



# Genome-wide copy number variants associated with calving ease and retained placenta in Holstein cows

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## Understanding Calving Disorders

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### Calving ease

The ability of a cow to give birth without assistance from the farmer

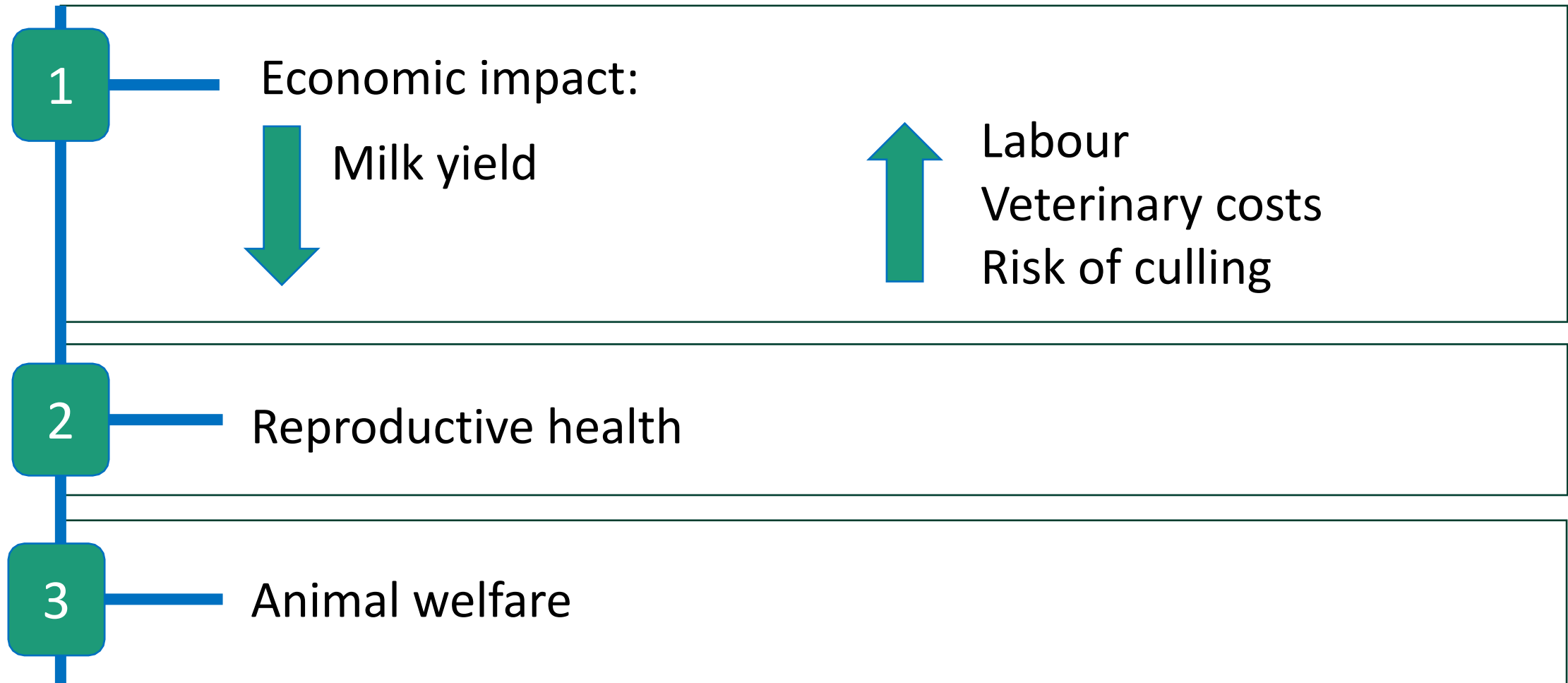
### Retained placenta

A condition where the cow fails to expel the fetal membranes after calving



Photo credit: freepic.com - 2023

## Impact of calving disorders on dairy production



## Genomics: Unleashing the Potential

Fertility traits in dairy cows, have long been known for their low heritability

**Inclusion of genomic information**

Early identification of genetically superior animals

Increasing genetic gain

**Table 1.** Heritabilities for the traits analysed in the present study

Trait	Heritability
Calving Ease <sup>1</sup>	0.121
Calving Ease <sup>2</sup>	0.085
Retained Placenta <sup>1</sup>	0.033
Retained Placenta <sup>2</sup>	0.030

<sup>1</sup>: measured in heifers

<sup>2</sup>: measured in cows

Oliveira, et al., in prep.

