Genetic parameters and genome-wide association studies of disease in growing pigs under a polymicrobial natural disease challenge

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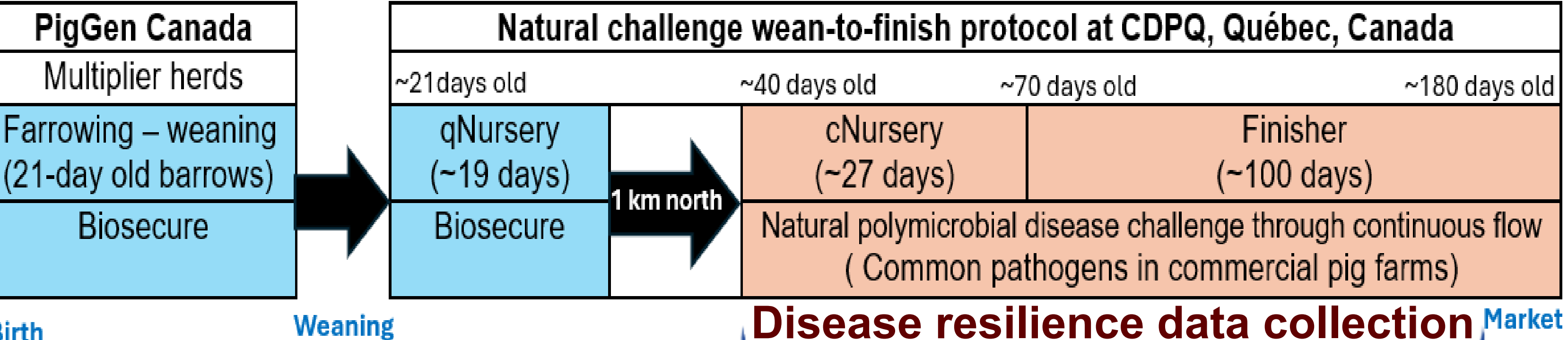
Introduction

- Selection in most pig breeding programs is conducted in high-health nucleus herds, while pigs typically encounter multiple pathogens in commercial herds.
- A knowledge gap remains on genetic parameters and genomics of disease-related traits of growing pigs under a polymicrobial disease challenge.

