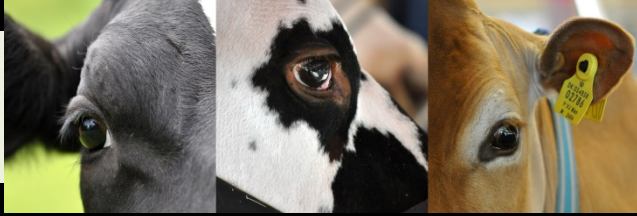


Across breed QTL detection and genomic prediction in French and Danish dairy cattle breeds

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R. F. Brøndum¹, G. Sahana¹, D. Boichard^{2,3} and M. S. Lund¹

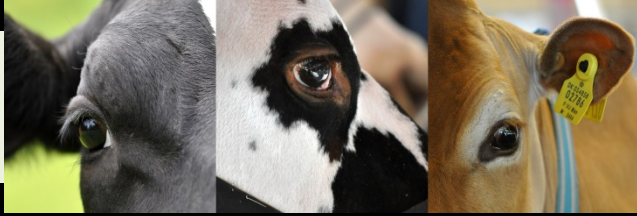


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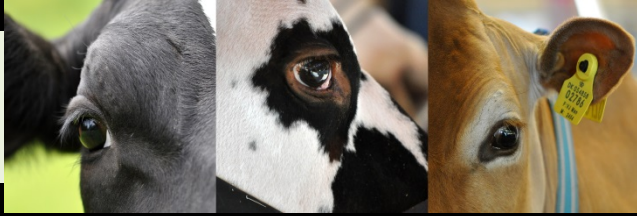
Introduction

- Across breed prediction in dairy cattle
- Low accuracy when using 50K/HD chips
- Sequence data: causative mutations
 - improve across breed prediction?



Objectives

- 1) How many QTL are shared across breeds?
- 2) How close should prediction markers be to the causative mutations?



QTL detection

1) How many QTL are shared across breeds?

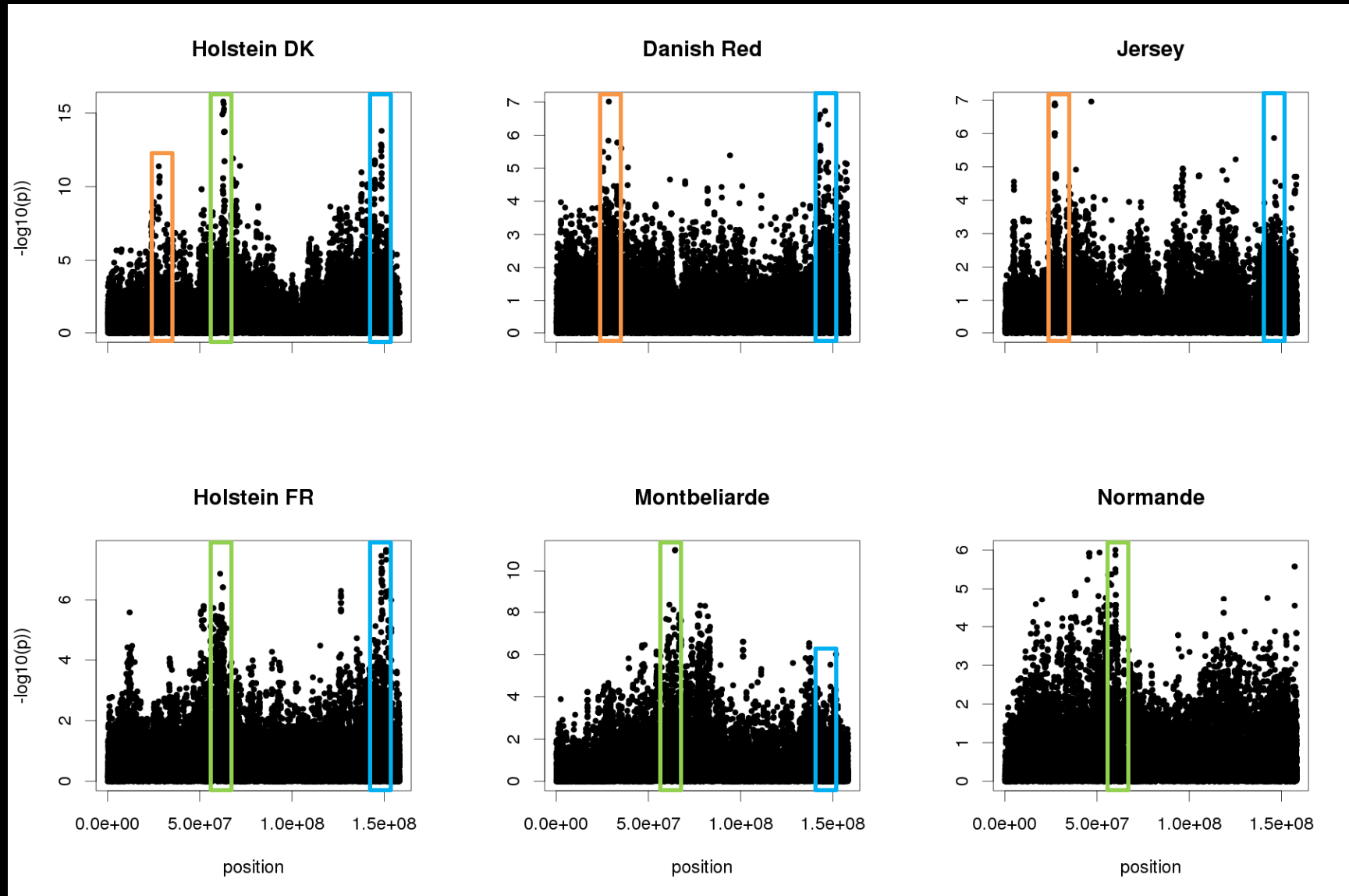


QTL detection – Material & Methods

- HD genotypes, imputed from 50K chip
- Deregressed proofs for protein yield
- 5642 Nordic Holstein, 3130 French Holstein, 1238 Jersey, 2236 Montbéliarde, 1970 Normande and 1019 Danish Red bulls
- Single marker sire model
- First QTL detection within breed: $p\text{-value} \leq 10^{-6}$
- QTL shared across breed if there is a marker with $p\text{-value} \leq 10^{-5}$ within 1 Mb in second breed



