



Sveriges lantbruksuniversitet  
Swedish University of Agricultural Sciences



# ***Fine-mapping of a QTL region on BTA18 affecting non-coagulating milk in Swedish Red cows***

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# Acknowledgements



Stiftelsen Lantbruksforskning



LUND  
UNIVERSITY



# Introduction

## Bovine milk:

Important source of proteins

Main proteins in milk → caseins



## In Sweden:

36% of total bovine milk → cheese-making purposes

# Non-coagulating (NC) milk

Milk does not coagulate within 40min after rennet addition



# NC milk



# NC milk



Potential big losses for cheese manufacturing industry



## Gustavsson et al. (2014):

Frequency at **18%** in **Swedish Red** cows

**Heritability estimate = 0.45**

Genetic correlation with protein content → **+0.38**

## Gregersen et al. (2015):

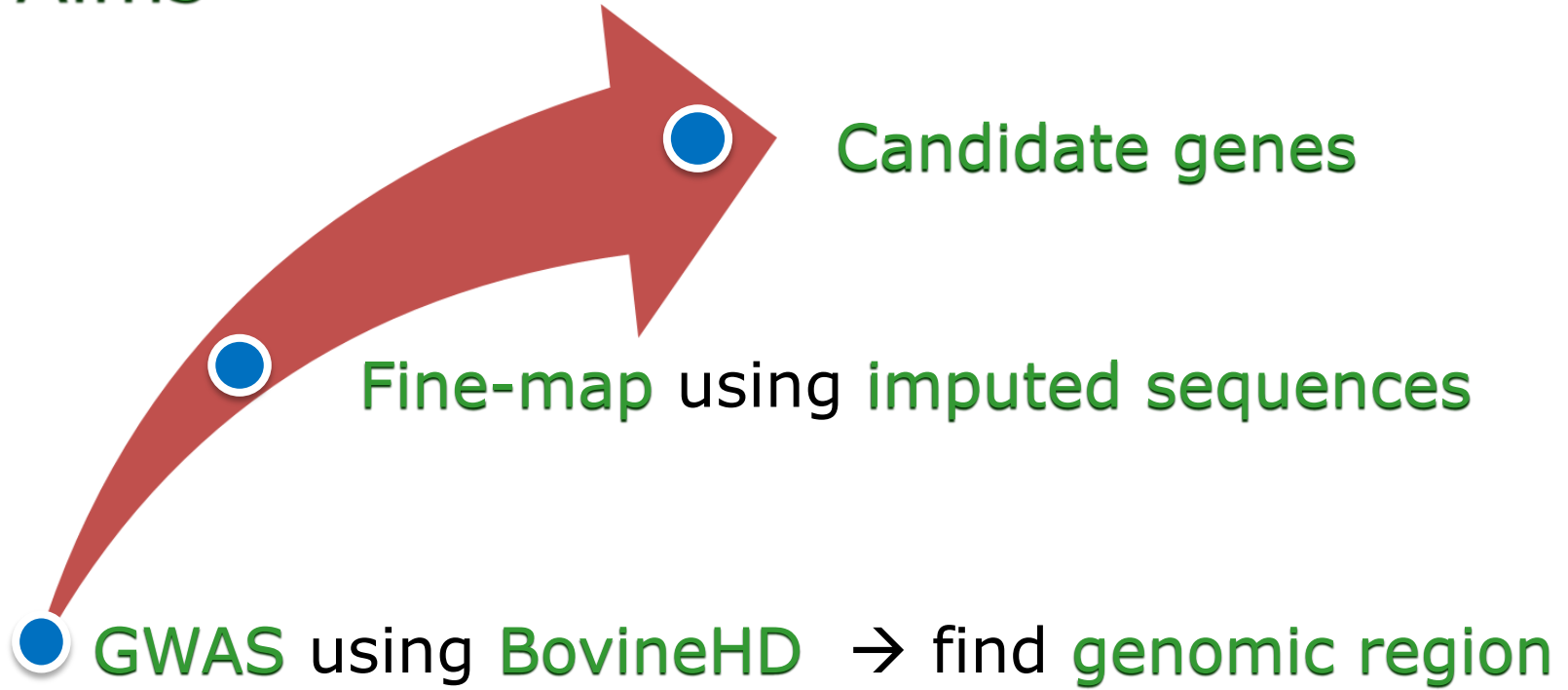
Genome-wide association study (**GWAS**)

Milk coagulation properties as phenotypes

777,963 SNP (**BovineHD**) as genotypes

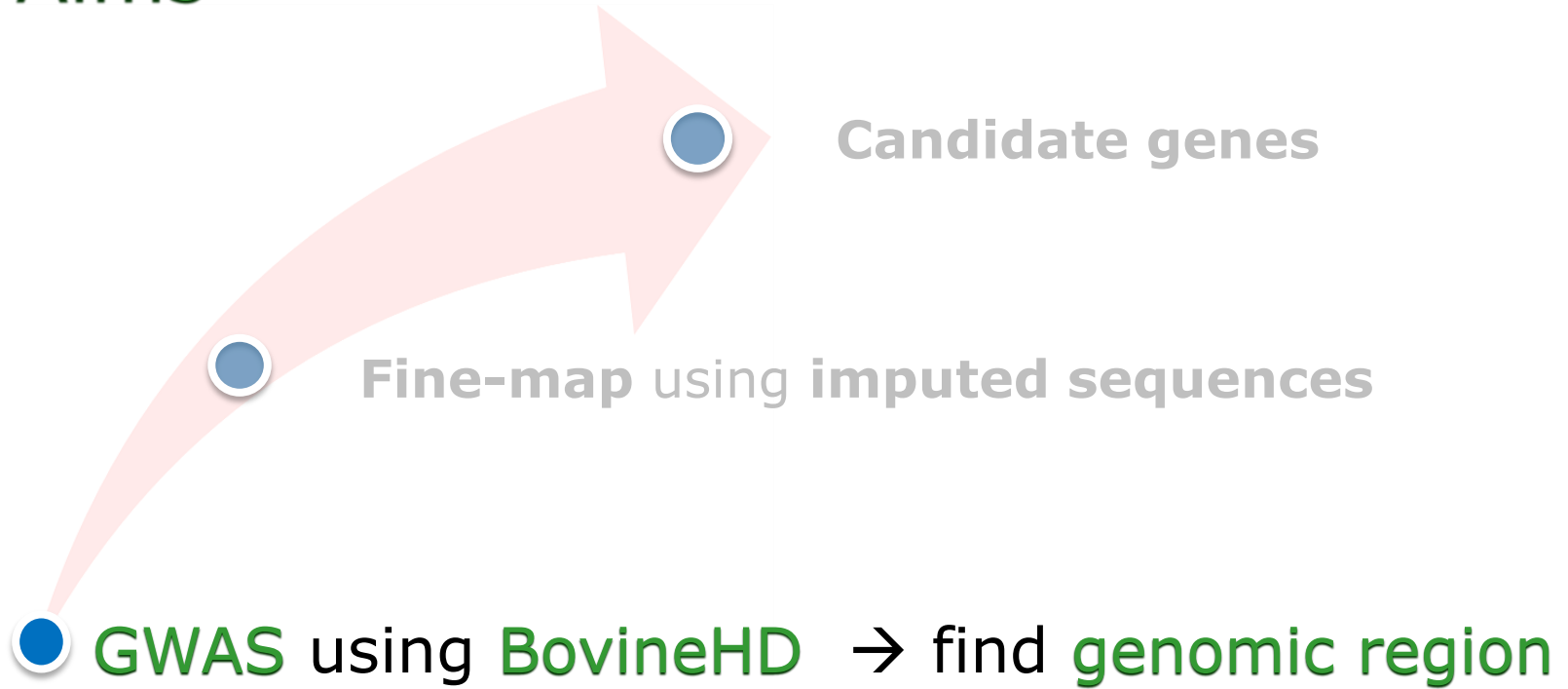
**However, they did not include NC milk...**

# Aims





# Aims



# Phenotypes

382 cows from 21 herds located in the south of Sweden  
NC milk was scored as 0/1

# Genotypes

- BovineHD ~ **624,302 SNP** after quality control  
(Call-Rate > 0.95%, MAF < 1%, and removal of X chromosome)
- Combined genotypes of  **$\alpha_{s1}$ -**,  **$\alpha_{s2}$ -**,  **$\beta$ -**, and  **$\kappa$ - caseins**