Objective

- Estimate genetic parameters and identify genomic regions and pathways associated with disease of growing pigs exposed to a natural polymicrobial disease challenge.
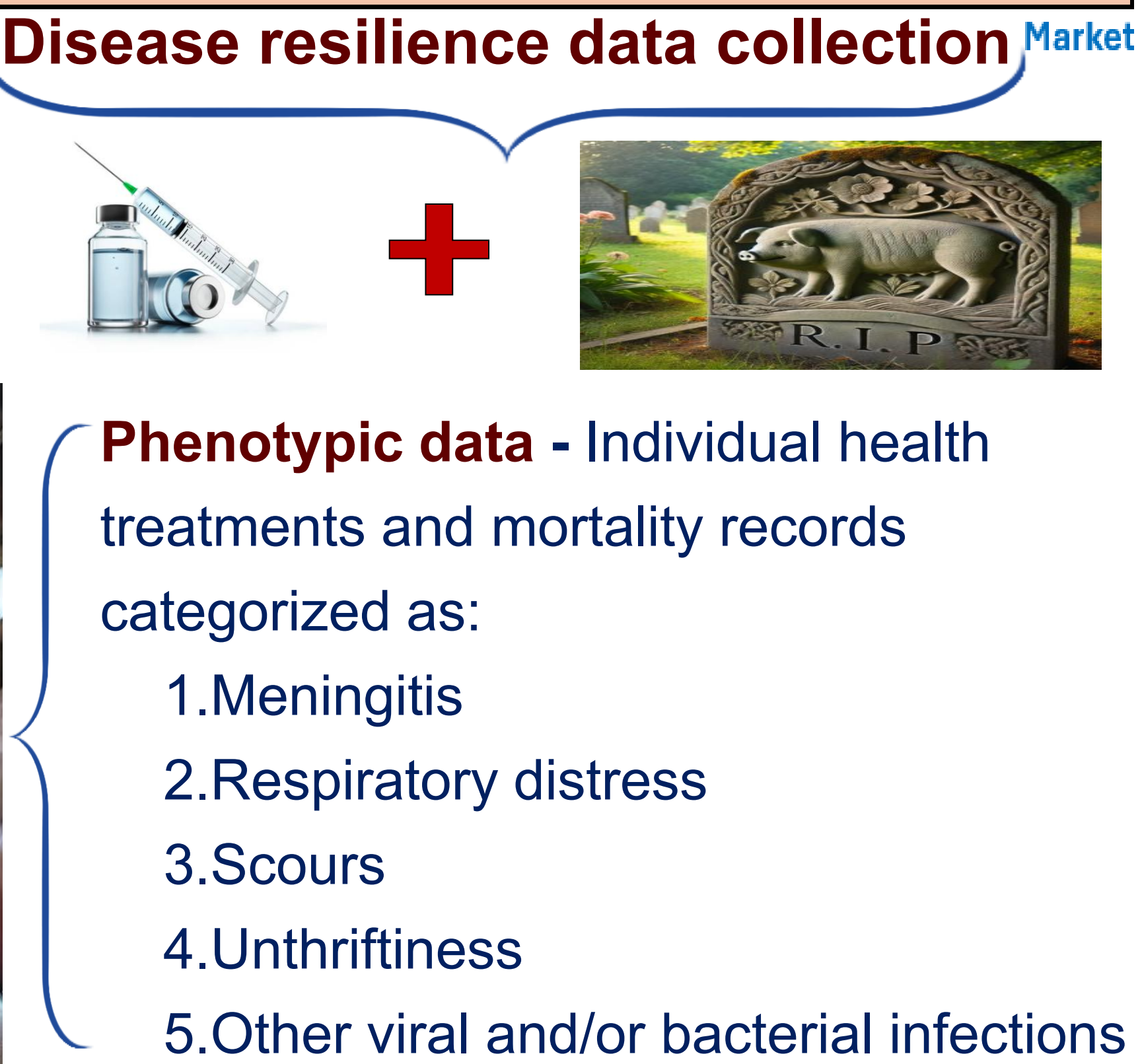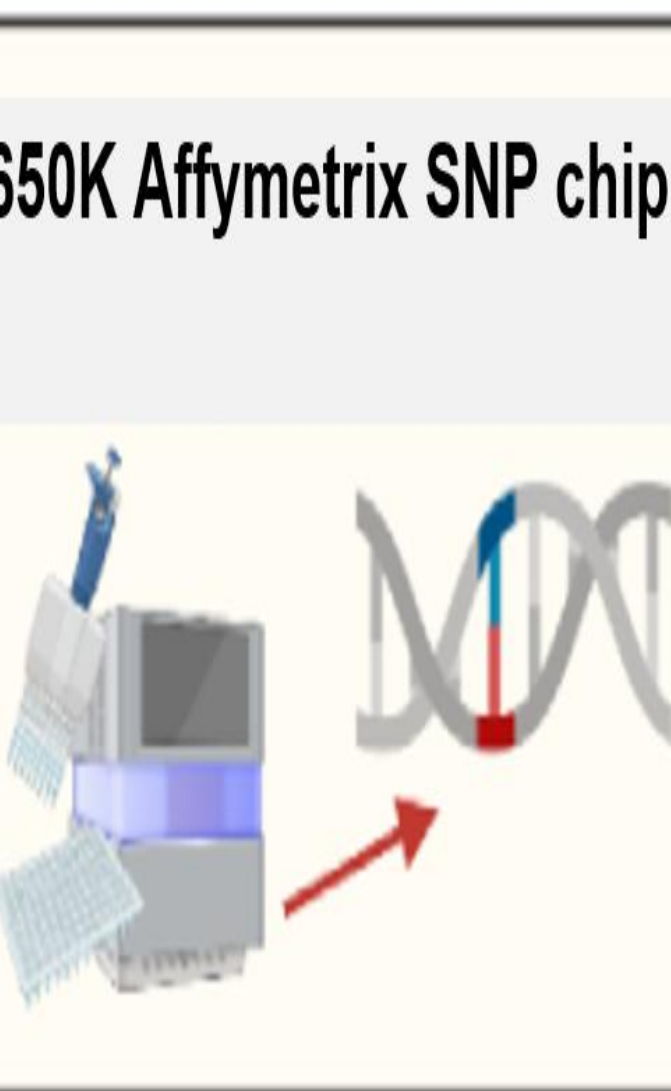
Materials and methods

- A three-phase natural polymicrobial disease challenge (Putz et al.,2019, Frontiers in Genetics)

- **Animals and genotyping**
  - 4,095 Y × LR barrows
  - 65 batches (each ~60 -75 pigs)

650K Affymetrix SNP chip

Phenotypic data - Individual health treatments and mortality records categorized as:
1. Meningitis
2. Respiratory distress
3. Scours
4. Unthriftiness
5. Other viral and/or bacterial infections

- **Variance Component Estimation and GWAS**: Uni- and bi-variate analyses using generalized and mixed linear models with genomics (ASReml 4.2) and GWAS using JWAS software.