QTL detection – Results – Chromosome 1



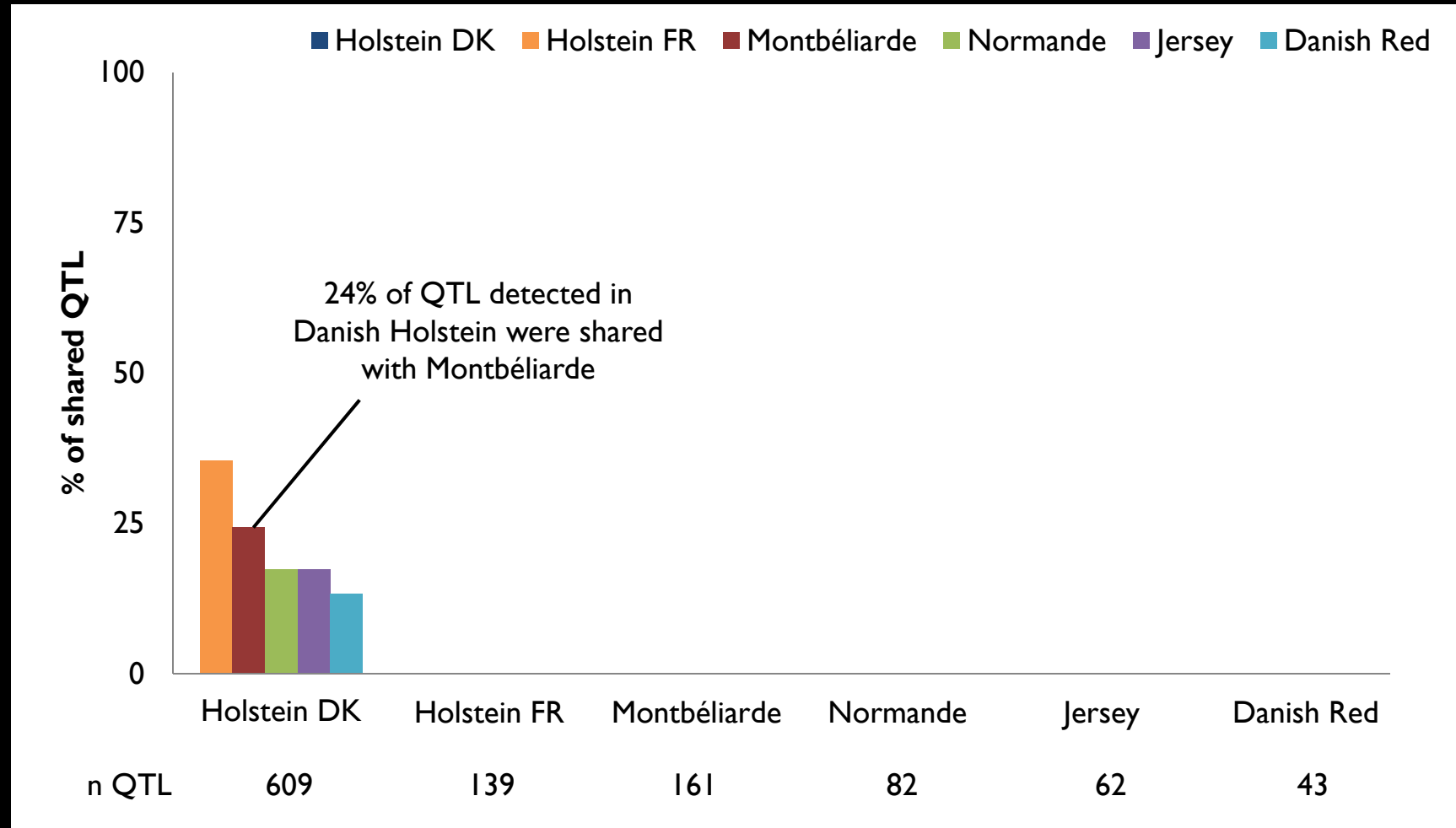


QTL detection – Results

	Holstein DK	Holstein FR	Montbéliarde	Normande	Jersey	Danish Red
n QTL	609	139	161	82	62	43