# Statistical analysis

**Single-SNP analyses** were run using an animal model in ASReml 4.0 (**Gilmour et al., 2009**):

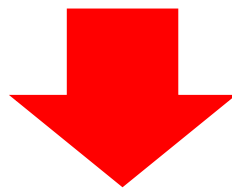
$$NCmilk = \mu + herd + parity + wim + e^{-0.05*wim} + CNcluster + \mathbf{SNP} + a + e$$

where:

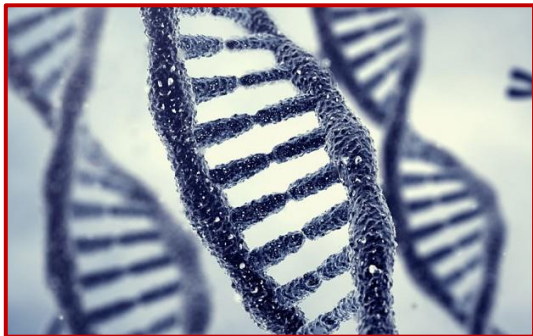
<b>Fixed effects</b>	<ul style="list-style-type: none"> <li><i>herd</i> → effect of herd</li> <li><i>parity</i> → effect of number of partuitions</li> <li><i>wim</i> → effect of weeks in milk</li> <li><i>CNcluster</i> → effect of combined genotypes of caseins</li> <li><b>SNP</b> → effect of marker</li> </ul>
<b>Random effects</b>	<ul style="list-style-type: none"> <li><i>a</i> → additive genetic effect</li> <li><i>e</i> → residual effect</li> </ul>

# Results of GWAS using BovineHD

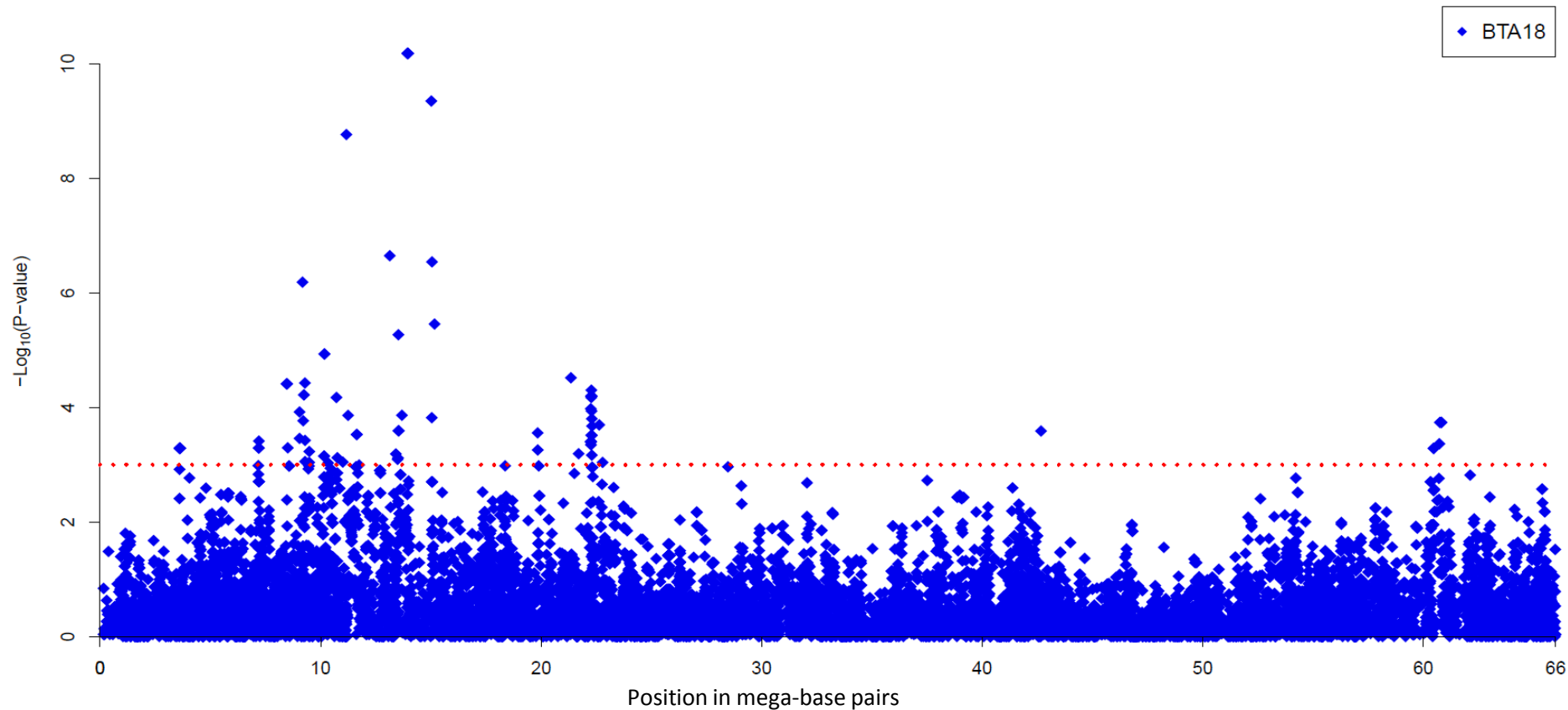
**49 significant SNP** across the genome  
at  **$-\text{Log}_{10}(\text{P-value}) > 4.5$**