## Copy number variants (CNVs) What we need to know

CNVs usually occur due to deletions or duplications of DNA segments larger than 50bp

Sudmant et al., 2015

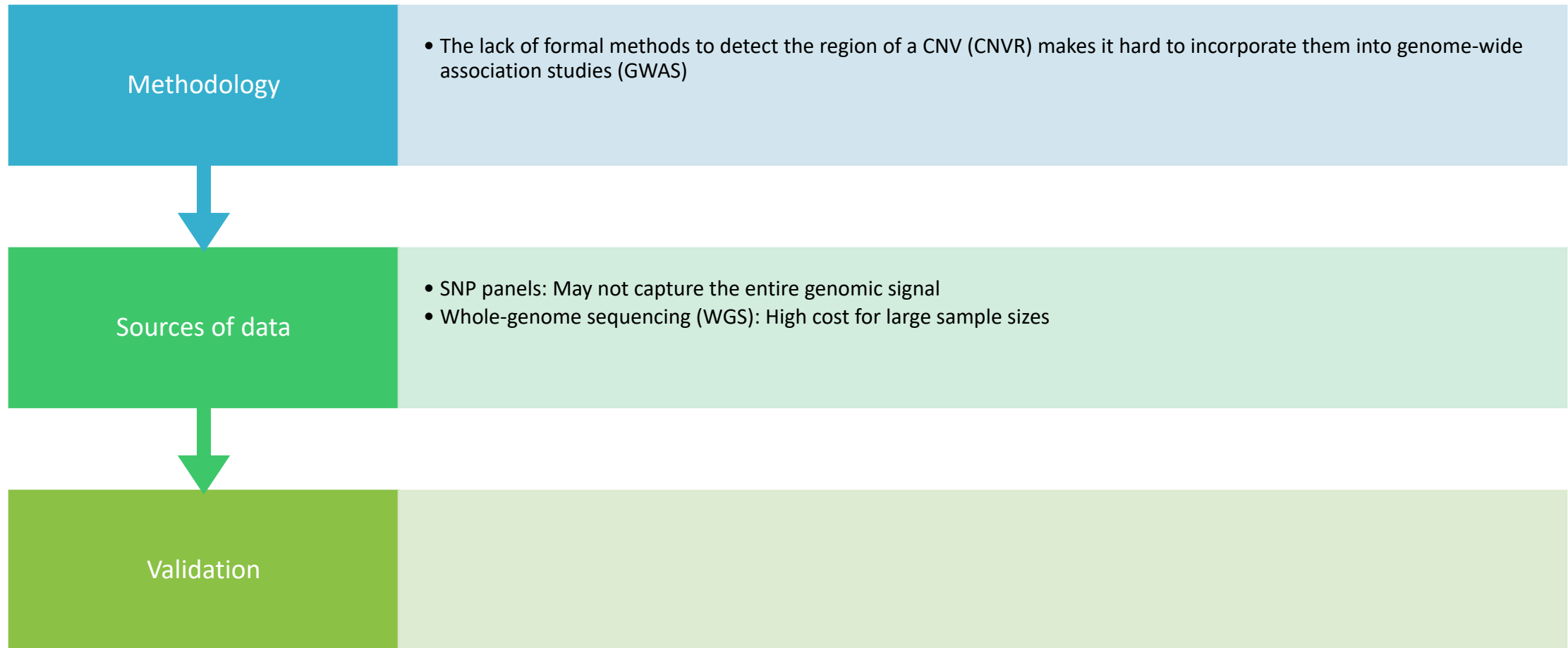
CNVs have strong effects on gene expression as they may alter coding sequences and regulatory elements