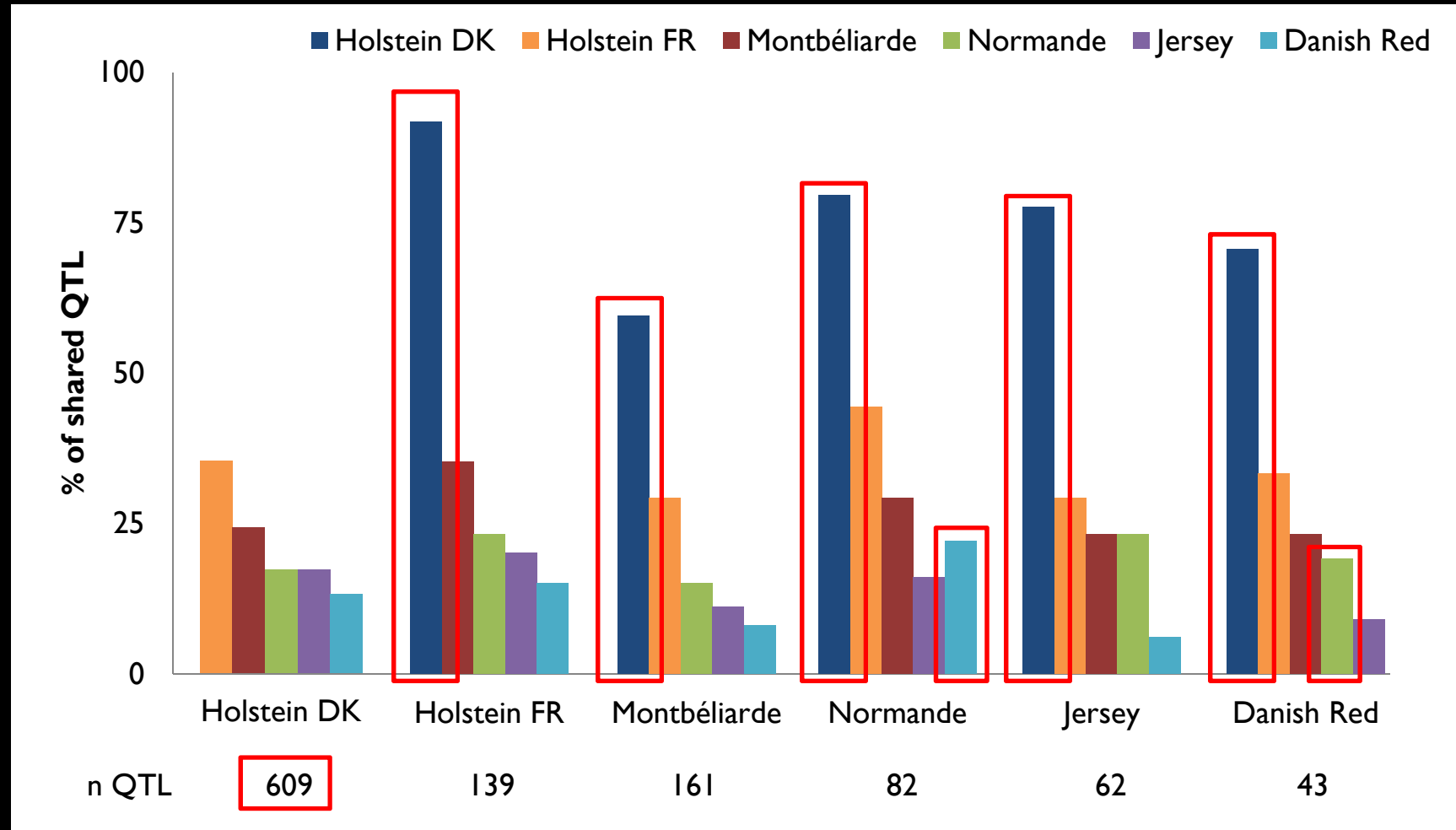


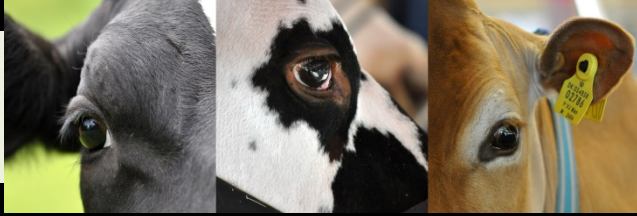
QTL detection – Results





QTL detection – Results

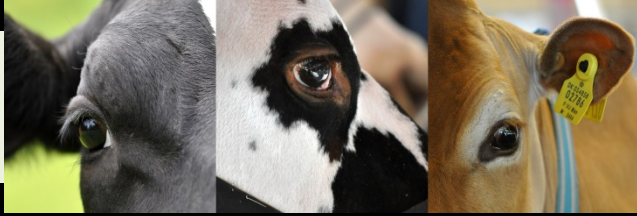




QTL detection – Conclusion

A substantial part of QTL detected in one breed show a significant association in another breed

→ Can be targeted for across breed prediction



Across breed prediction

2) How close should prediction makers be to the causative mutations to enable across breed prediction?



Across breed prediction - Methods

Following de los Campos *et al.* (2013):

$1 - (1 - b)^2$:

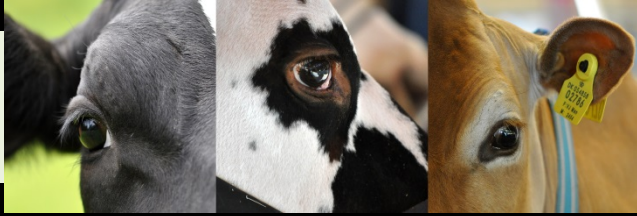
$$\bar{R}_{n+1,y}^2 \leq R_{n+1,y}^2 [1 - (1 - b_{n+1})^2]$$

R^2 if markers are in perfect LD with causative mutations
 minimum R^2 reduction factor
 R^2 if markers are not in perfect LD with causative mutations

b :