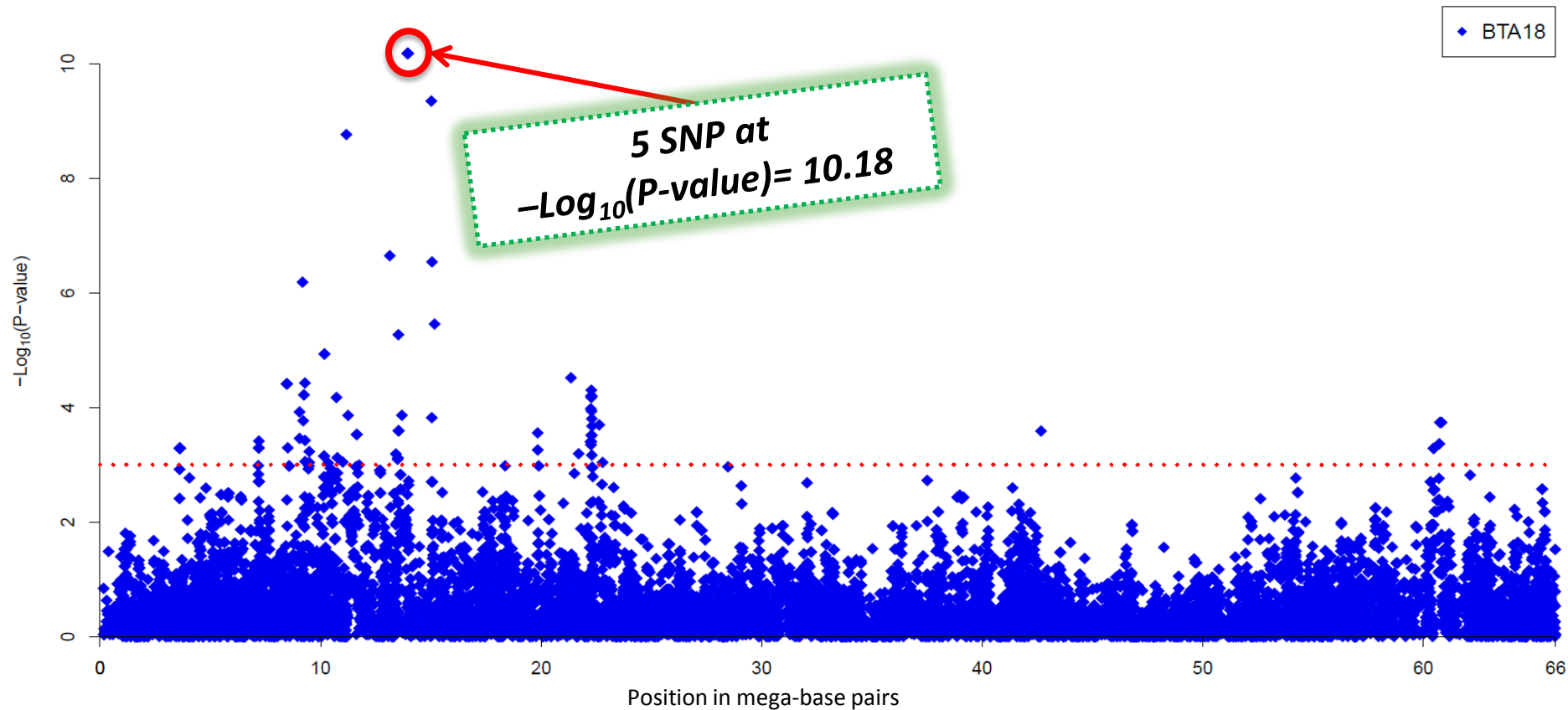
Manhattan plots



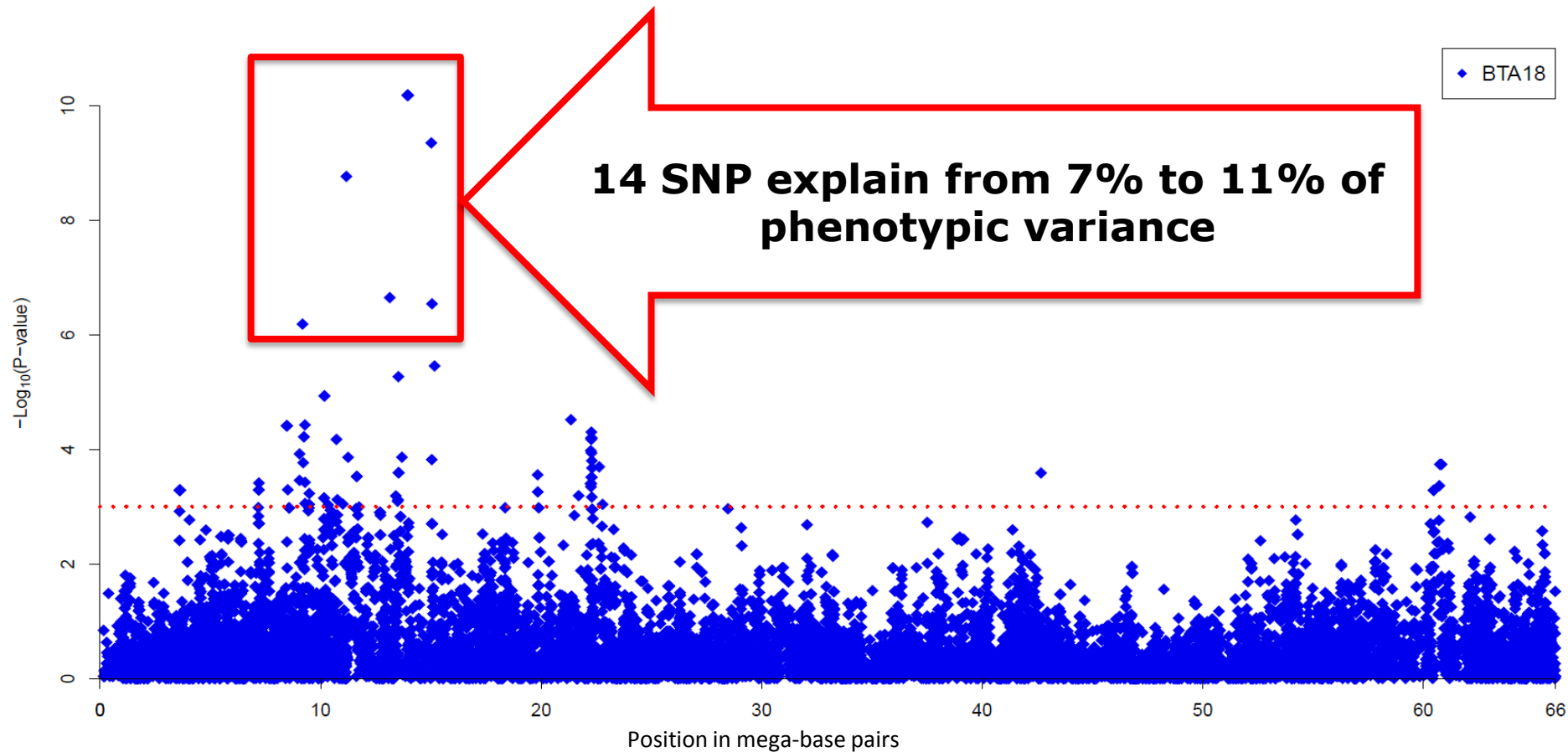
# GWAS on BTA18 using BovineHD



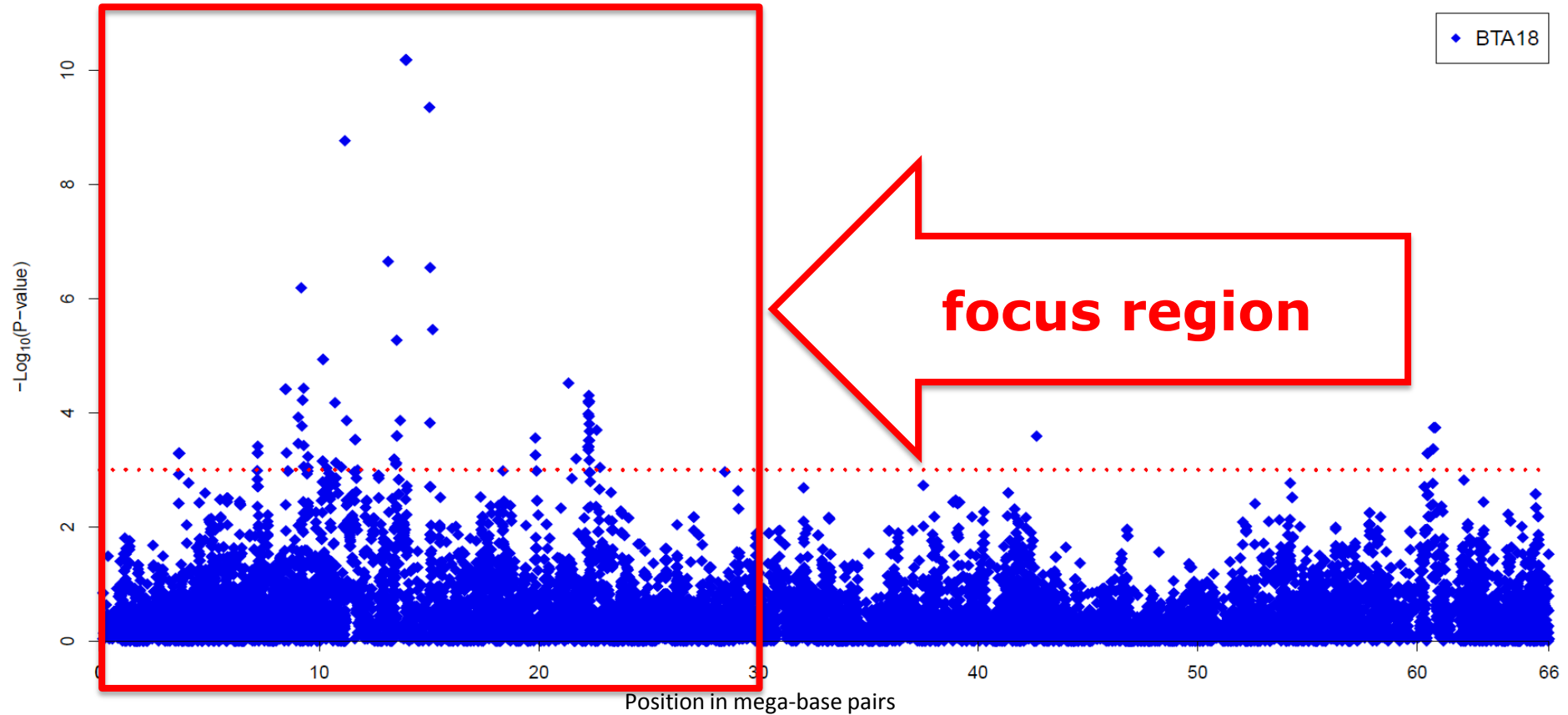
# GWAS on BTA18 using BovineHD



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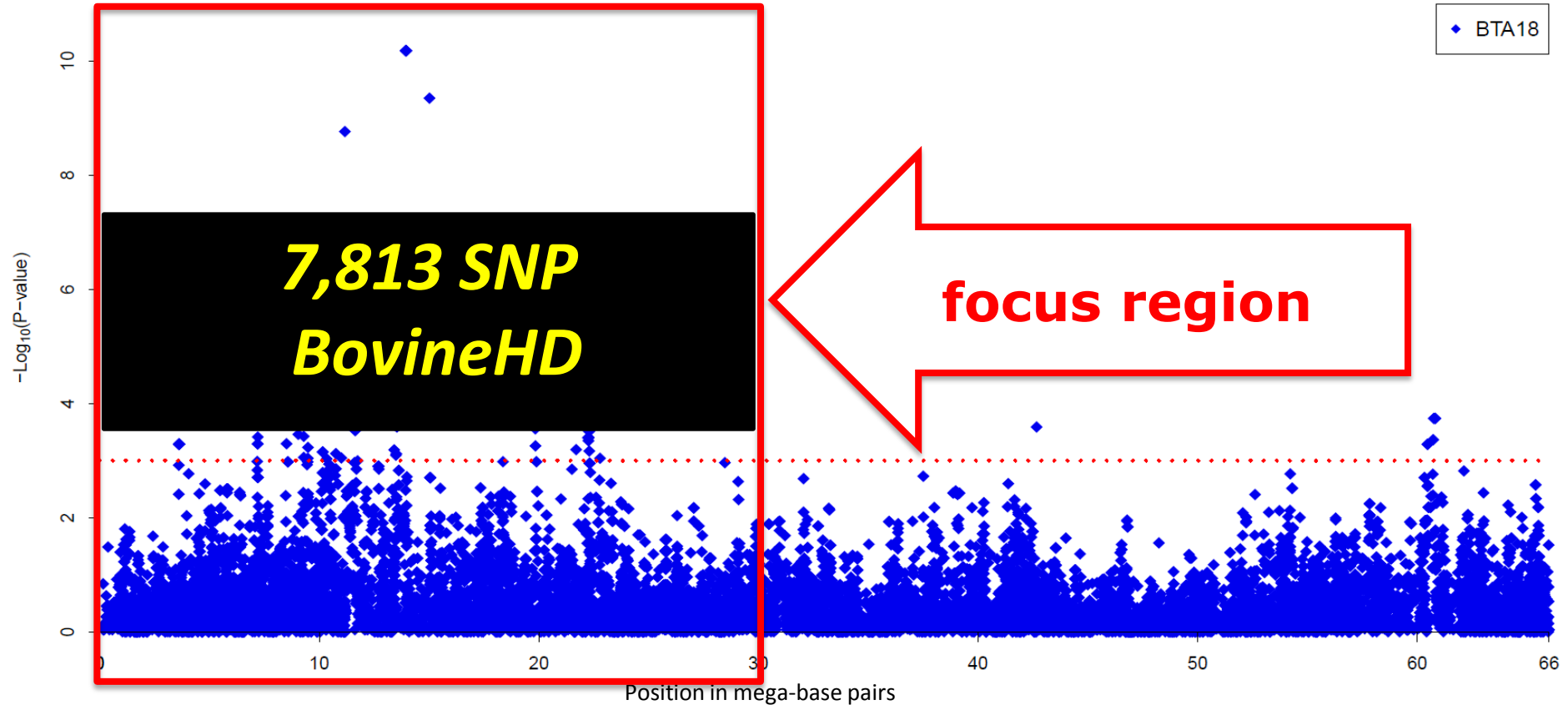


