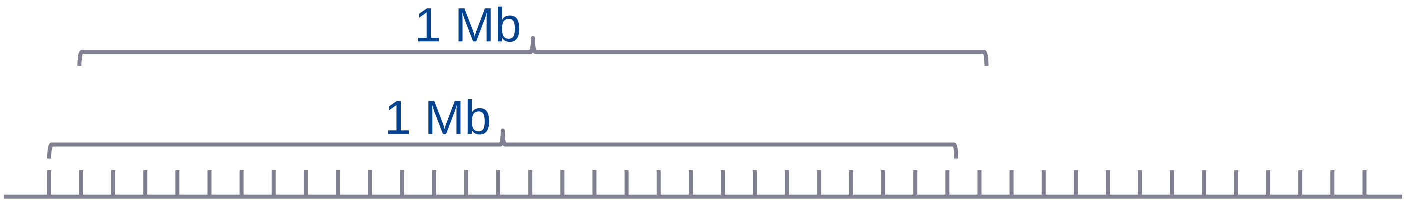
| | Landrace | Yorkshire |
|---|---|---|
| **Marker** | 37,060 | 36,058 |
| **Animal** | 5,977 | 6,000 |
| **Boar** | 1,788 | 1,761 |
| **Sow** | 4,189 | 4,239 |
| **Birth** | 1998 to 2014 | |

# Bayesian Mixture Model (BM)

- $\mathbf{y_c} = \mathbf{1}\mu + \sum_{i=1}^{m} \boldsymbol{x}_i g_i + \boldsymbol{Z}\boldsymbol{u} + \boldsymbol{e}$
  - $\mathbf{y_c}$: corrected phenotypic value
  - $g_i \sim \begin{cases} \mathrm{N}\left(0, \sigma_{g_0}^2\right) & \text{with probability } \pi_0 \\ \mathrm{N}\left(0, \sigma_{g_1}^2\right) & \text{with probability } \pi_1 = 1 - \pi_0 \end{cases}$
  - $\boldsymbol{u}$: polygenic effect
  - BayZ Package

# QTL region analysis

- Sliding window



- Posterior probability of interval ($PP_{int}$)

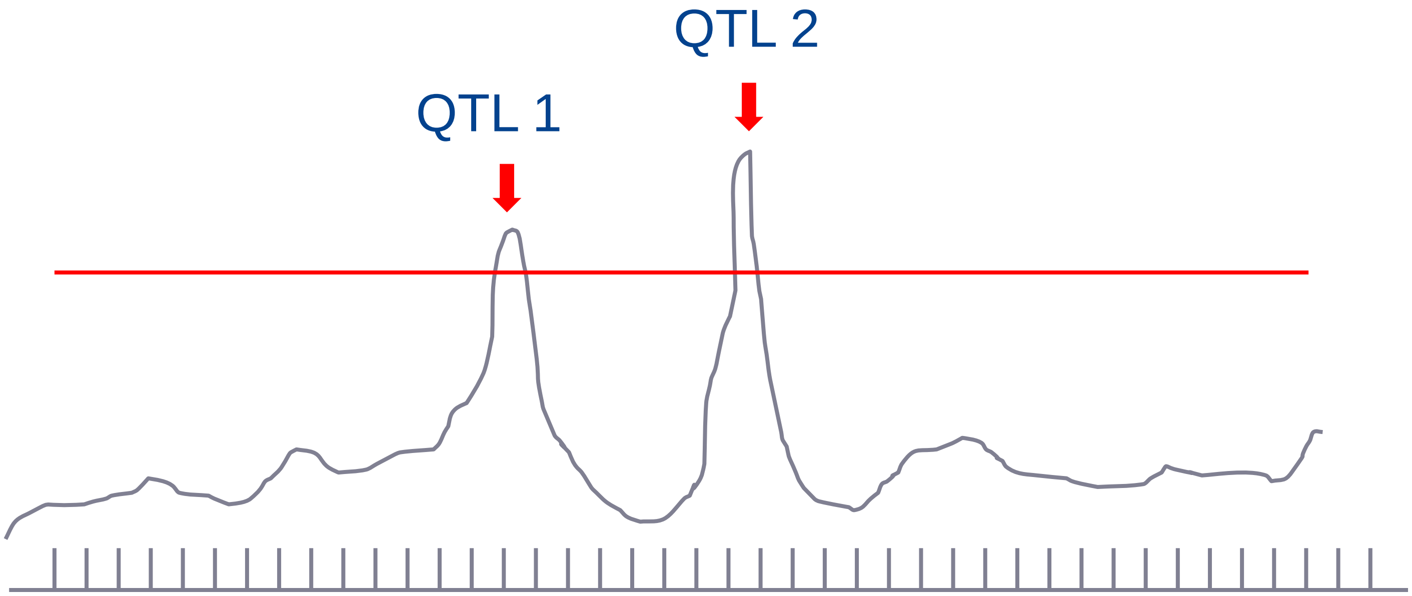
the proportion of samples where at least one SNP within the window was falling into the second distribution