Levy et al., 2011

CNVs can account for up to 18% of the genetic variation in gene expression

Stranger et al., 2007

# Challenges in Detecting CNVs





Identify CNVs using  
genotypes obtained  
from two different SNP  
arrays (50K and 95K)



Validate the CNVR  
identified using WGS  
data



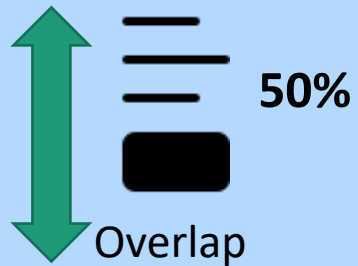
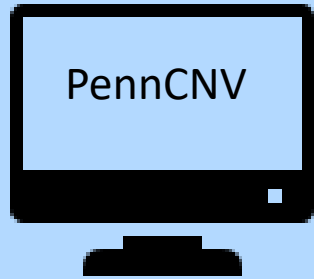
Association between  
CNVRs and calving ease  
and retained placenta

# Materials and Methods

1



10,101 (95k)  
5,353 (50k)  
log R ratio  
B allele frequency



126 WGS



CNV identification – CNVR creation

2



Calving ease<sup>1</sup>

2,464

dEBV<sup>3</sup>

102.76  
(3.67)

Calving ease<sup>2</sup>

2,275

101.58  
(3.15)

Retained placenta<sup>1</sup>

2,465

101.64  
(4.67)

Retained placenta<sup>2</sup>

2,461

99.78  
(4.01)

<sup>1</sup>: measured in heifers; <sup>2</sup>: measured in cows; <sup>3</sup>: dEBV mean (SD)