$$\bar{G}_{n+1,i} = b_{n+1} G_{n+1,i} + \xi_{n+1,i} \quad (i = 1, \dots, n)$$

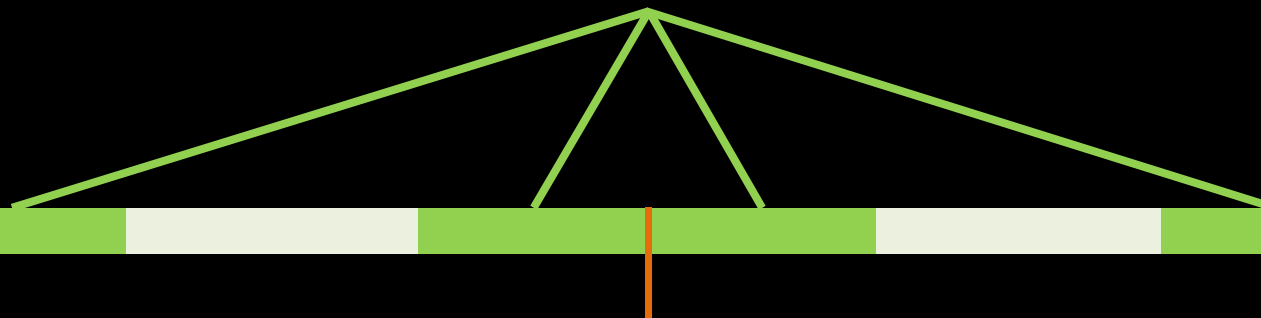
regression coefficient
 genomic relationship at causative mutations
 genomic relationship at prediction markers between individual $n + 1$ and individual i
 residuals



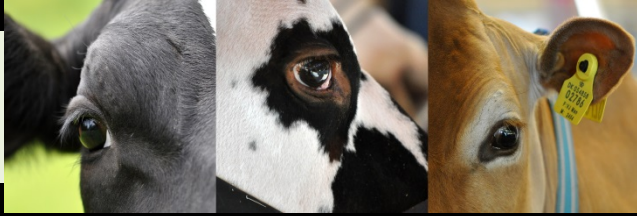
Across breed prediction - Material & Methods

- Genomic relationship matrix at causative mutations:
 - 100 randomly sampled variants
- Genomic relationship matrix at prediction markers:
 - 50K / HD: SNP on 50K / HD chip
 - 50K / HD closest: for each causative mutation, the closest 50K / HD marker
 - Two 1 Kb intervals on both sides of the causative mutations, distance between causative mutations and intervals between 1b and 1Mb

Intervals with prediction markers

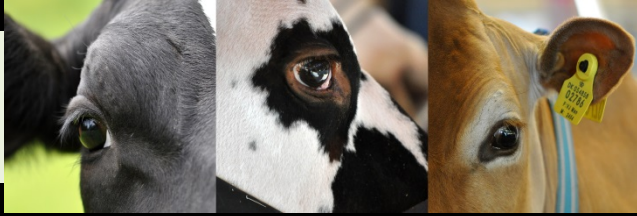


Causative mutation



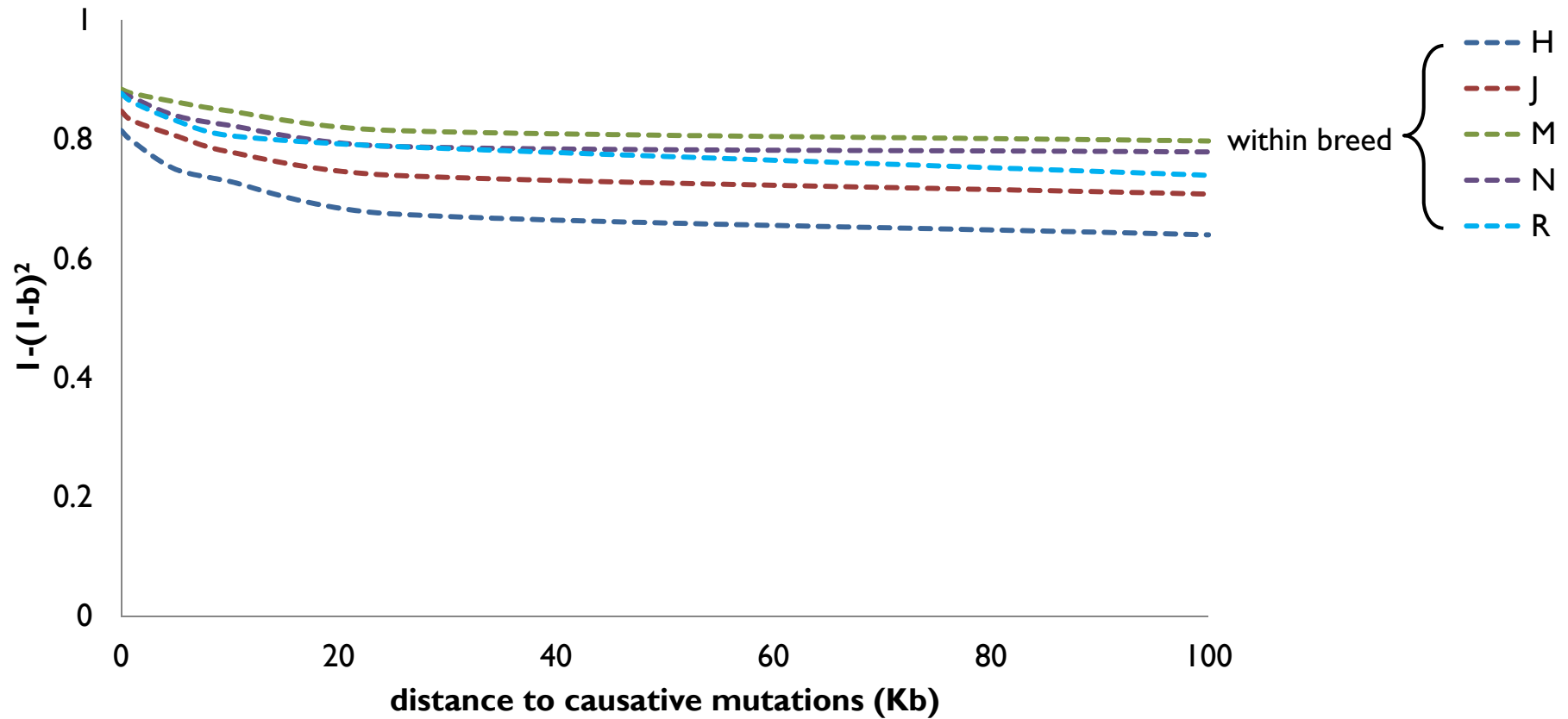
Across breed prediction - Material & Methods

