Using expression data to detect small QTL in dairy cattle

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Introduction

- Most QTL have small effect → difficult to detect

- Use additional information to detect QTL → gene expression?

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Objective | *Combine Bayesian prediction model, GWAS, and eQTL to detect variants associated both with QTL and gene expression*

Local GEBVS

- 35K Holstein & Jersey: HD SNPs, milk traits & fertility
- Bayes R hybrid→ SNP effects
→ **Local GEBVs for intervals of 250kb**

Gene expression

- Gene expression from milk (131 Holstein & Jersey) and blood (105 Holstein)
→ **Expression of genes within 1 Mb of interval**

1. Correlate

2. Select

p-value correlation $\leq 10^{-5}$ & var(interval) ≥ total genetic variance/10,000
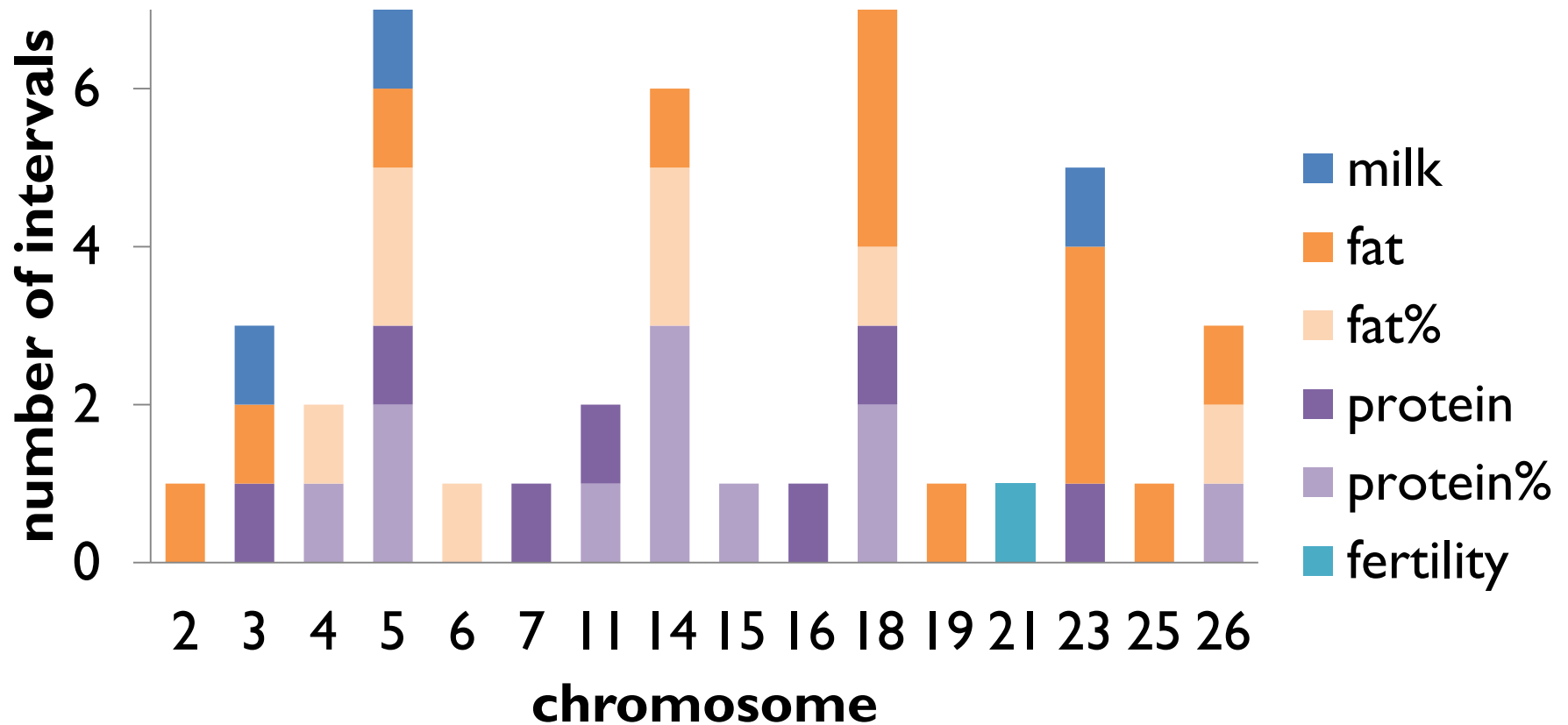
3. Compare