Pseudo-phenotypes

3

Theoretical reliability > 0.1

CNVRs identified >1% of animals

Linear regression CNVRs X dEBVs

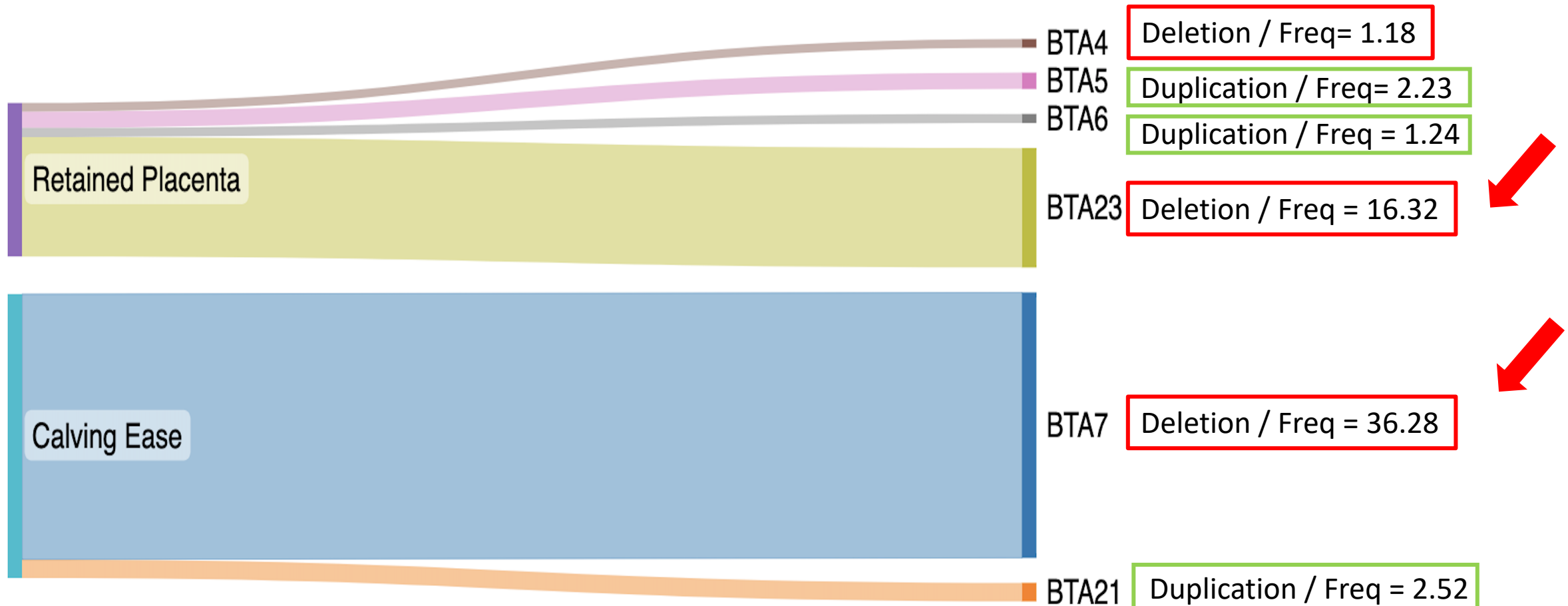
Population stratification

False discovery rate < 0.05

Association analyses

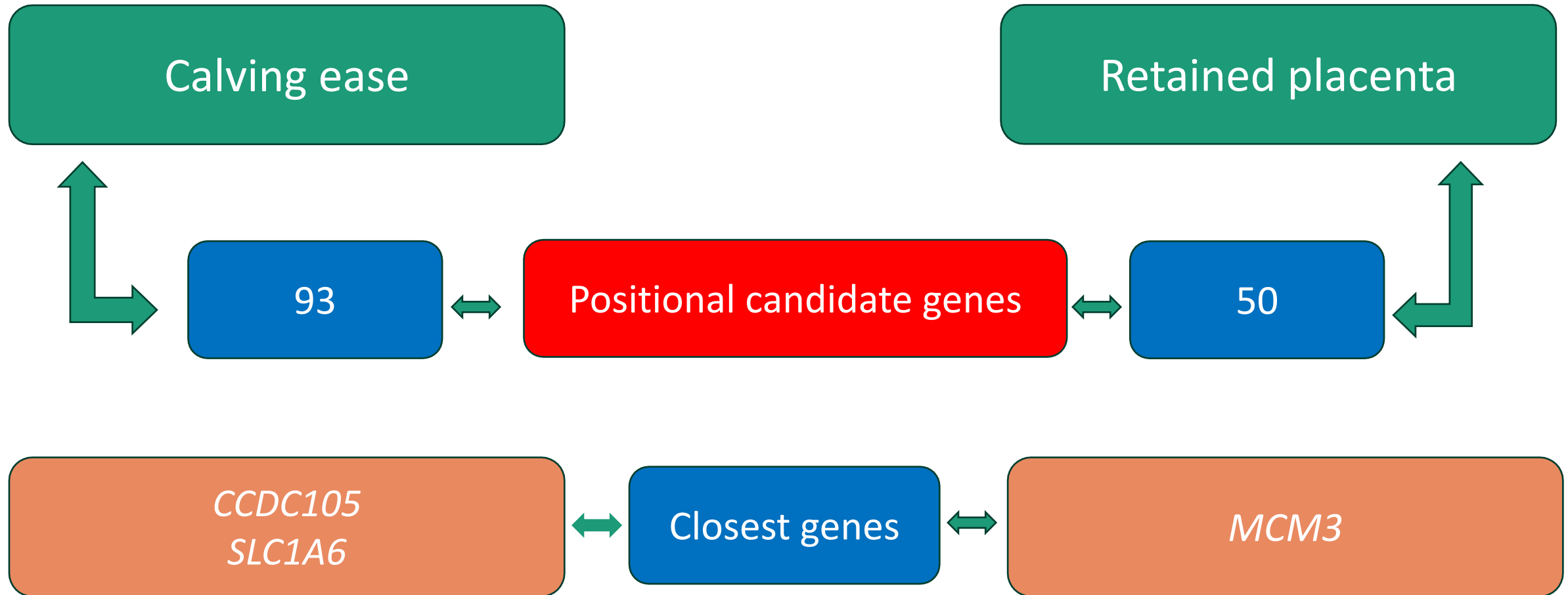