# GWAS on BTA18 using BovineHD

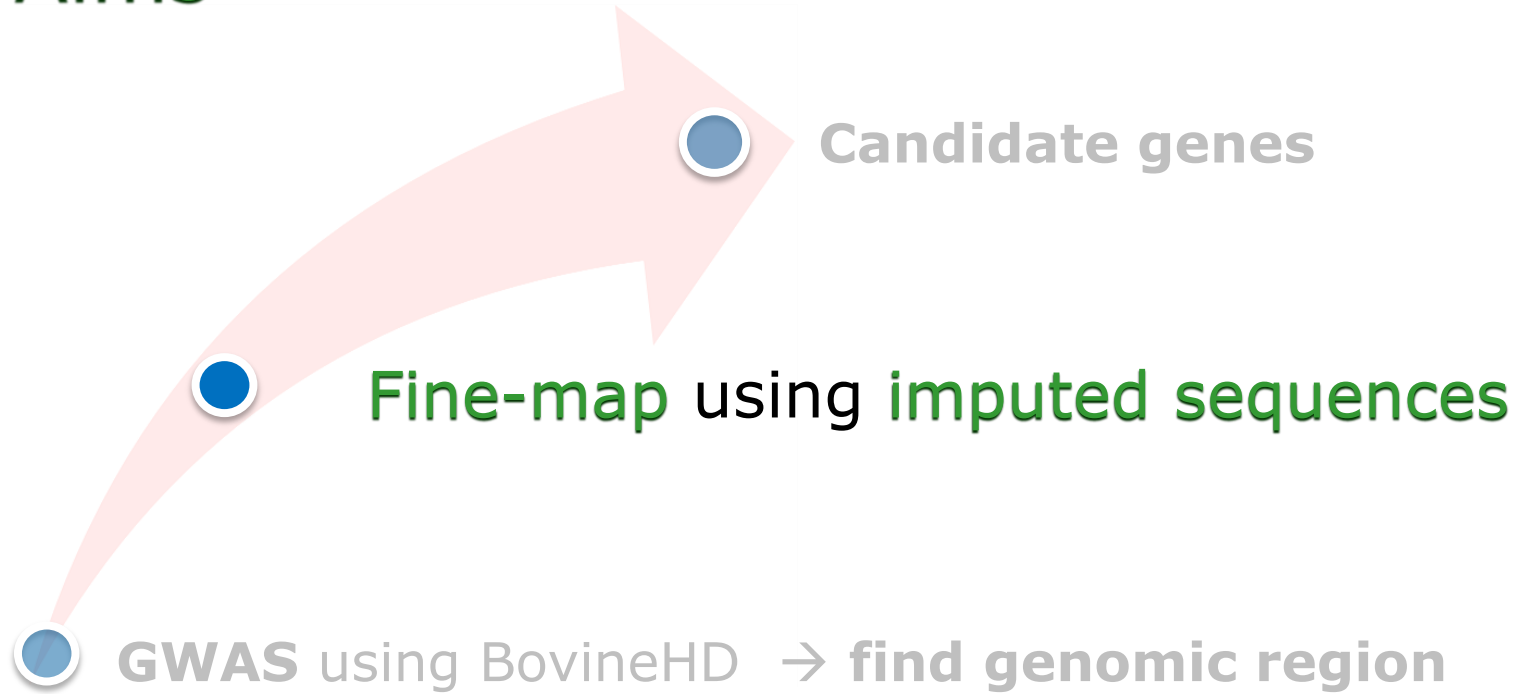




# GWAS on BTA18 using BovineHD



# Aims



# Imputation from BovineHD to sequences

**382 SR**

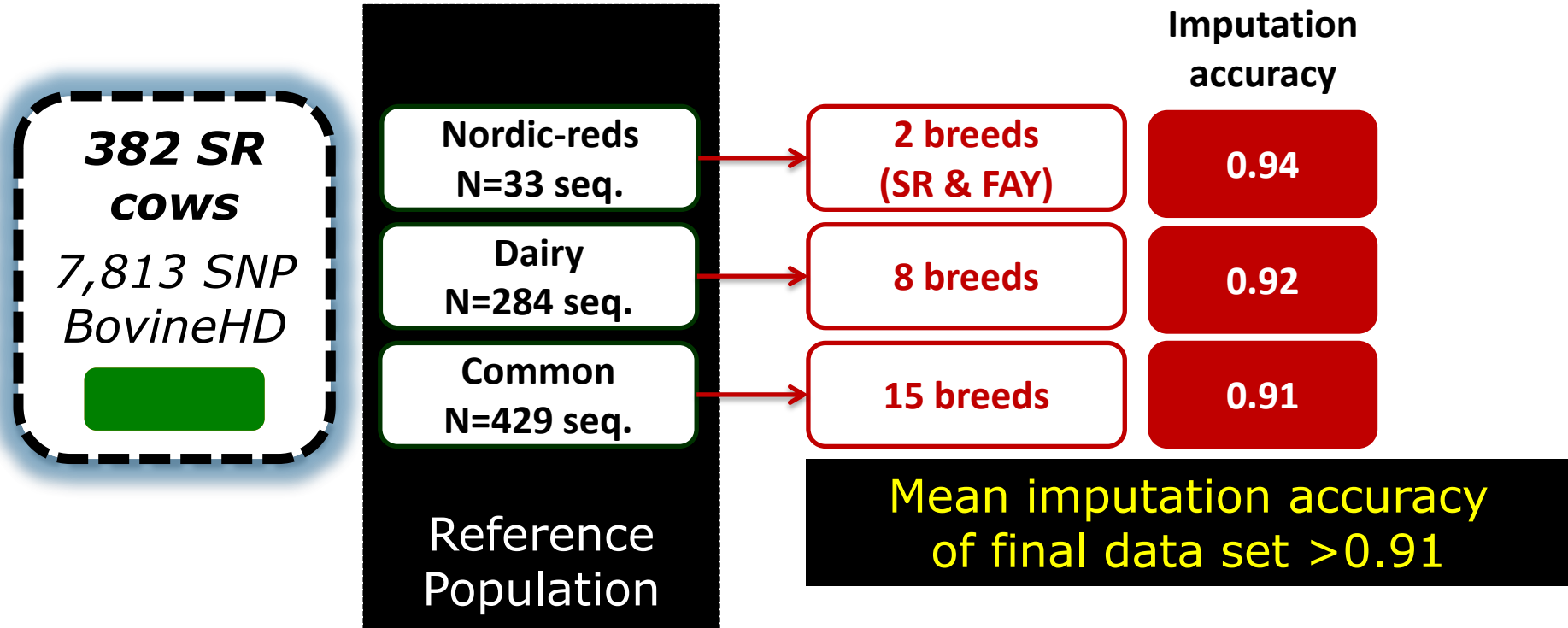
**COWS**

7,813 SNP

BovineHD

