

Different types of data for predicting genomic EBV

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How to increase genomic reliabilities

- **Increase reference population**

- Join populations of same breed
- Cows in reference population
- Across breeds predictions

- **Increase LD information**

- Haplotype models
- Sequence information

How to increase genomic reliabilities

- **Genotyping and sequencing technologies**
 - 7K, 9K, 50K, 700K
 - WGS
- **Statistical models**
 - GBLUP/SNP-BLUP
 - Haplotype models
 - Bayesian VSM
 - One step
- **Take home message**
 - Combination of genomic technologies
 - Need multiple models

SNP-chip vs. WGS

- SNP chip

- Sample of SNP (higher minor allele frequency)
- Limited linkage disequilibrium depending on number of SNP
- High informativity for imputation
- Opportunity for custom made chip

- Sequence

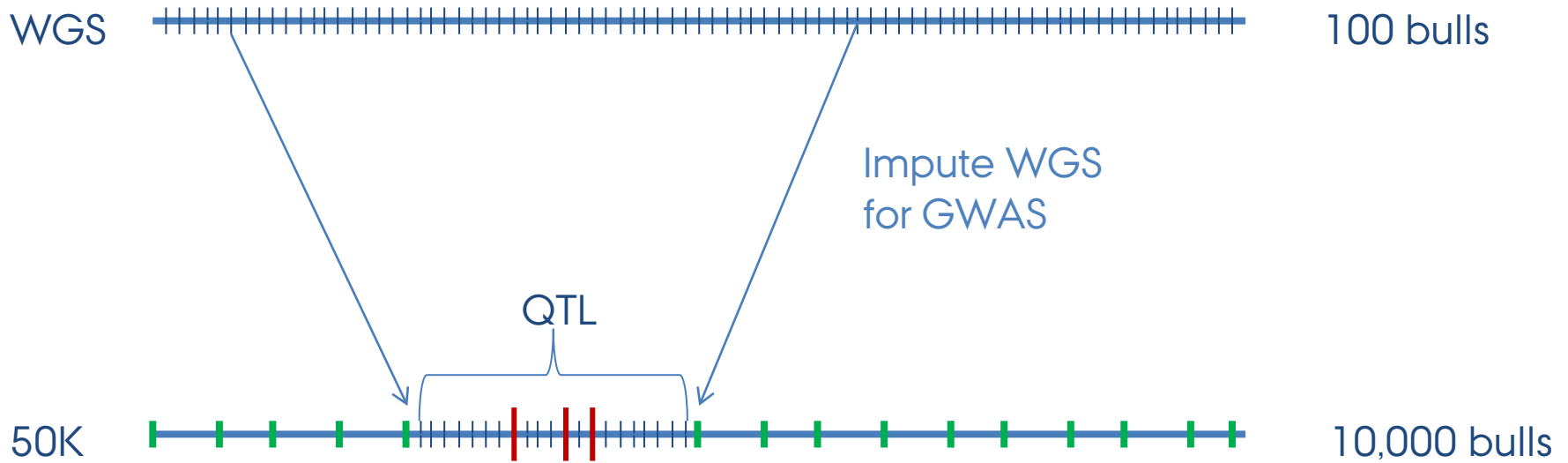
- Contains most variants (>20 mio SNP, indels, CNVs, etc)
- Causative variants included (no bias in selection of SNP)
- High linkage disequilibrium between markers and causative variants
- Sequence GWAS improve associations substantially (Goutam)

