

Concordance analysis: from QTL to candidate causative mutations

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Objective

To narrow down from a QTL region containing a large number of polymorphisms to a limited number of candidate causative mutations

Trait – rear leg set side view (RLSV)

Illustration adapted from primholstein.com

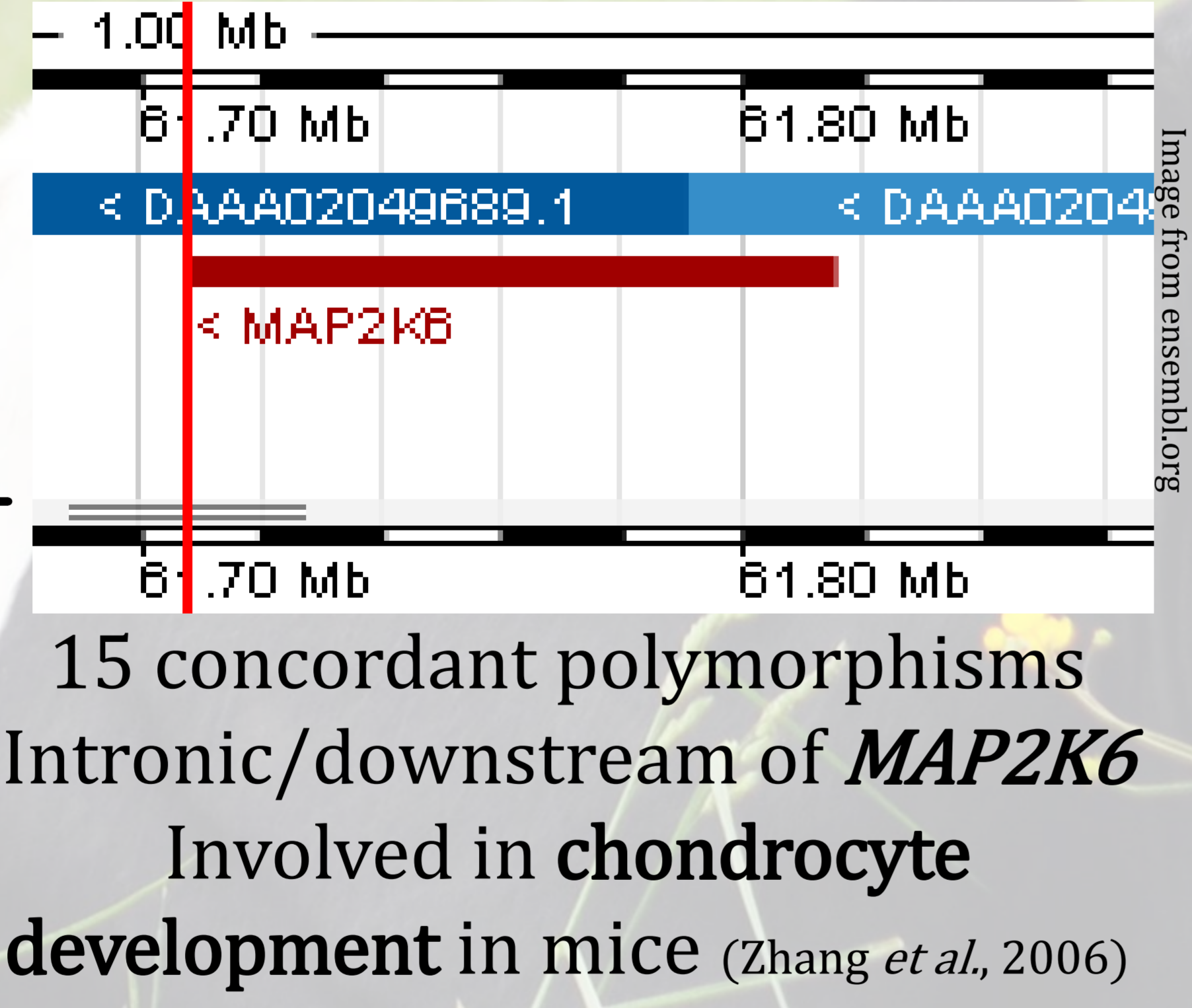
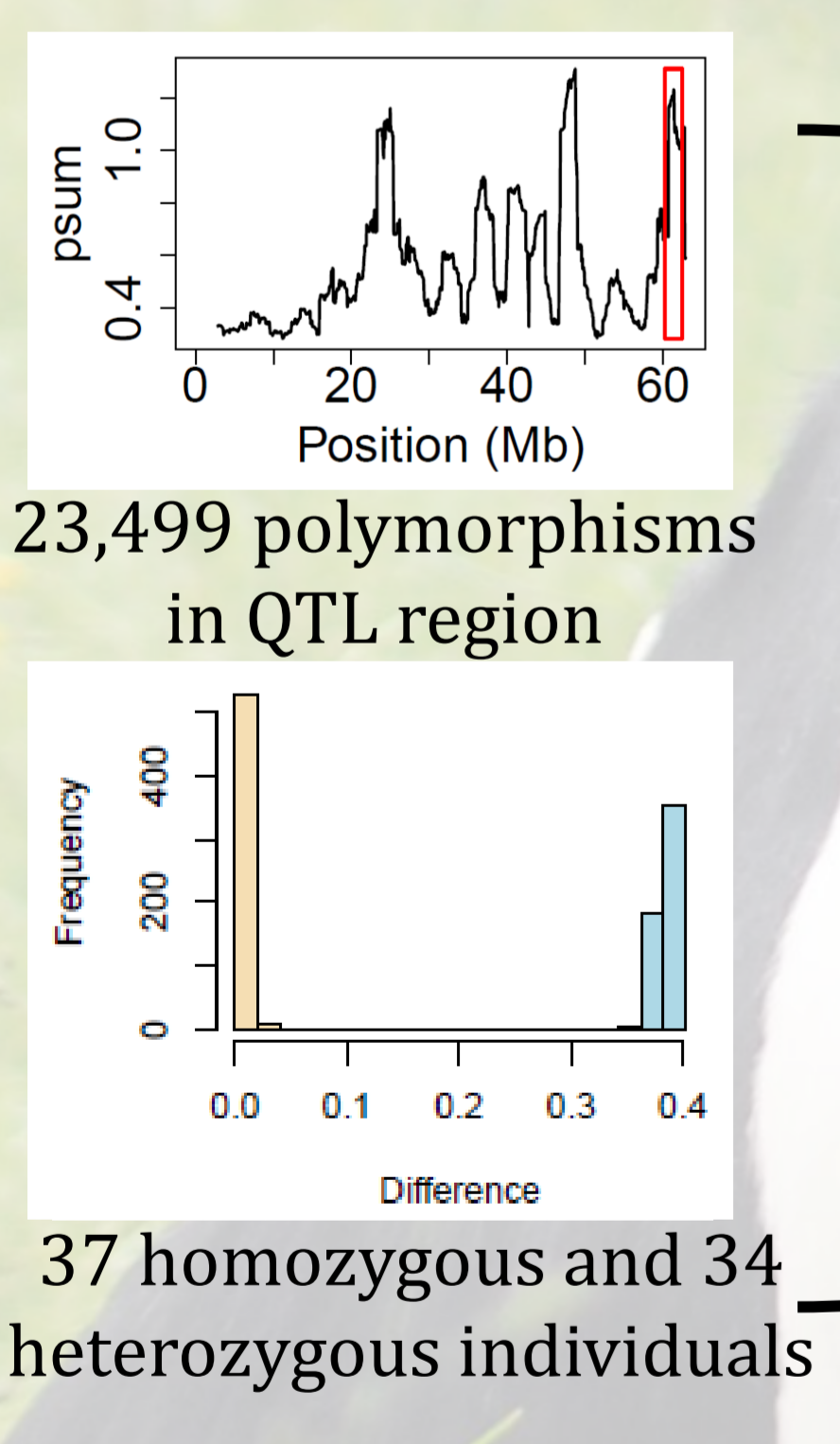