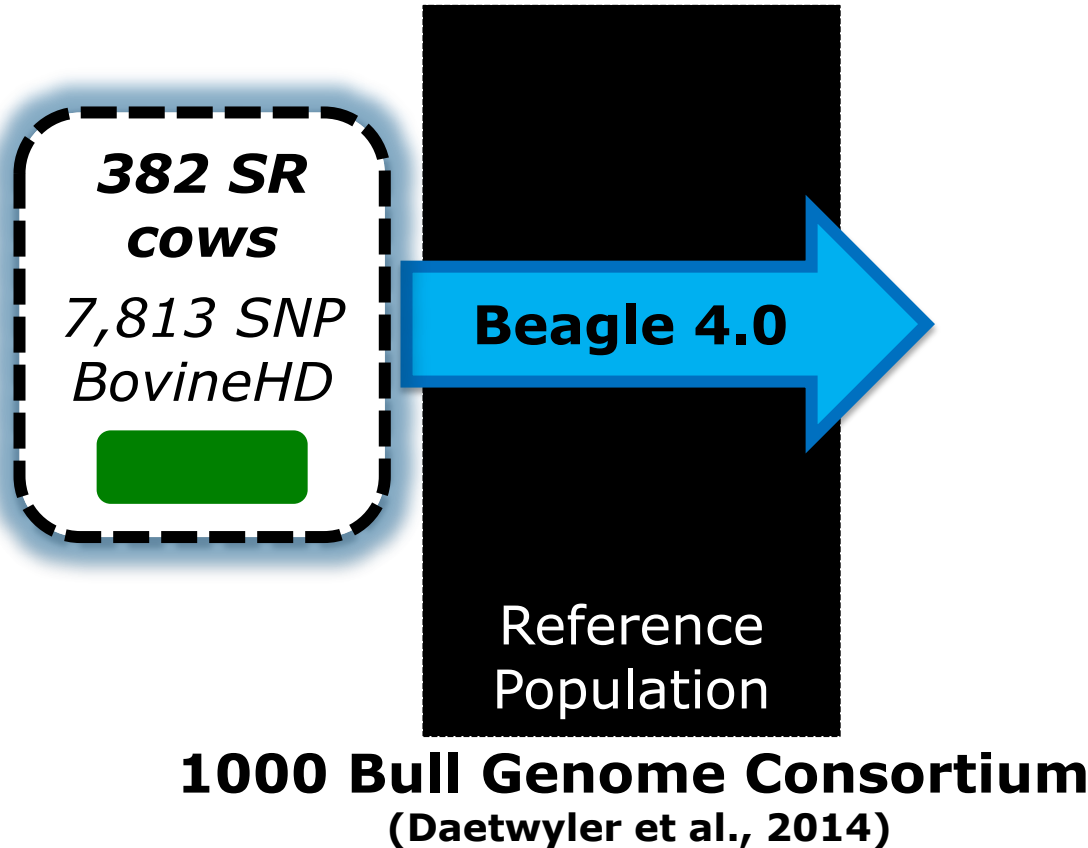


# Imputation from BovineHD to sequences

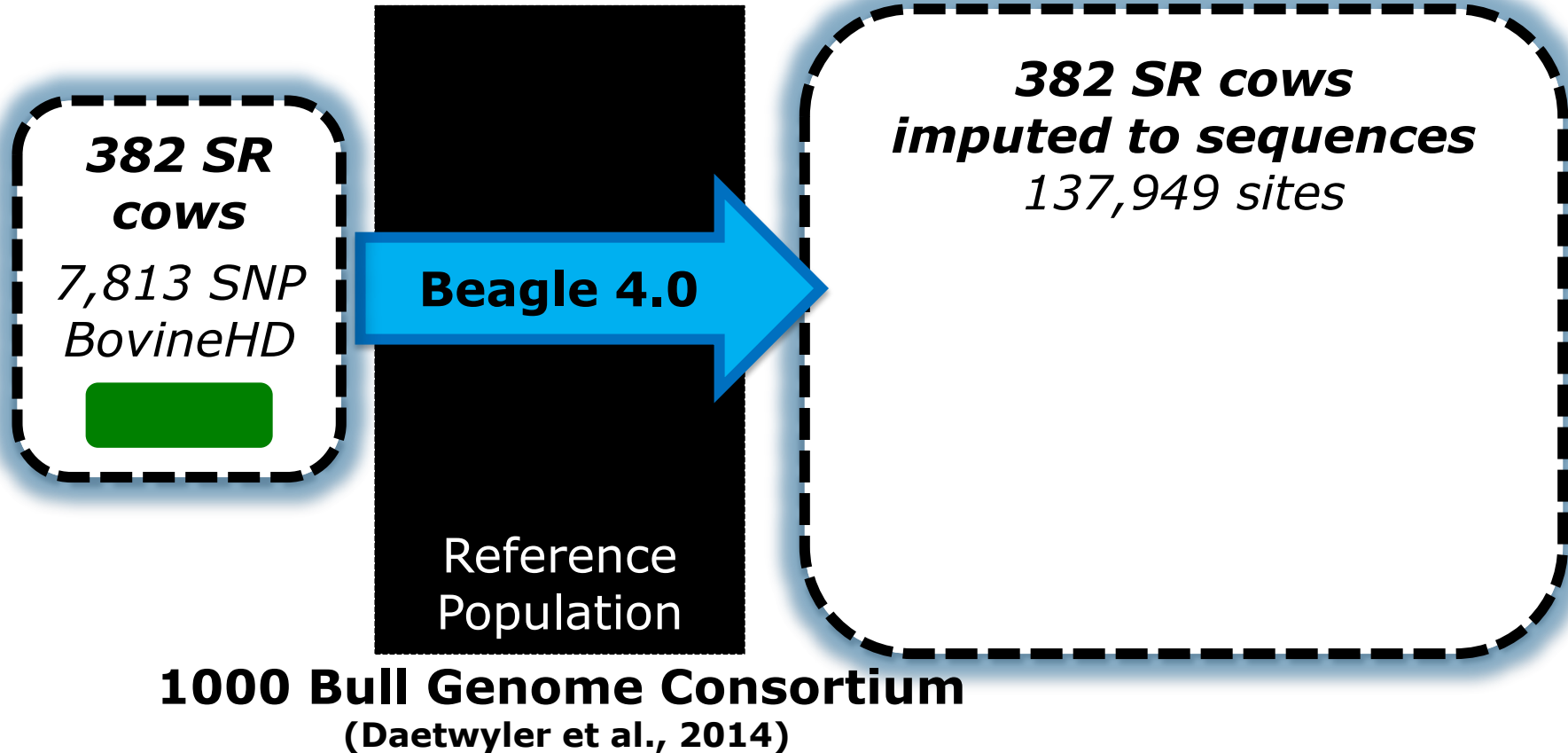


**1000 Bull Genome Consortium**  
(Daetwyler et al., 2014)

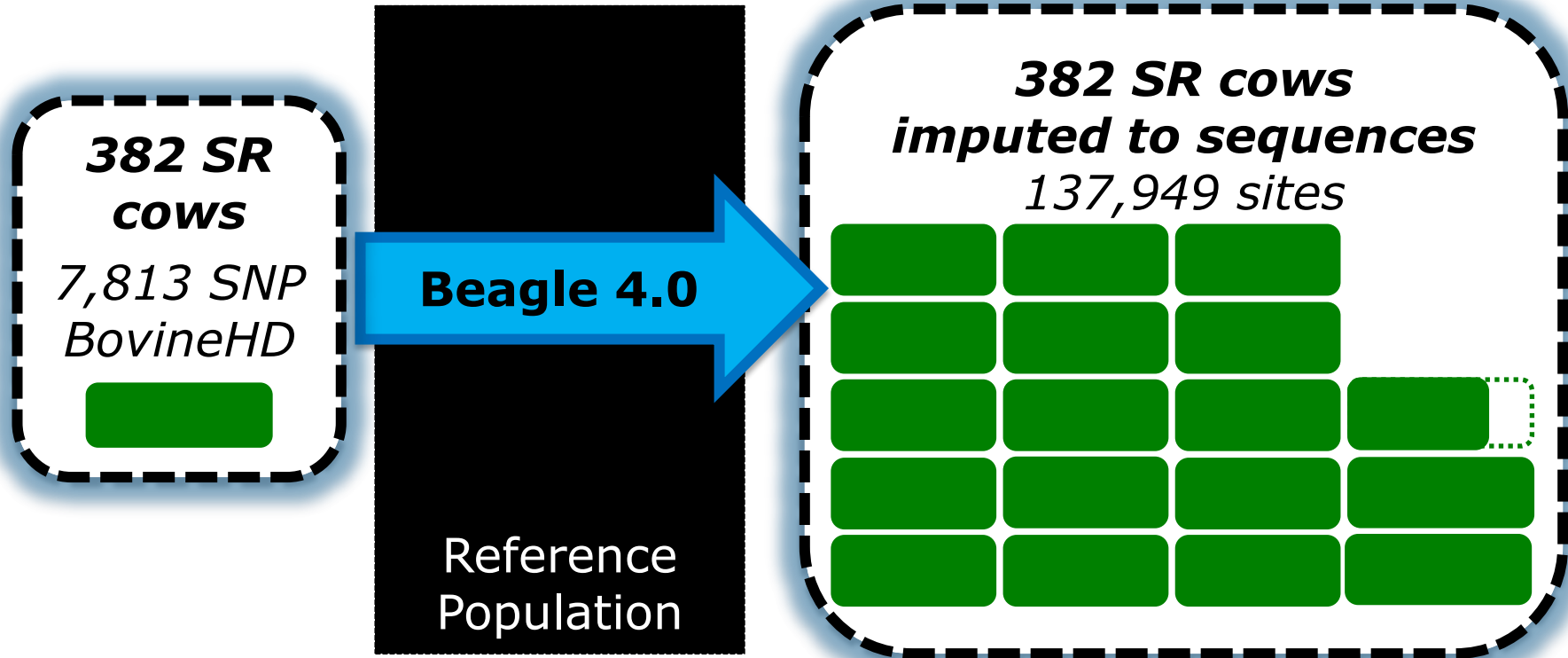
# Imputation from BovineHD to sequences