# Interval posterior probability ($PP_{int}$)

| | M1 | M2 | M3 | M4 | M5 | M6 | M7 | M8 |
|---|---|---|---|---|---|---|---|---|
| **S1** | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| **S2** | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| **S3** | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| **S4** | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| **S5** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| $PP_{snp}$ | 0/5 | 1/5 | 0/5 | 2/5 | 0/5 | 0/5 | 2/5 | 1/5 |

# QTL region analysis

- $PP_{int} > 0.8$



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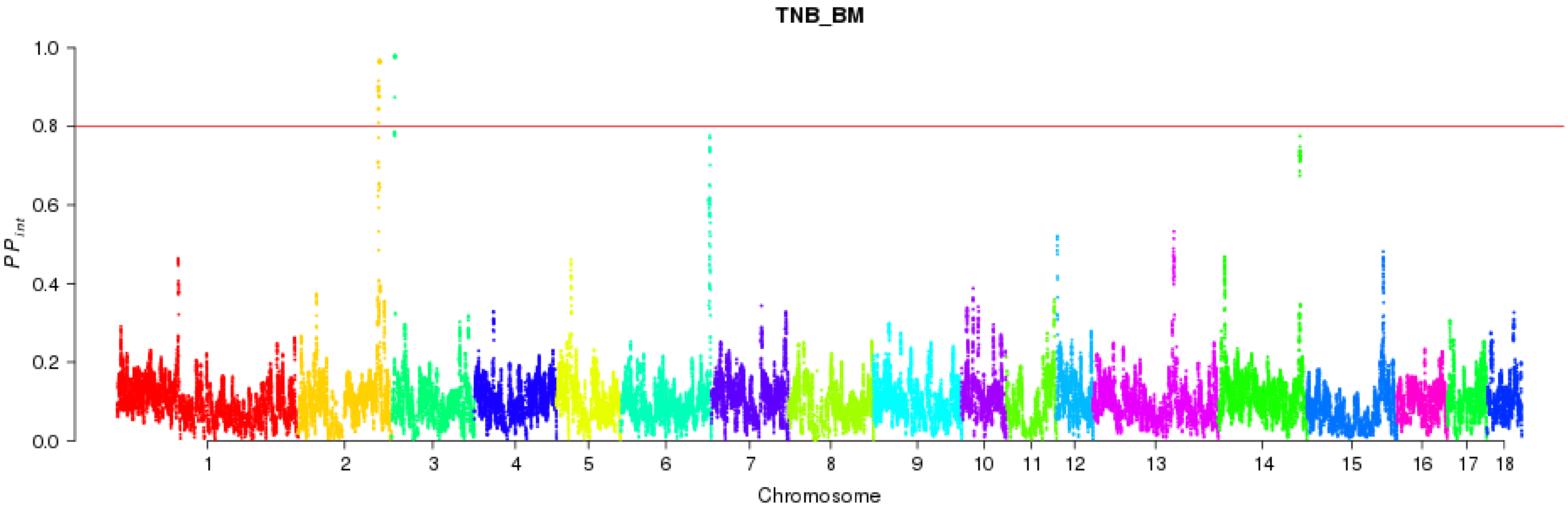
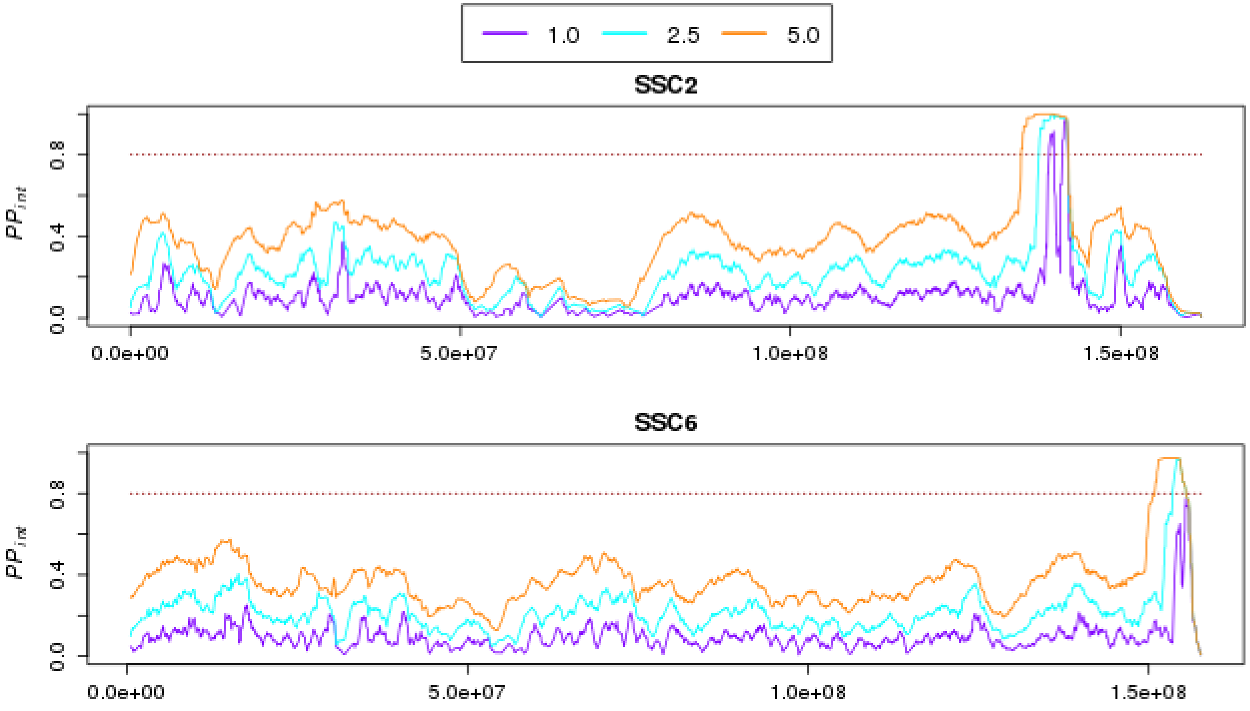
# GWAS for TNB Landrace