- **Model:** $y_{ijkl} = Batch_i + EntryAge_{ijkl} + Pen_j + Sow_{ijk} + Pig(grm)_{ijkl} + e_{ijkl}$

- **Gene Ontology term enrichment analyses:** of 0.25 Mb windows that did not reach significance, using GSEA 4.3.3 software.
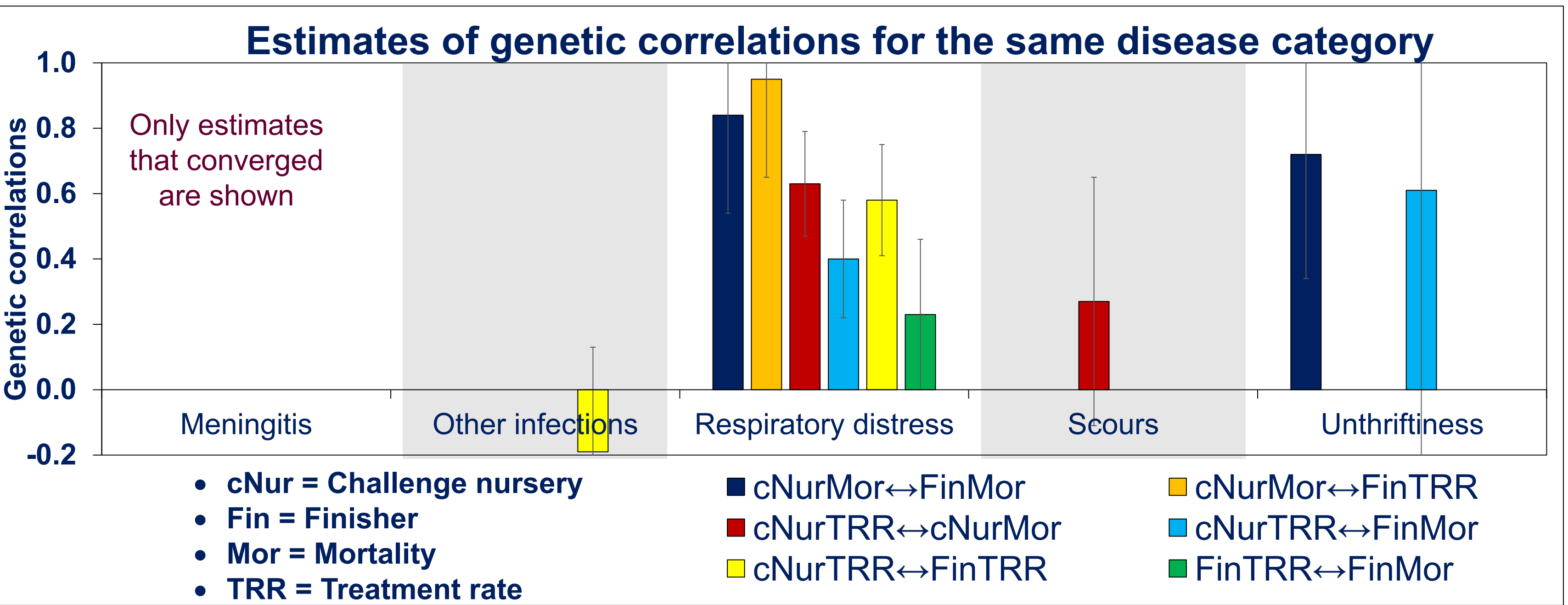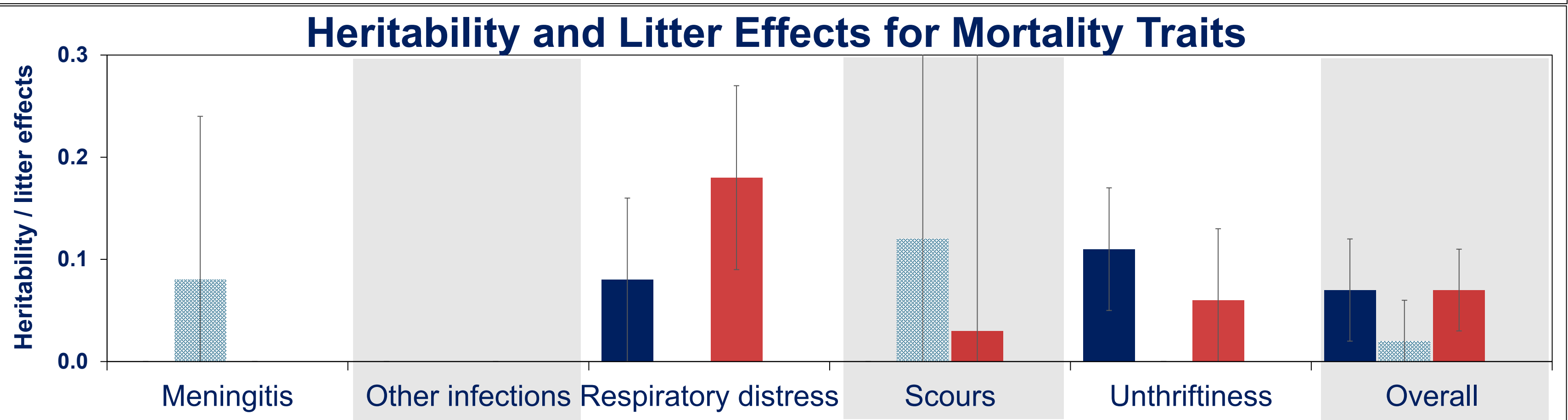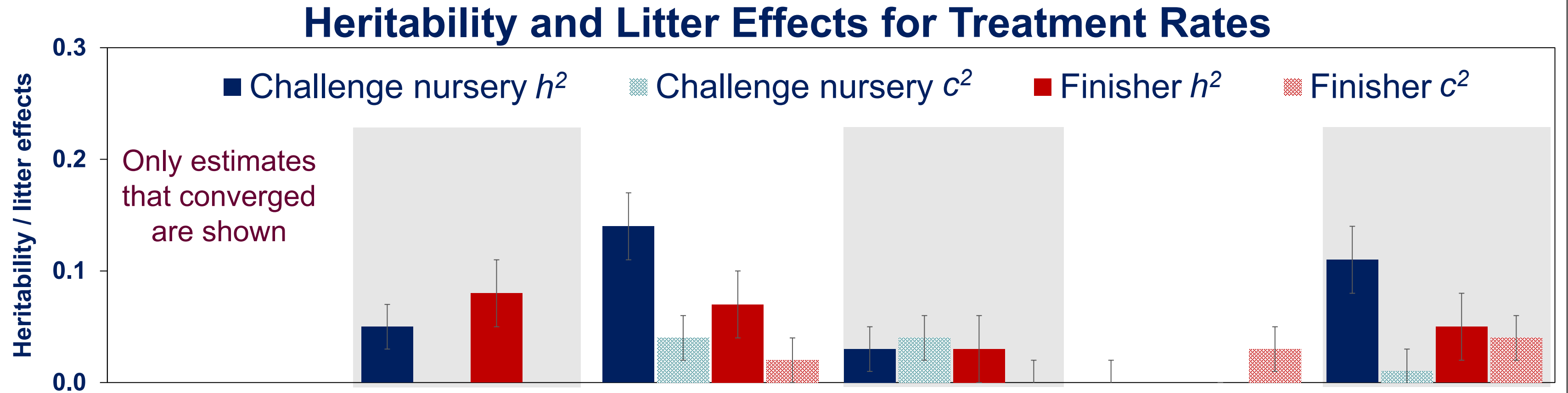
Discussion