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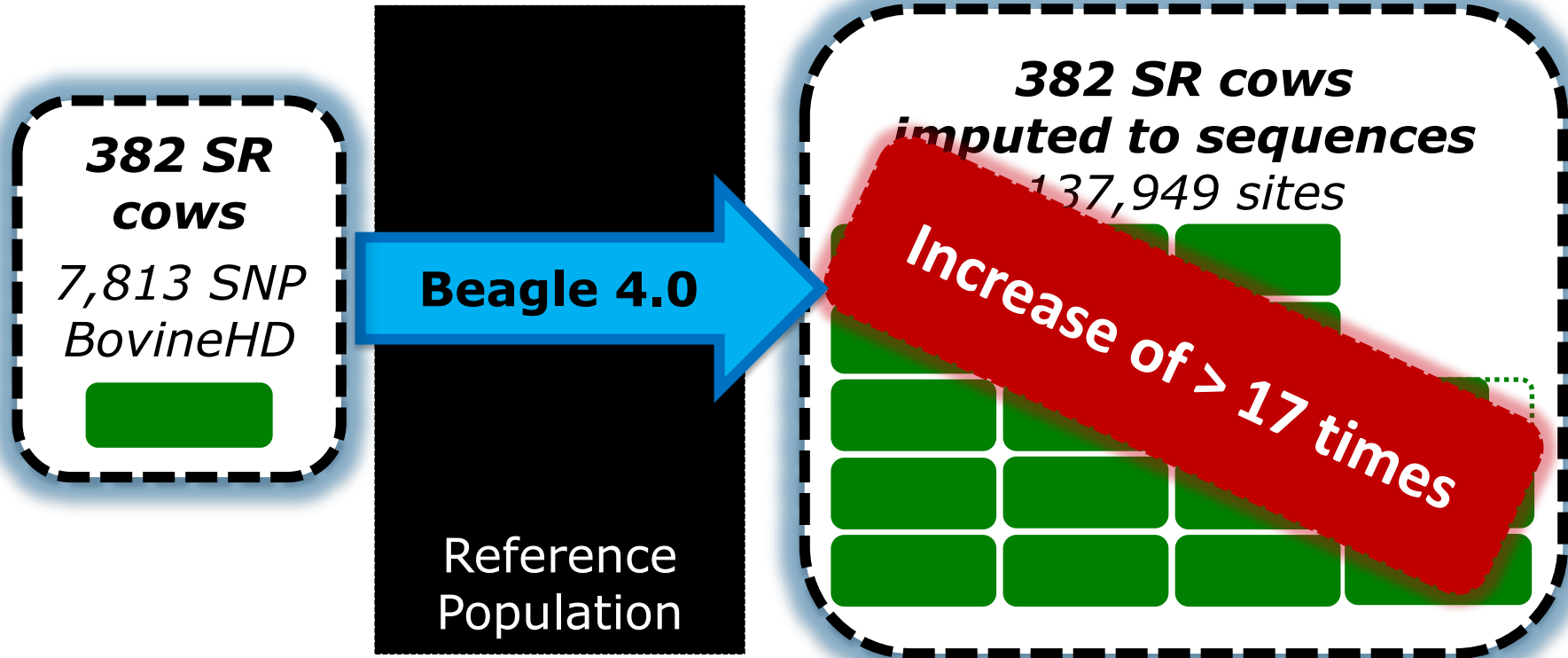


# Imputation from BovineHD to sequences



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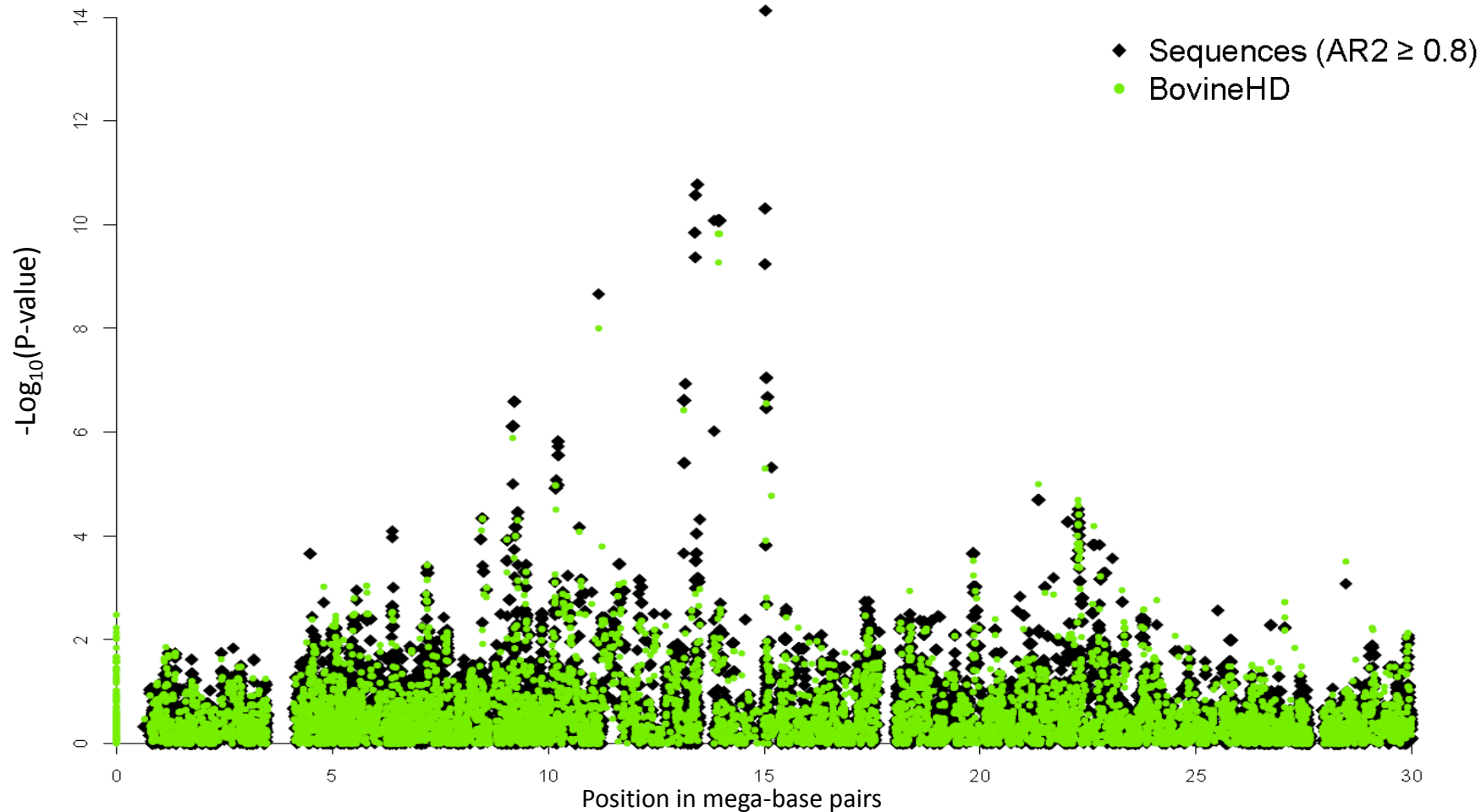
# Imputation from BovineHD to sequences



