

# Genome-wide associations for atypical progesterone profiles in Holstein-Friesian dairy cows

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# BACKGROUND

Female fertility has a major role in the dairy production

Economically important trait affecting profitability

Endocrine fertility traits, such as progesterone profiles, are interesting indicators

- more accurately reflect the cow's physiology
- higher heritability compared to traditional fertility traits

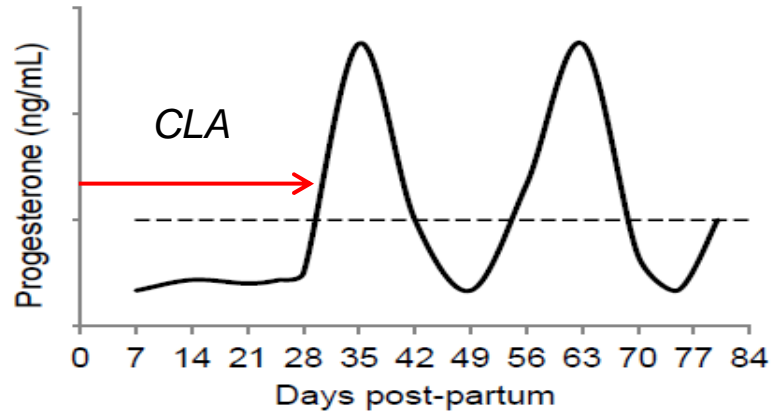
Atypical progesterone profiles have been associated with compromised fertility



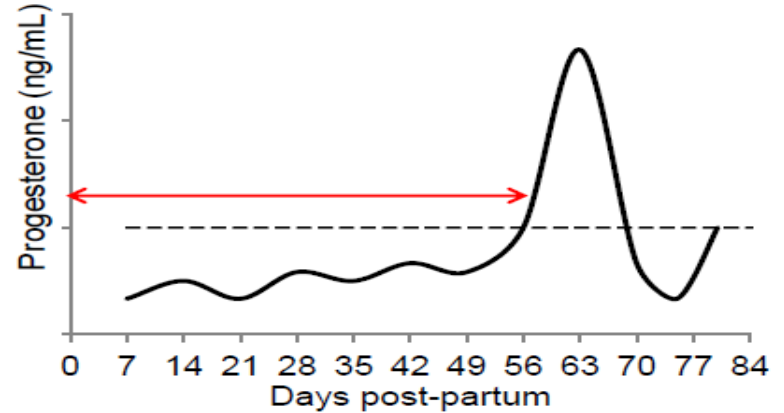
# Progesterone profiles

CLA=  
Commencement  
of Luteal Activity

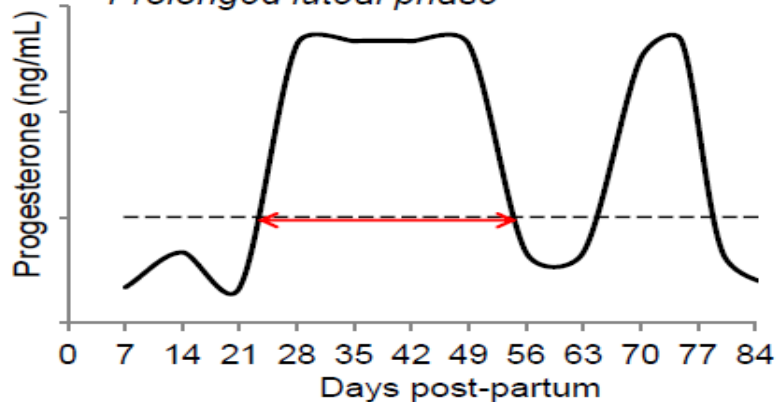
*Normal oestrus cycle*



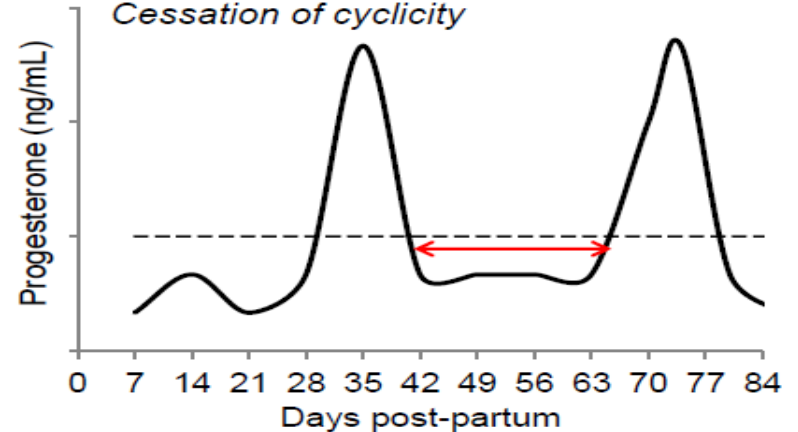
*Delayed cyclicity*



*Prolonged luteal phase*



*Cessation of cyclicity*



# OBJECTIVE

To perform a genome-wide association study (**GWAS**) in order to identify genomic regions associated with atypical progesterone profiles in the Holstein-Friesian breed