## Association Analyses

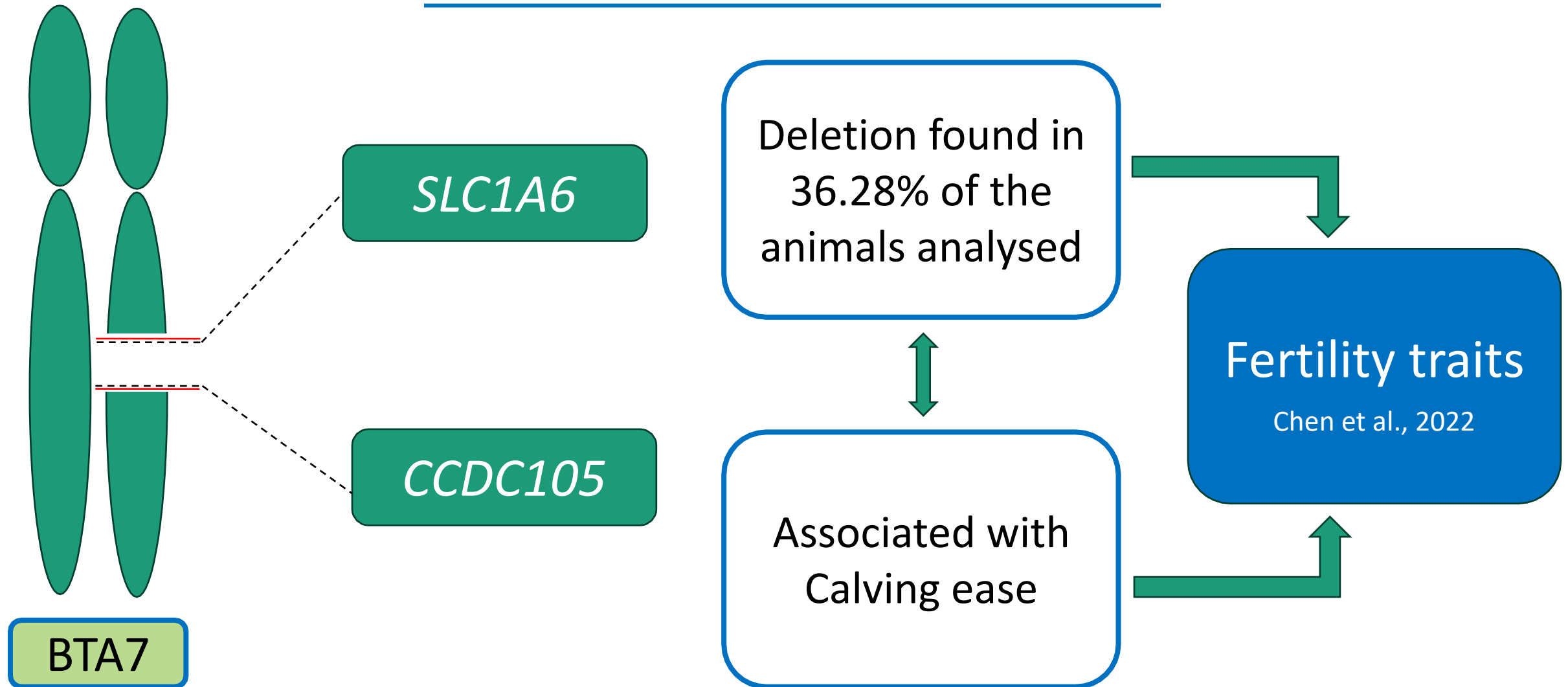


**Figure 1.** Sankey diagram illustrating the relationship between CNVRs and the analysed traits, along with the frequency of significantly ( $P < 0.05$ ) associated CNVRs across chromosomes.