- Several peaks when using sliding window with 1Mb

# QTL regions



1.0 Mb

2.5 Mb

- ➢ The narrowest region among three scenarios was chosen as the QTL region

# Overlap with reported region

- 15 QTL regions on SSC1, 2, 3, 6, 7, 9, 13 and 14

| | |
|---|---|
| **Reproduction** | corpus luteum number<br>teat number<br>non-functional nipples<br>age at puberty<br>litter weight<br>embryo weight |

# Common QTL regions

| SSC | Breed 1 | Trait 1 | QTL 1 | Breed 2 | Trait 2 | QTL 2 |
|---|---|---|---|---|---|---|
| **3** | Landrace | TNB | 6.34 ~ 7.34 Mb | Yorkshire | TNB | 5.48 ~ 6.48 Mb |
| **7** | Landrace | LS5 | 34.74 ~ 35.74 Mb | Landrace | MORT | 34.74 ~ 35.74 Mb |

- 6 common QTL regions on SSC2, 3, 6, 7 and 13
  - SSC3: both Landrace & Yorkshire
  - SSC7: positive for LS5 & negative for MORT

# Candidate genes

- **KPNA7**: suggested the requirement for cleavage development
- **SPESP1**: involved in the sperm–oocyte binding and fusion in pigs
- **GDF9**: expression higher in oocytes than in cumulus/granulosa cells

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# Conclusions

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- 6 regions located on SSC2, 3, 6, 7 and 13 were associated with more than one trait.
- The QTL regions detected overlapped with the regions previously reported for reproduction traits.

# Thanks for your attention

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# Take-home messages

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