eQTL

- Gene expression (131/105 Holstein & Jersey)
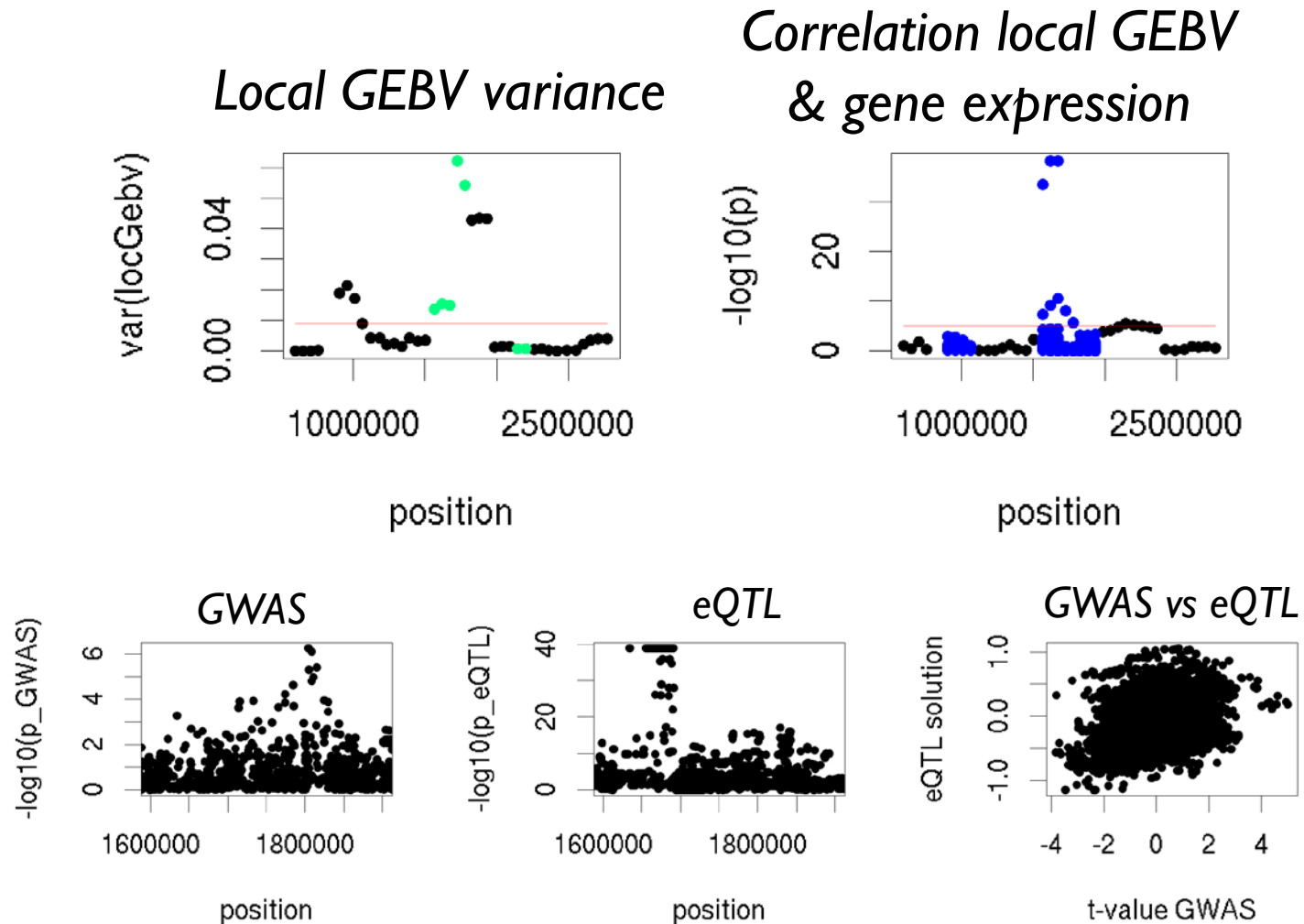- ~10 million sequence variants
→ **Detect eQTL**

GWAS

- Milk traits & fertility (35K Holstein & Jersey)
- ~5 million sequence variants
→ **Detect GWAS hits**

Example: chromosome 18, fat yield

Local GEBV variance

Correlation local GEBV & gene expression

GWAS

eQTL

GWAS vs eQTL

Conclusions

- *Expression data can be used to identify QTL regions*

- *Regions explained very small part of genetic variance*