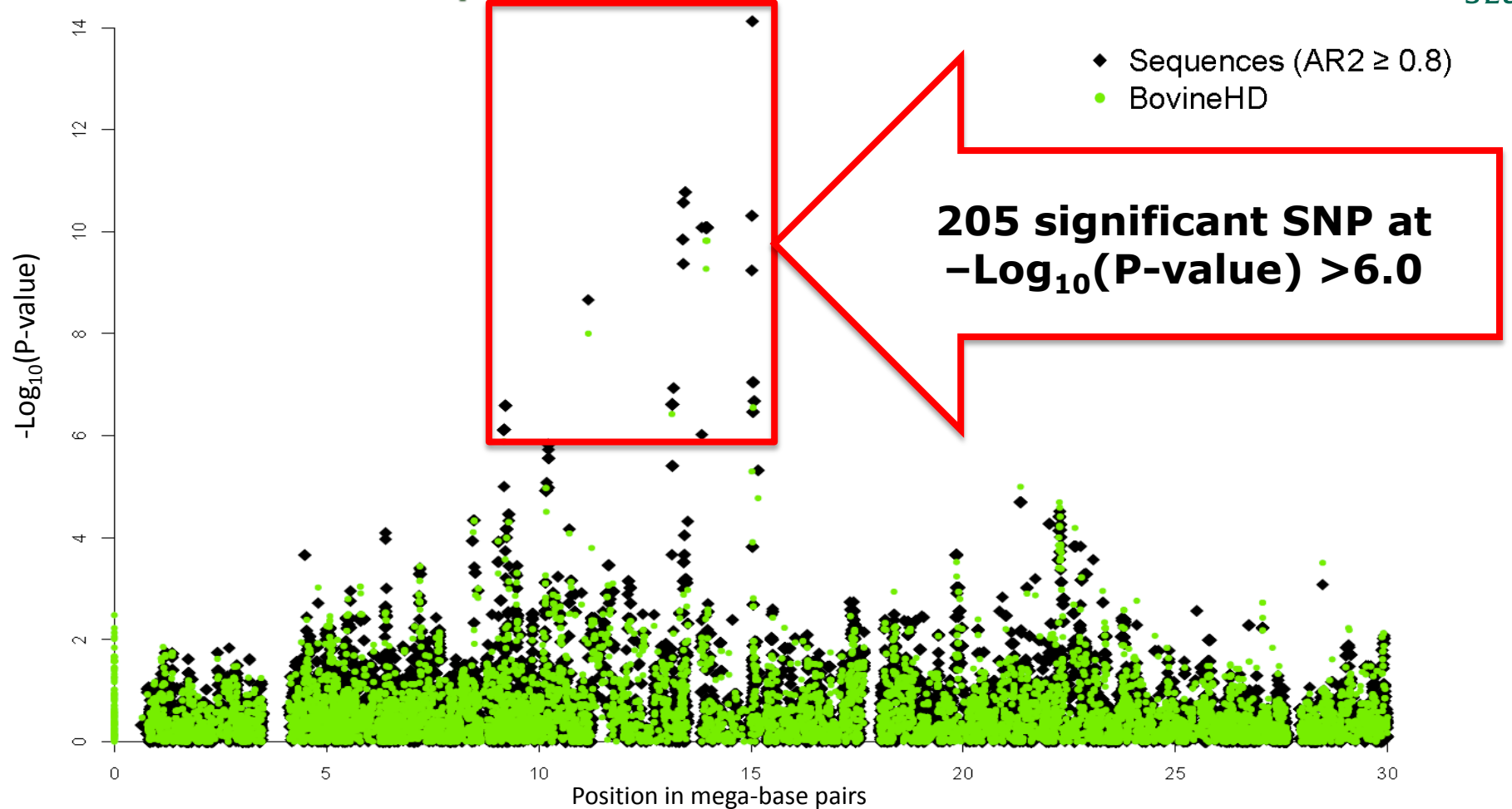
**1000 Bull Genome Consortium**  
(Daetwyler et al., 2014)