- Heritability estimates for treatment rate and mortality were generally higher in the challenge nursery than in the finisher.
- Compared to other diseases, respiratory distress treatment rate and mortality tended to have higher heritability estimates, both in the nursery and finisher.
- Litter effects were generally low, but stronger in the challenge nursery.
- Genetic correlation estimates for respiratory distress among treatment rate and mortality were generally positive, both in the challenge nursery and finisher.
- Corresponding genetic correlation estimates for other disease categories were either moderately negative, not positive definite, or did not converge.
- GWAS identified several genomic regions and candidate genes, on chromosomes 7, 8, 13, and 18 for other infections and respiratory distress treatment rate in the challenge nursery and finisher.
- Gene set enrichment analyses identified several enriched biological processes for genomic regions that explained more genetic variance but did not reach significance, including disease susceptibility and immune capacity.
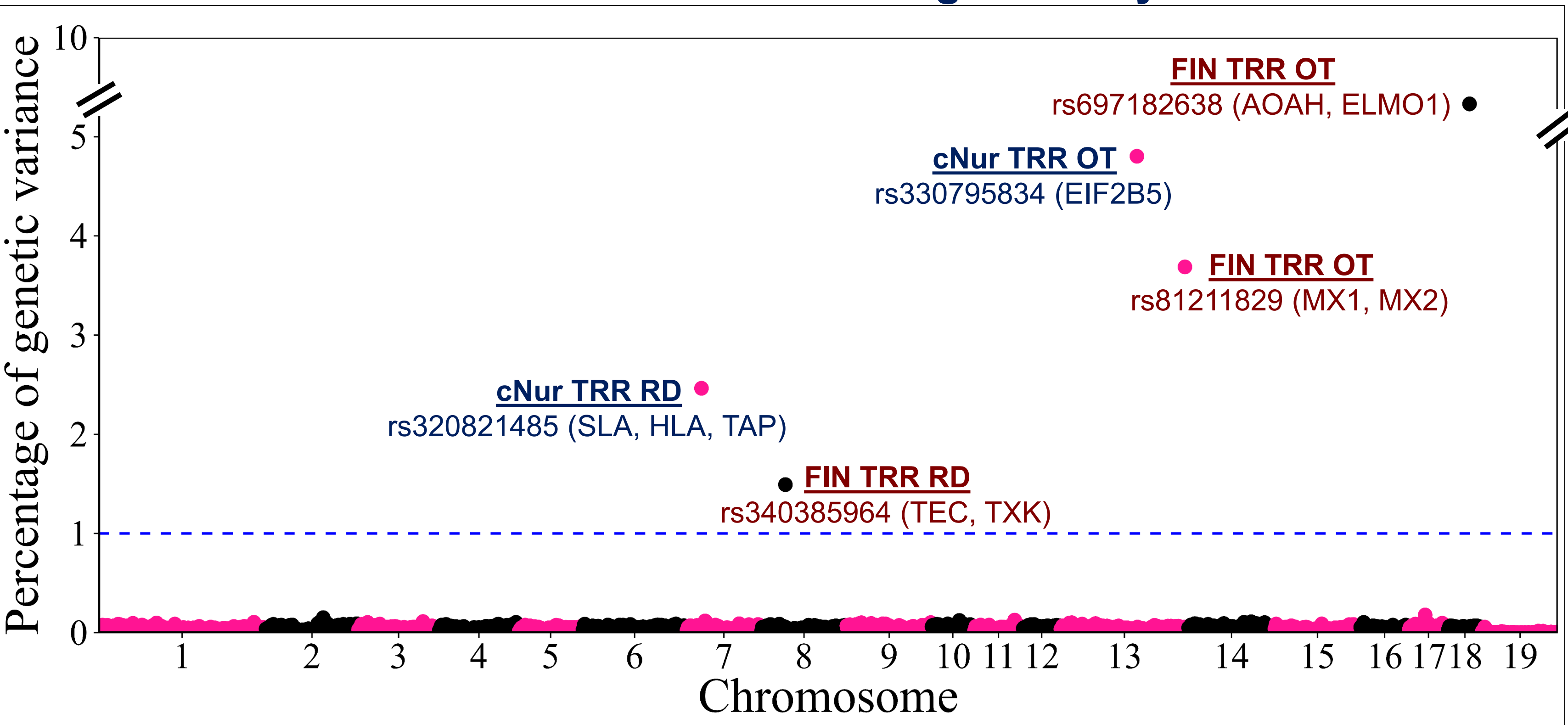
Conclusions

- Respiratory distress treatment rate and mortality are substantially influenced by genetics, making it a key target for genetic selection.
- Litter effects are critical in early life stages but diminish as the pigs mature.
- Selection strategies to improve health treatment and mortality traits should be balanced to avoid unintended consequences.
- Genetic parameters and genomics provide the roadmap for breeding programs, and this study provides valuable information to breed for disease resilience in pigs.

Results

Heritability and Litter Effects for Treatment Rates

Heritability and Litter Effects for Mortality Traits

Estimates of genetic correlations for the same disease category

GWAS for disease traits in the challenge nursery and finisher

Heatmap of GO enrichment analysis of GWAS results for Respiratory Distress