Bull reference

50K



10,000 bulls



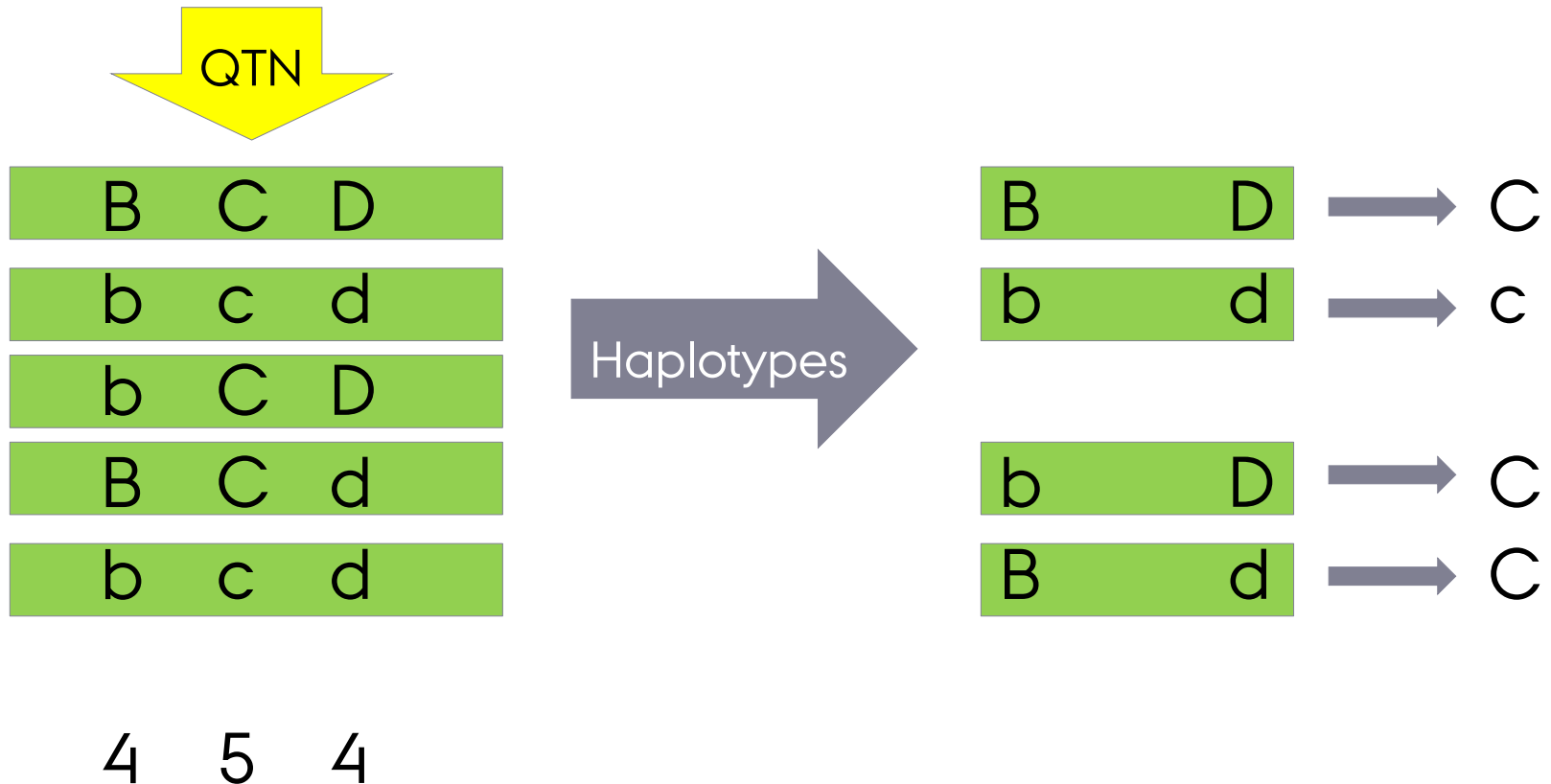
Include sequence SNPs (QTL regions, general)