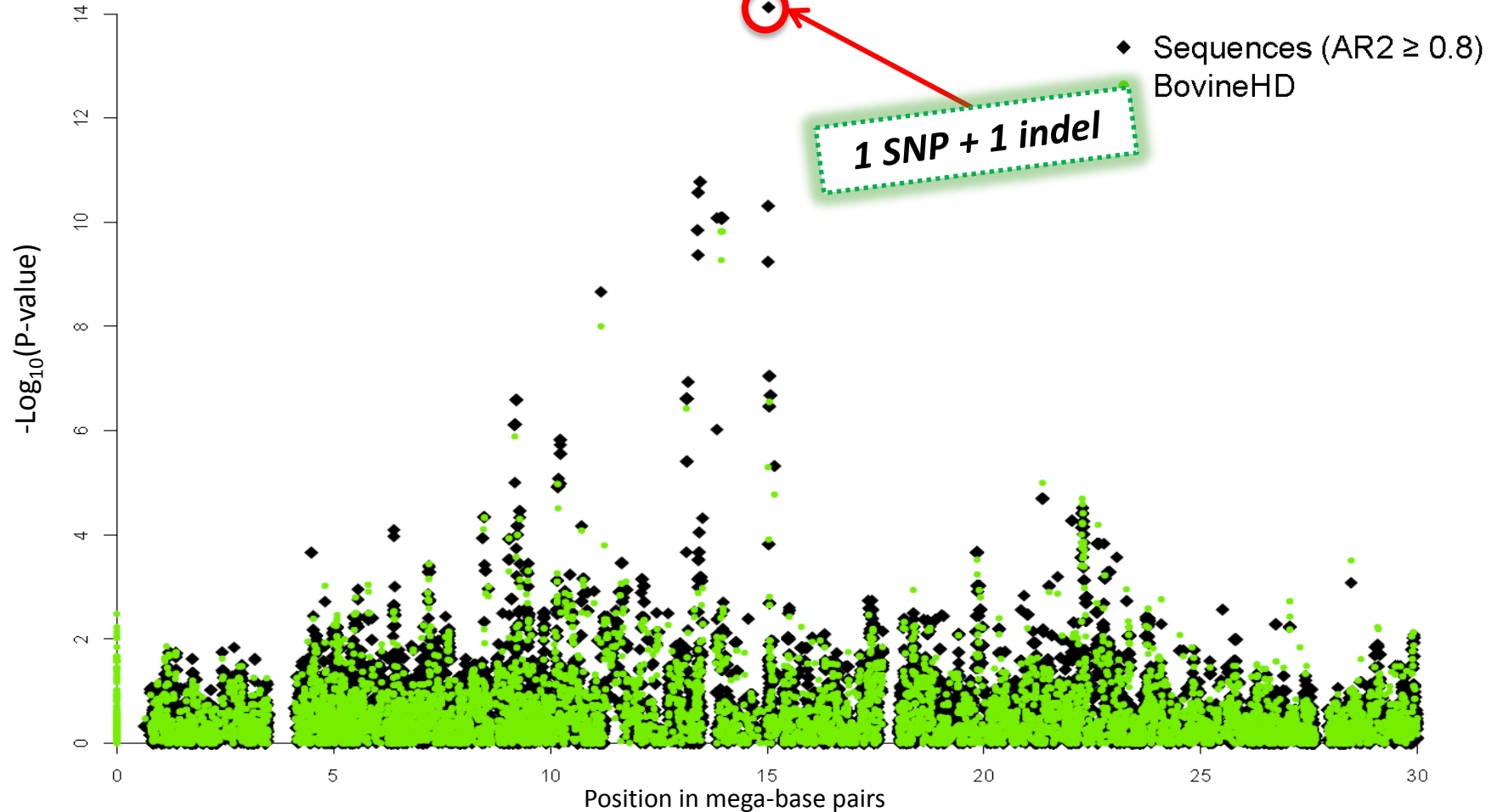
# Fine-mapping on half of BTA18



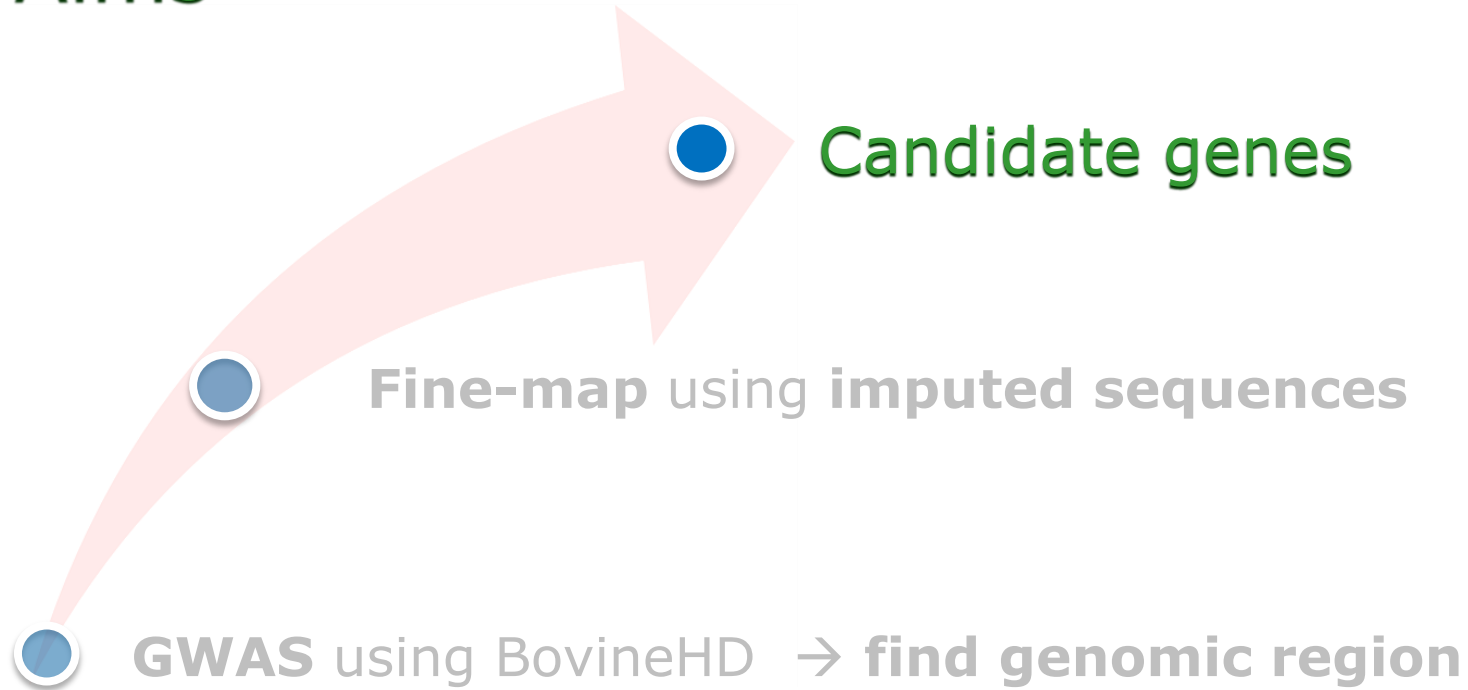
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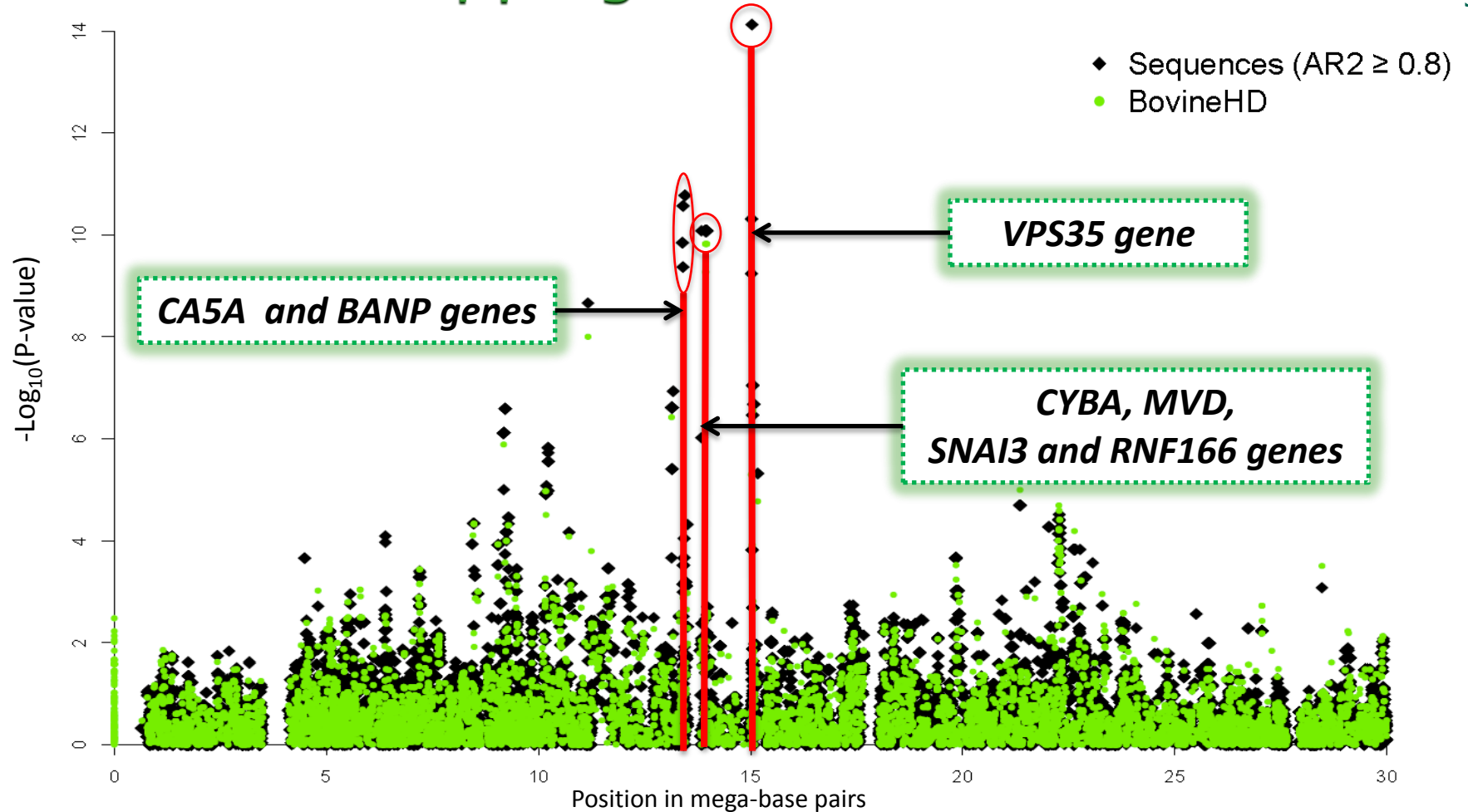
# Fine-mapping on half of BTA18



# Aims



# Fine-mapping on half of BTA18





# Conclusions

- *Genomic region is located **between 0-30 MBP on BTA18***
- *At least one QTL was found in this focus region*
- *Candidate gene for this QTL: **VPS35 gene***

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