- Genomic relationship matrix at causative mutations:
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- Genomic relationship matrix at prediction markers:
 - 50K / HD: SNP on 50K / HD chip
 - 50K / HD closest: for each causative mutation, the closest 50K / HD marker
 - Two 1 Kb intervals on both sides of the causative mutations, distance between causative mutations and intervals between 1b and 1Mb
- Sequences, chromosome 1:
 - 122 Holstein, 27 Jersey, 28 Montbéliarde, 23 Normande and 45 Danish Red
 - Chromosome 1, ~1,5 million polymorphisms
- Each scenario was repeated 50 times



Across breed prediction - Results

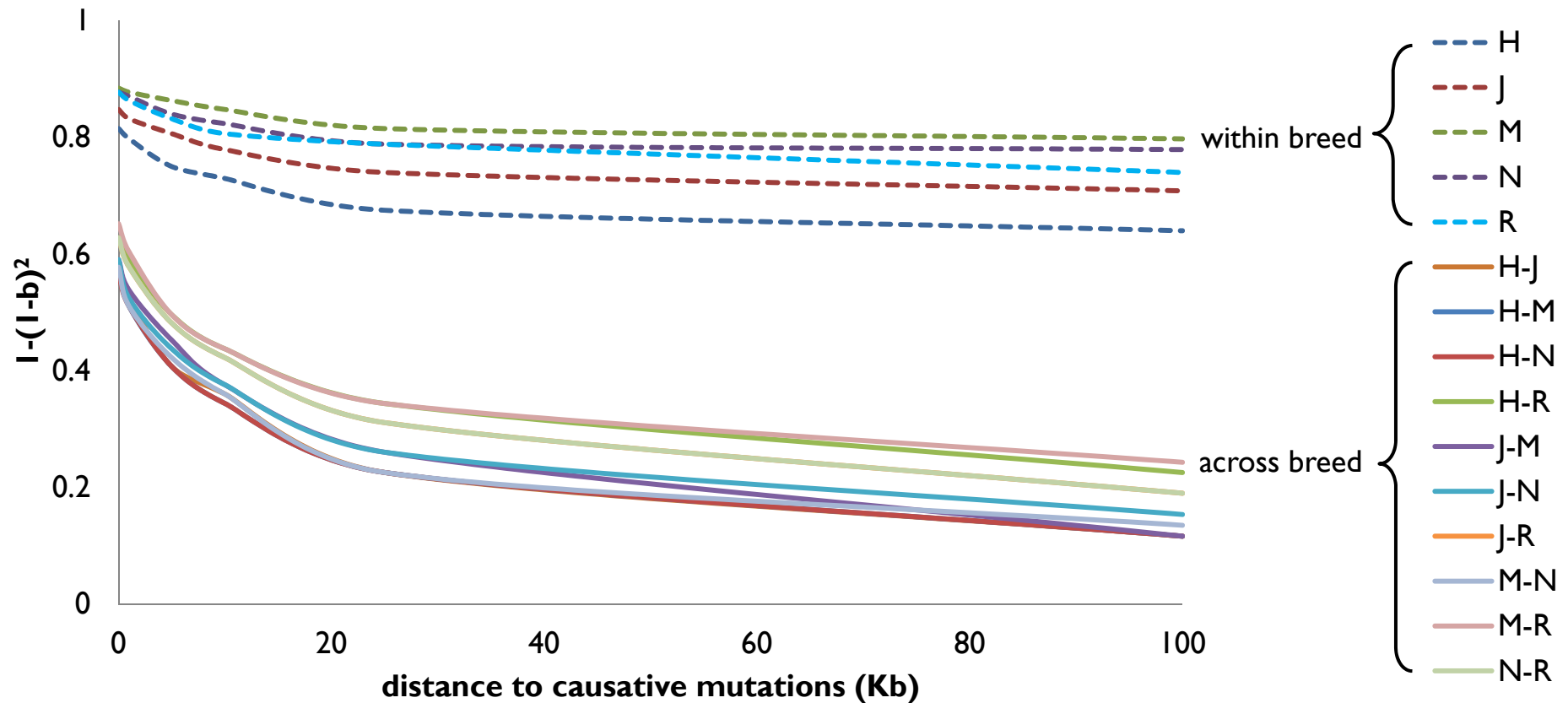
H = Holstein, J = Jersey, M = Montbéliarde, N = Normande, R = Danish Red