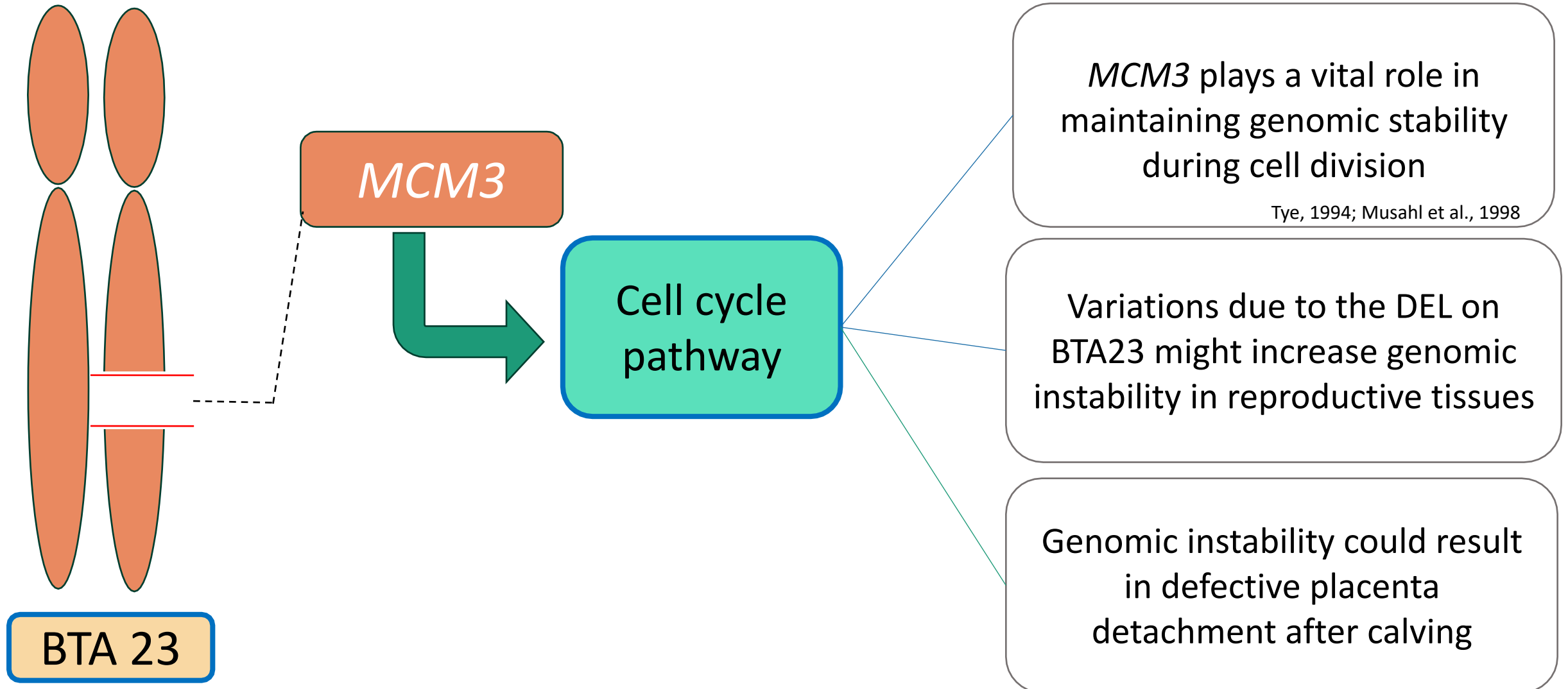
## Candidate genes identified



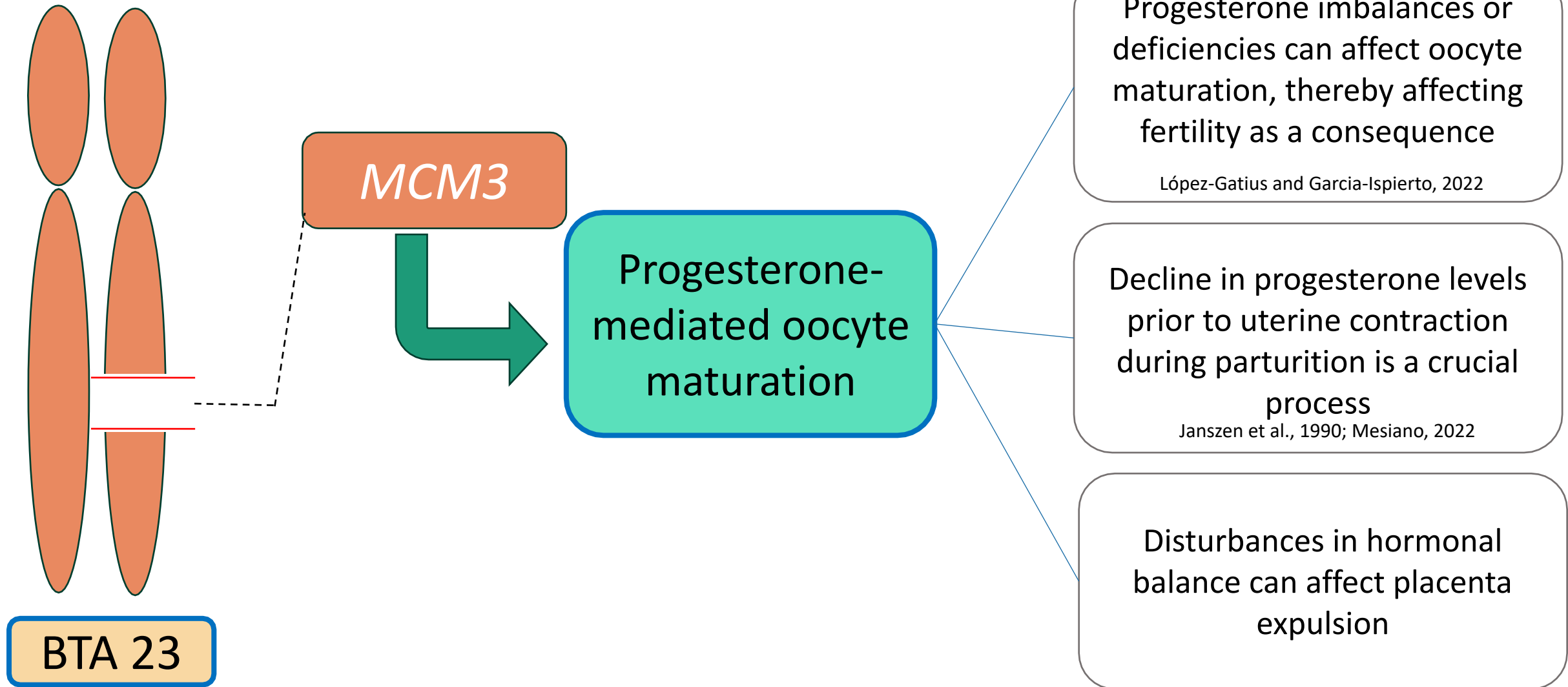
## Calving Ease



## Retained Placenta



## Retained Placenta



## CNV Insights:

Valuable insights for low heritable traits in dairy cattle

## High Frequency Associations:

CNVRs on BTA7 and BTA23

## Improving EBVs:

Incorporating this information might increase the accuracy of genomic selection

## Advancing the Dairy Industry:

Strategy for healthier and more productive cattle

## Future Directions:

Further investigations are needed to fully understand the implications of these CNVRs

# Acknowledgments



IOWA STATE UNIVERSITY