Correlated with culling rate (de Jong, 1997)

Data

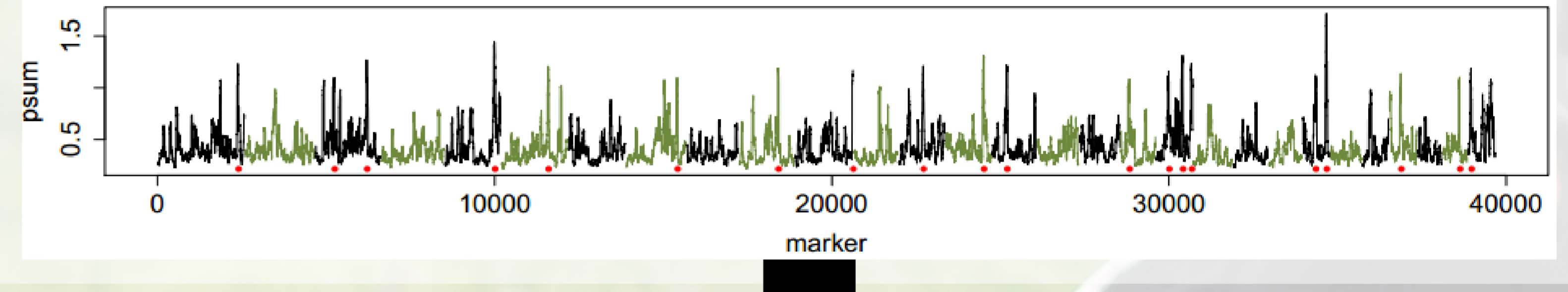
- QTL mapping & status prediction: 50K SNP data
- 3,154 Holstein bulls
- Deregressed proofs for RLSV
- Concordance analysis: 71 sequences from 1000 bull genome project

Example – chr 19:60.2-62.5 Mb



1) QTL mapping

- Bayes C using GS3 (Legarra *et al.*, 2009), π fixed at 0.01
- Selection of regions based on the sum of posterior marker inclusion probabilities
- 20 intervals of 40 markers (~ 2.5 Mb) selected

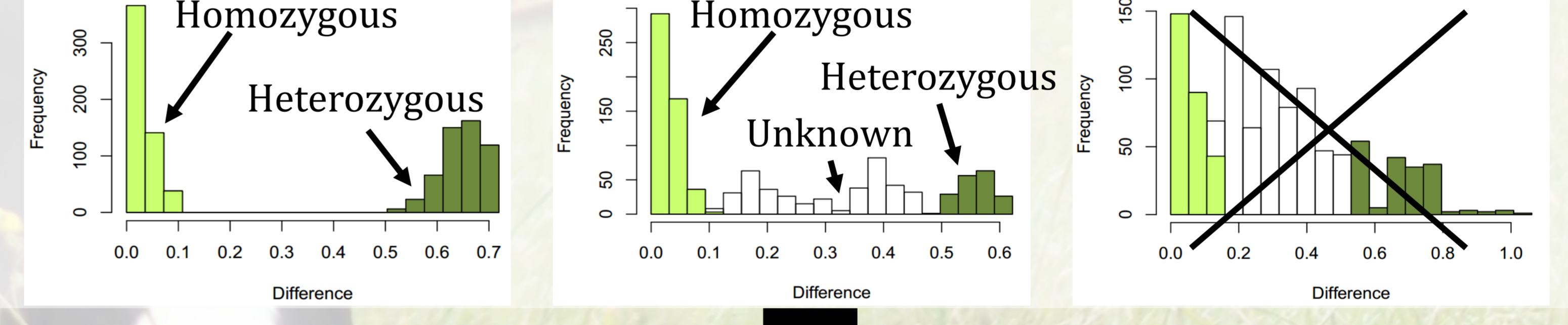


2) Status prediction

- Marker effects estimated during QTL mapping used to derive QTL status
- Subinterval of 10 markers to reduce noise

Effect haplotype 1	0+	0-	0.1+	0.1+	0+	0+	0-	0.2+	0+	0.1	= -0.1
Haplotype 1	1	1	2	2	1	1	1	2	1	2	
Haplotype 2	2	1	2	2	2	2	1	2	1	1	
Effect haplotype 2	0.4+	0-	0.1+	0.1+	0.2+	0.3+	0-	0.2+	0+	0	= 0.7

Example: difference = 0.8 → clustering → heterozygous



3) Concordance analysis

- Sequences → keep polymorphisms in QTL region if:
- Polymorphisms concordant with QTL status for at least 90% of the individuals
 - Genotype quality ≥ 20 in at least 5 homozygous and 5 heterozygous individuals

QTL	Polymorphism
homozygous	1/1
homozygous	1/2
homozygous	2/2
heterozygous	1/1
heterozygous	1/2
heterozygous	2/2

Conclusions & Perspectives

Good results for some QTL, but not for QTL influenced by multiple mutations
→ Next steps: imputation, association study using multiple breeds



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