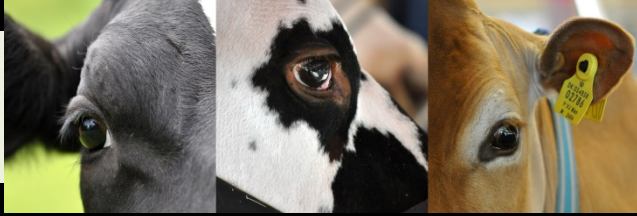


Across breed prediction - Results

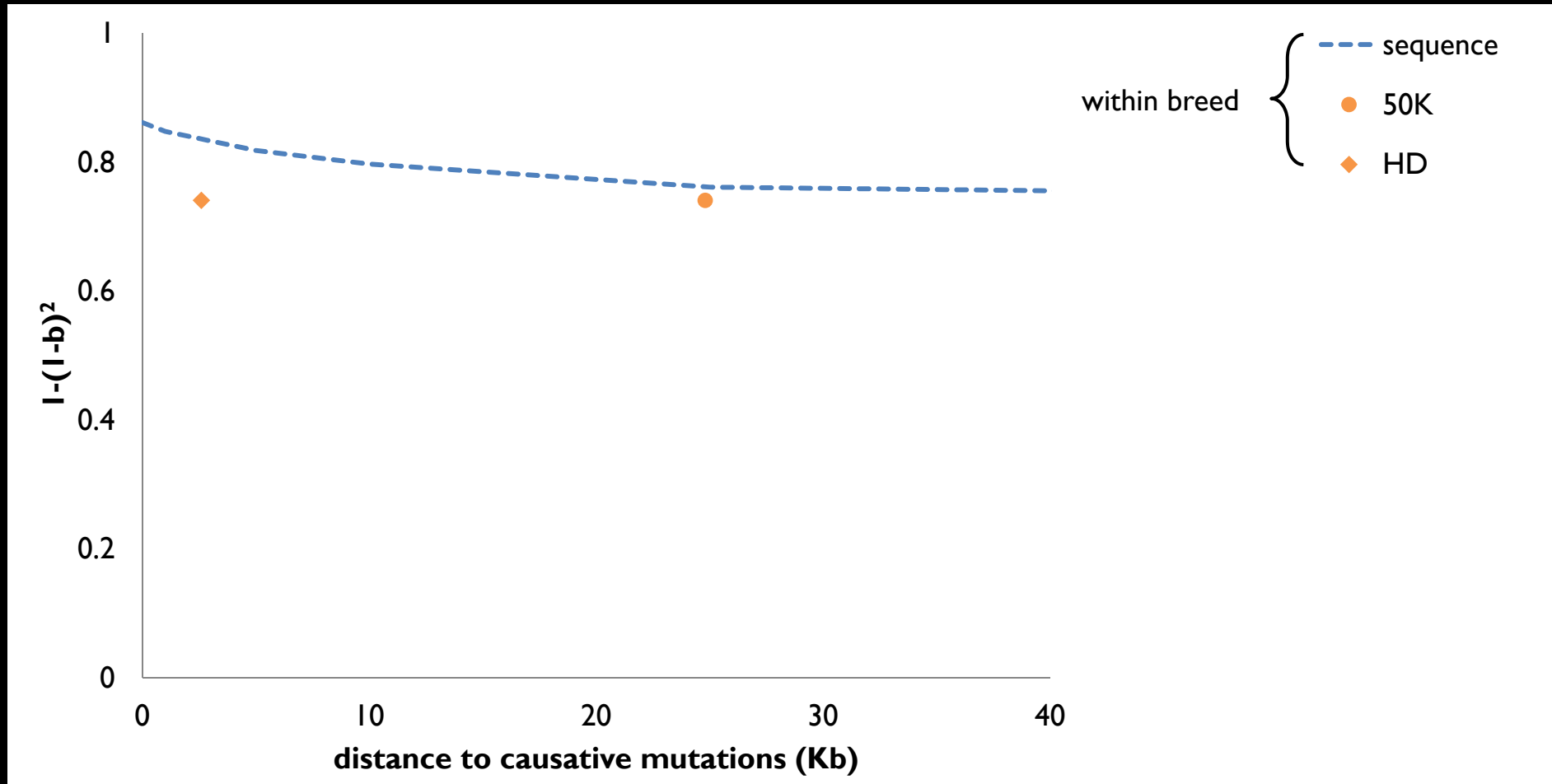
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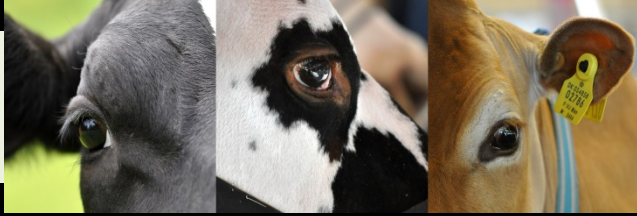


→ $I-(I-b)^2$ decreases when distance between prediction markers and causative mutations increases, faster decrease across breed