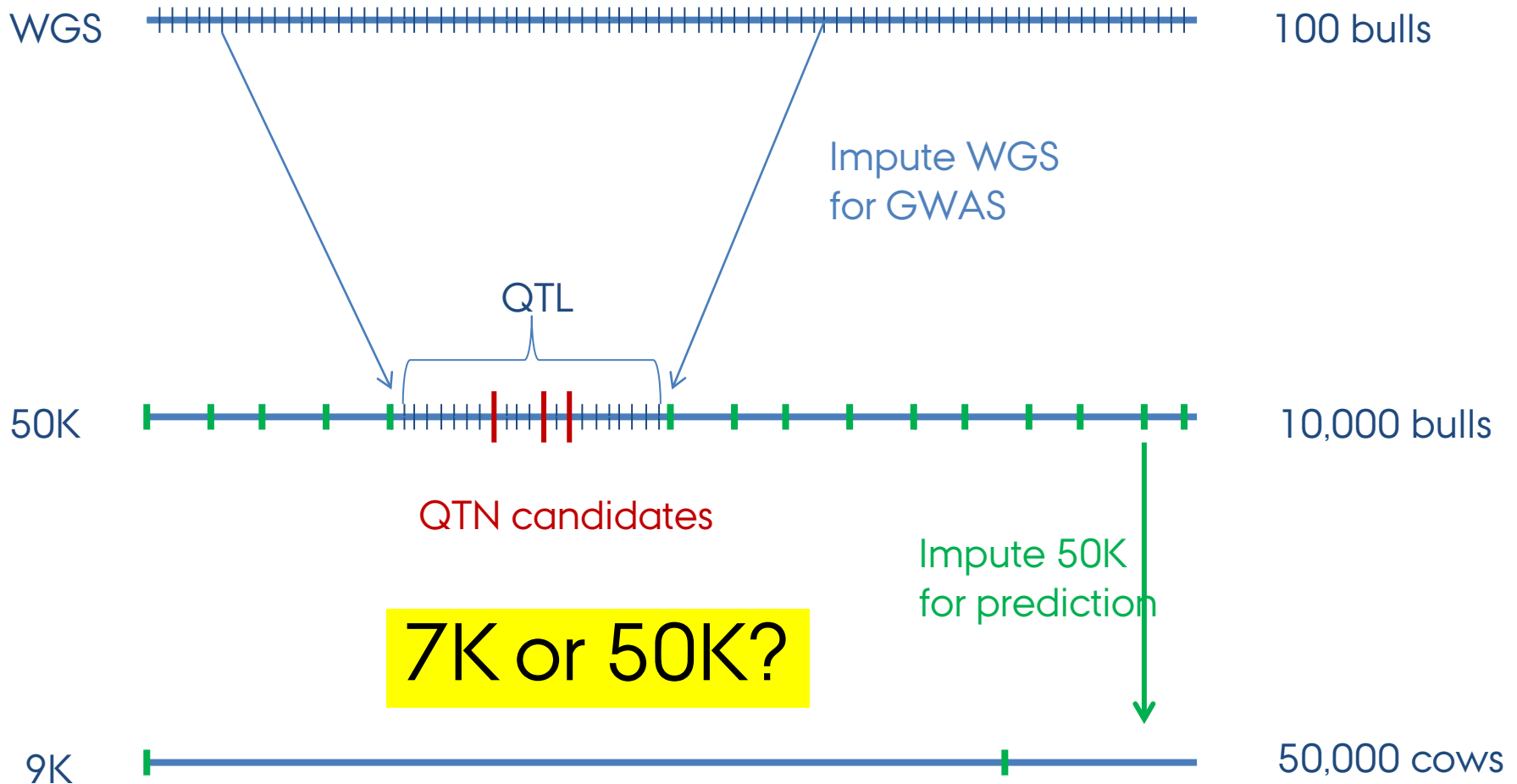
Or few potential QTN

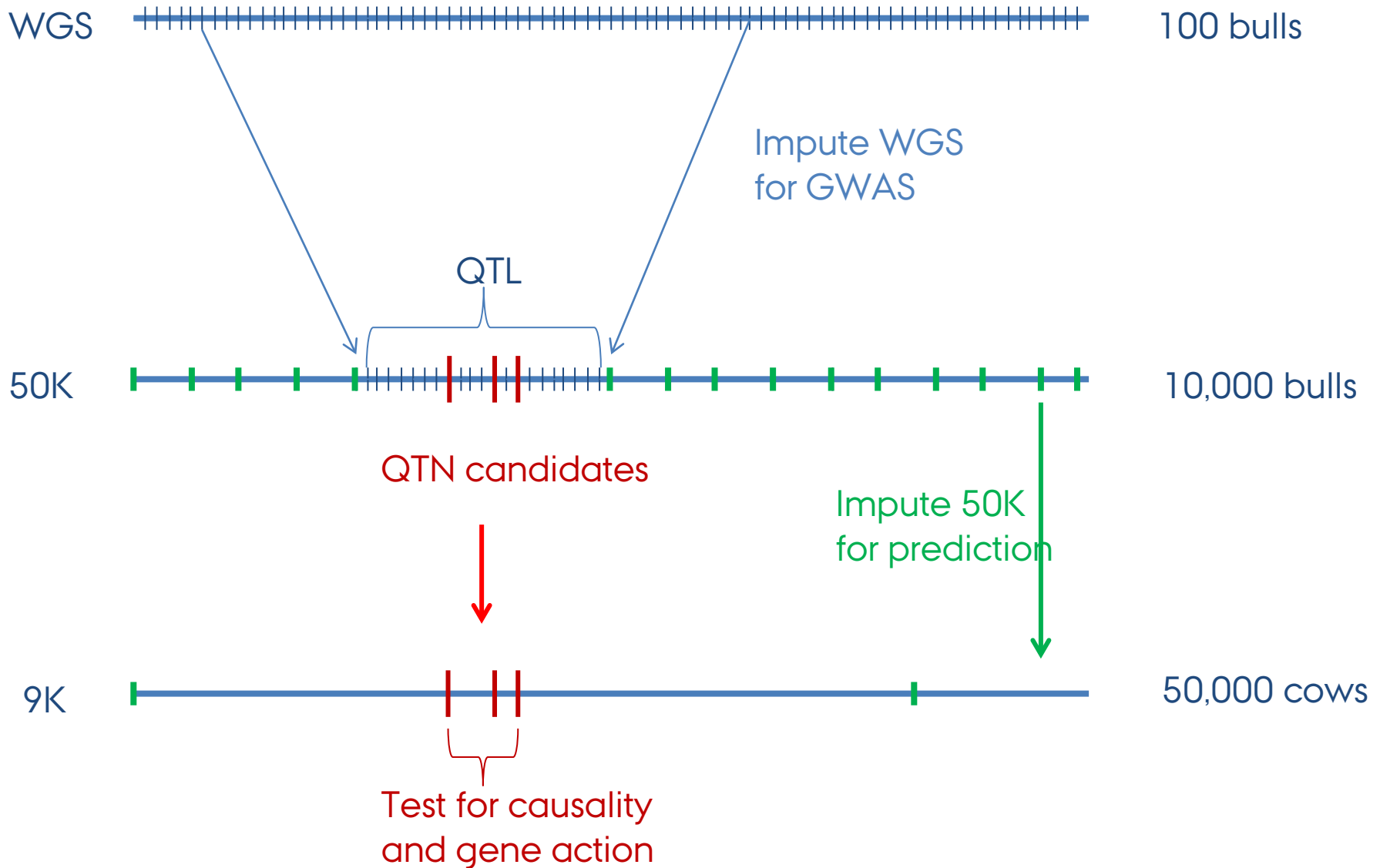
Bayesian models are needed

Haplotype models

Increased LD







Bull reference

- **50K**
 - Capture most genetic variance within breed
- **700K**
 - Haplotype models
 - Prediction over generations (and breeds)
- **Sequence data**
 - Causative variants
 - Prediction over generations and breeds

9K for reference cows

- **More cows in reference (cheaper)**
- **High imputation accuracy**
- **Add many potential causative variants**
 - Non-additive effects
 - Testing for causative variants
- **Better predictions across breeds**

Models

- **GBLUP → infinitesimal model**
 - No improvement from sequence data
 - Needed for large scale predictions
 - Can be modified to prioritise specific SNPs
- **BayesianVS models → causality model**
 - Select causal SNP or few SNP in high LD
 - Needed to extract prior knowledge for GBLUP/SNP-BLUP

Combining genotyping and modeling