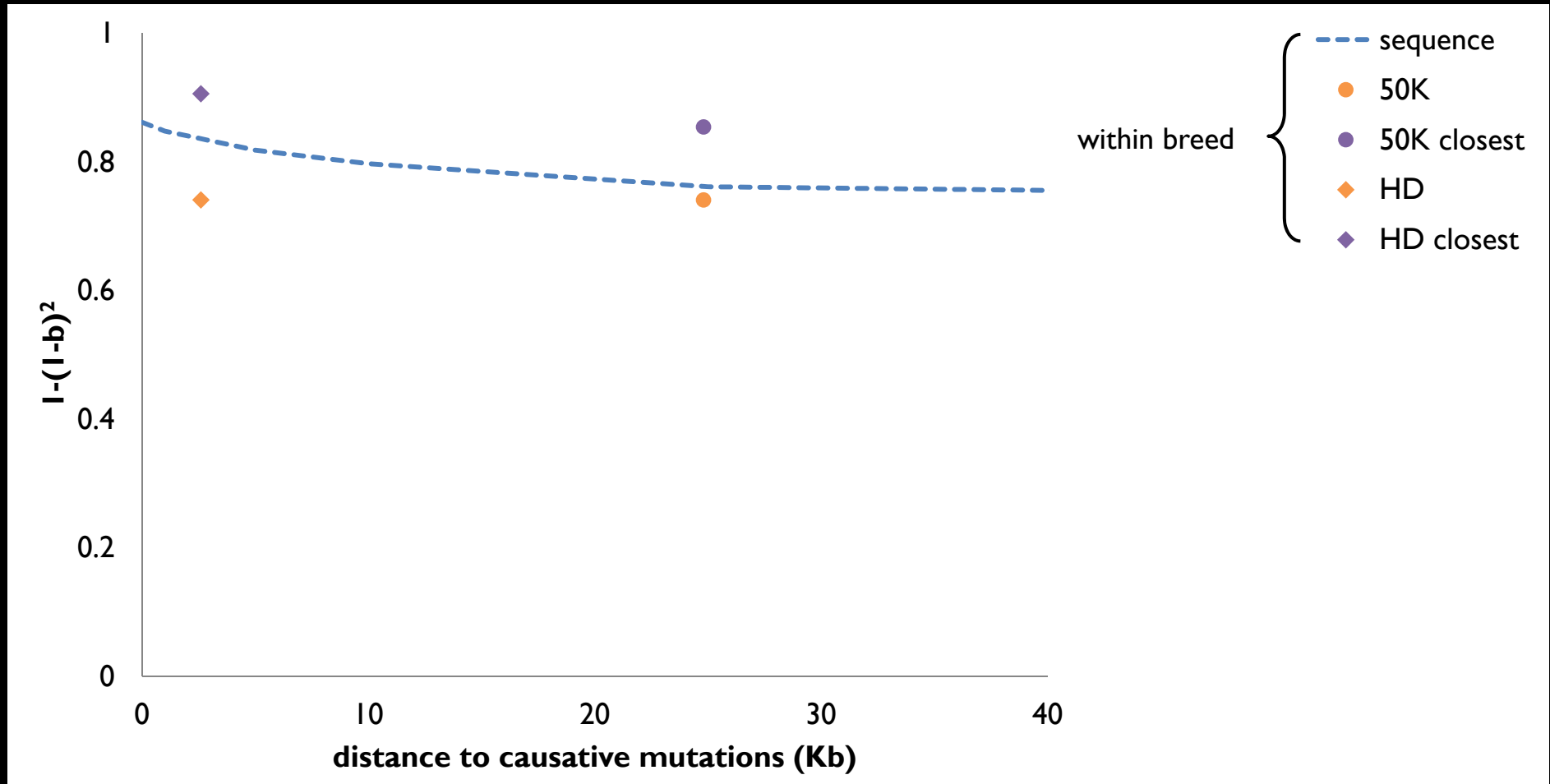


Across breed prediction - Results



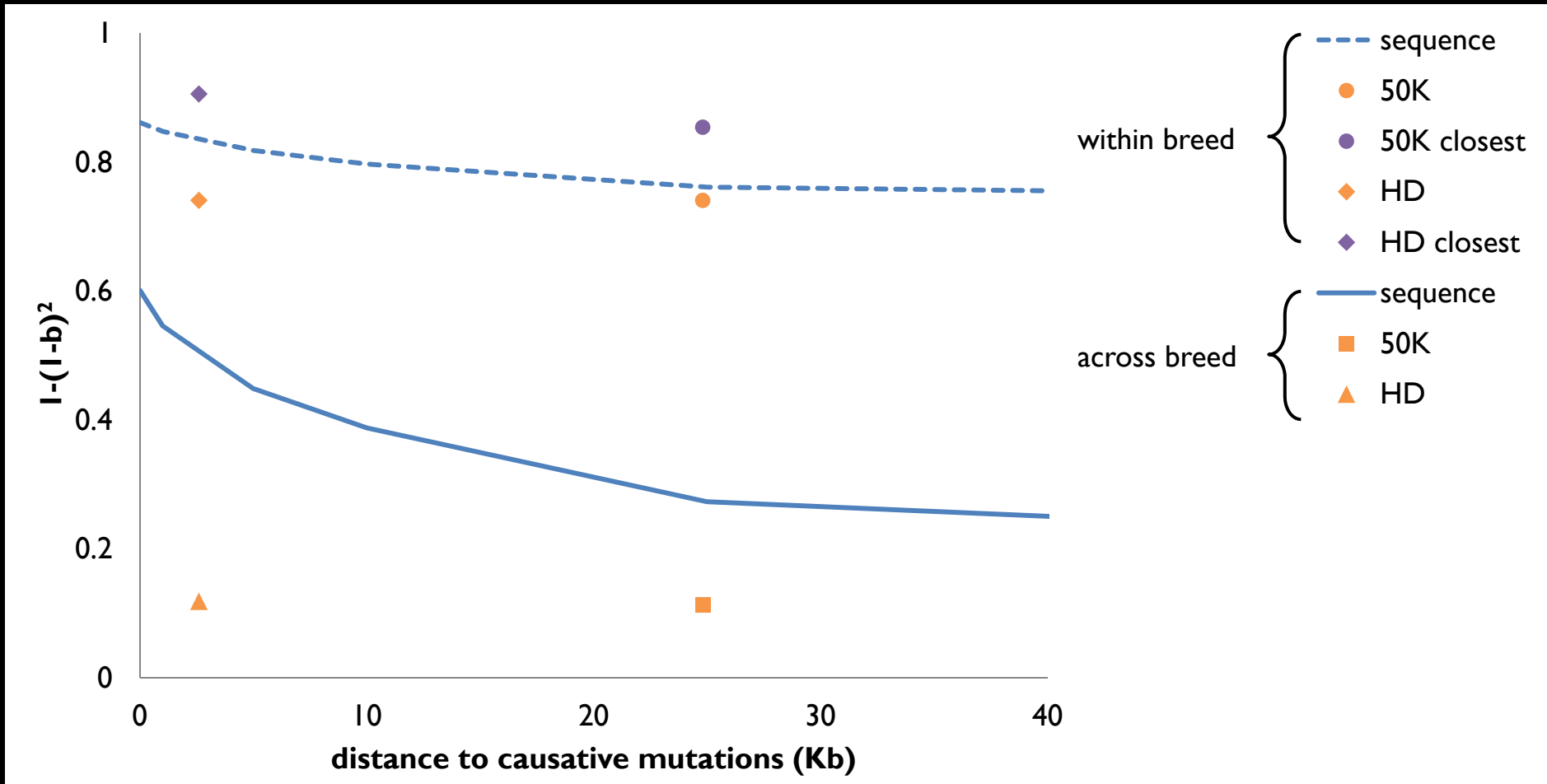


Across breed prediction - Results



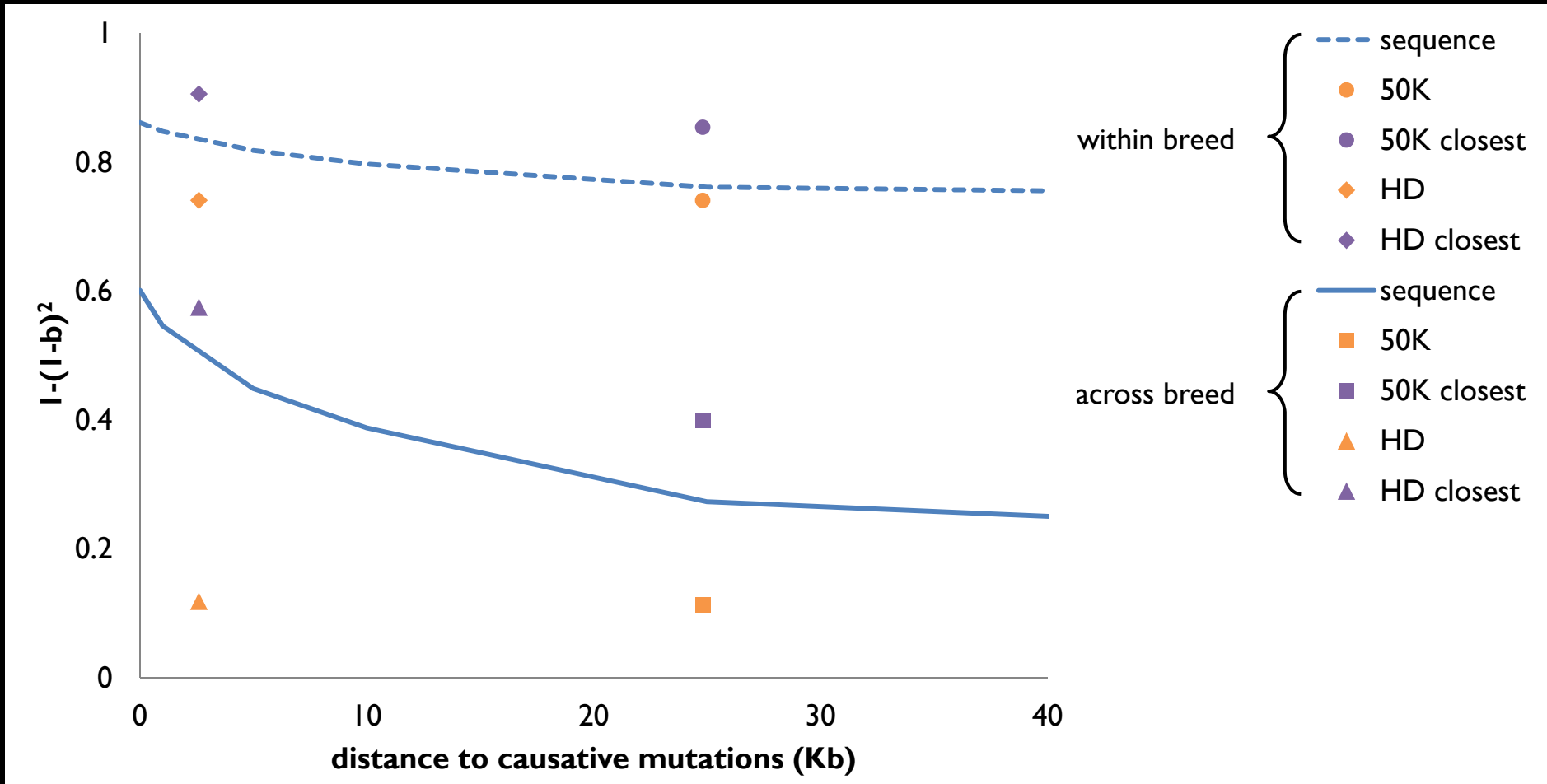


Across breed prediction - Results

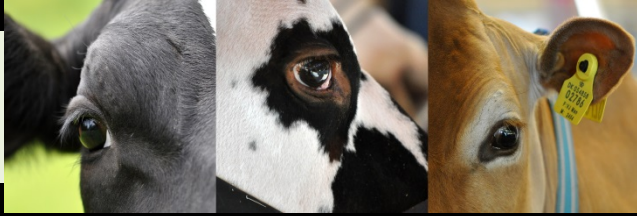




Across breed prediction - Results



→ Using all 50K/HD markers → lower $1-(1-b)^2$ compared to sequence, but higher when only the markers closest to the causative mutations are used



Across breed prediction - Conclusions

- Prediction markers close to the causative mutations:
 - $1-(1-b)^2$ decreases when the distance between prediction markers and causative mutations increases
 - This decrease is faster across breed than within breed
 - 50K/HD markers:
 - Lower $1-(1-b)^2$ when all markers are used
 - Highest $1-(1-b)^2$ when only the markers closest to the causative mutations are used
- Best prediction when a low number of markers close to the causative mutations is used



Conclusions

- A substantial part of QTL detected in one breed show a significant association in another breed
- This shared variance can be predicted across breed if prediction markers very close to the causative mutations are used
- Sequence data → locate QTL → select prediction markers
→ Improve across breed prediction