## Data from research herds in 4 different countries

- 1,126 primiparous and multiparous Holstein-Friesian (**HF**) cows
- 1,612 lactations with phenotypic data

## Progesterone measurements in milk

## Traditional fertility traits:

- *Calving interval* (**CI**)
- *Interval from calving to first observed heat* (**CFH**)
- *Interval from calving to first service* (**CFS**)
- *Pregnancy at first service* (**PFS**)
- *Interval from first to last service* (**FLS**)





# ANALYSIS

Illumina BovineSNP50 BeadChip (**Bovine50K**)

The GenABEL-package RepeatABEL

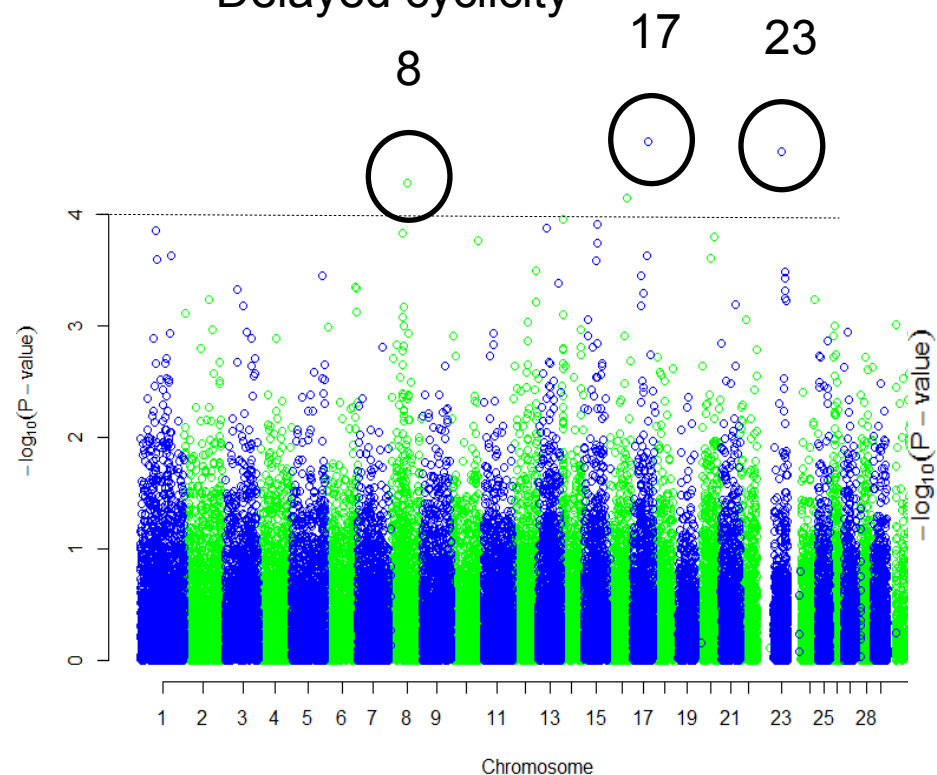
Model used:

$$y_{ijklmn} = \mu + P_i + Y_j + S_k + \text{SNP}_l + a_m + pe_n + e_{ijklmn}$$

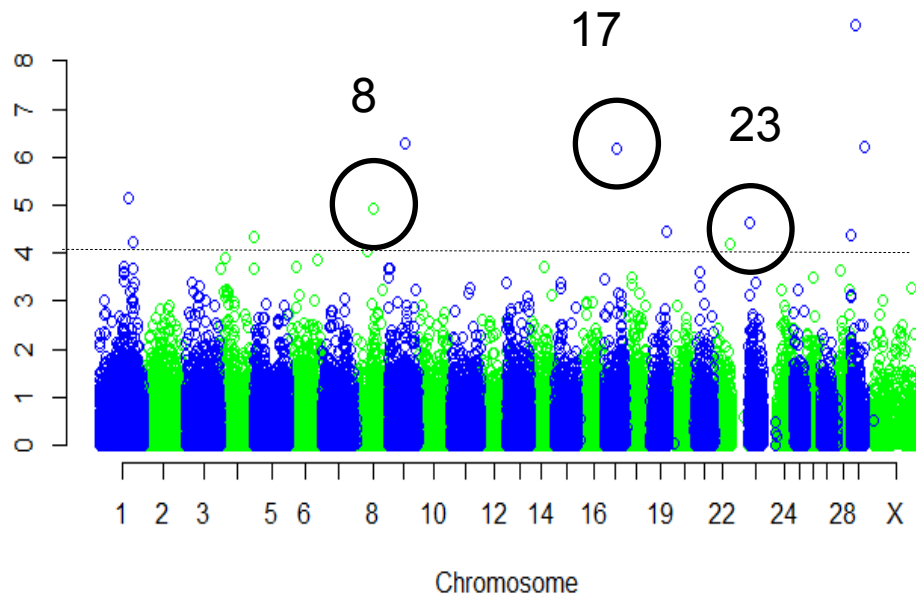


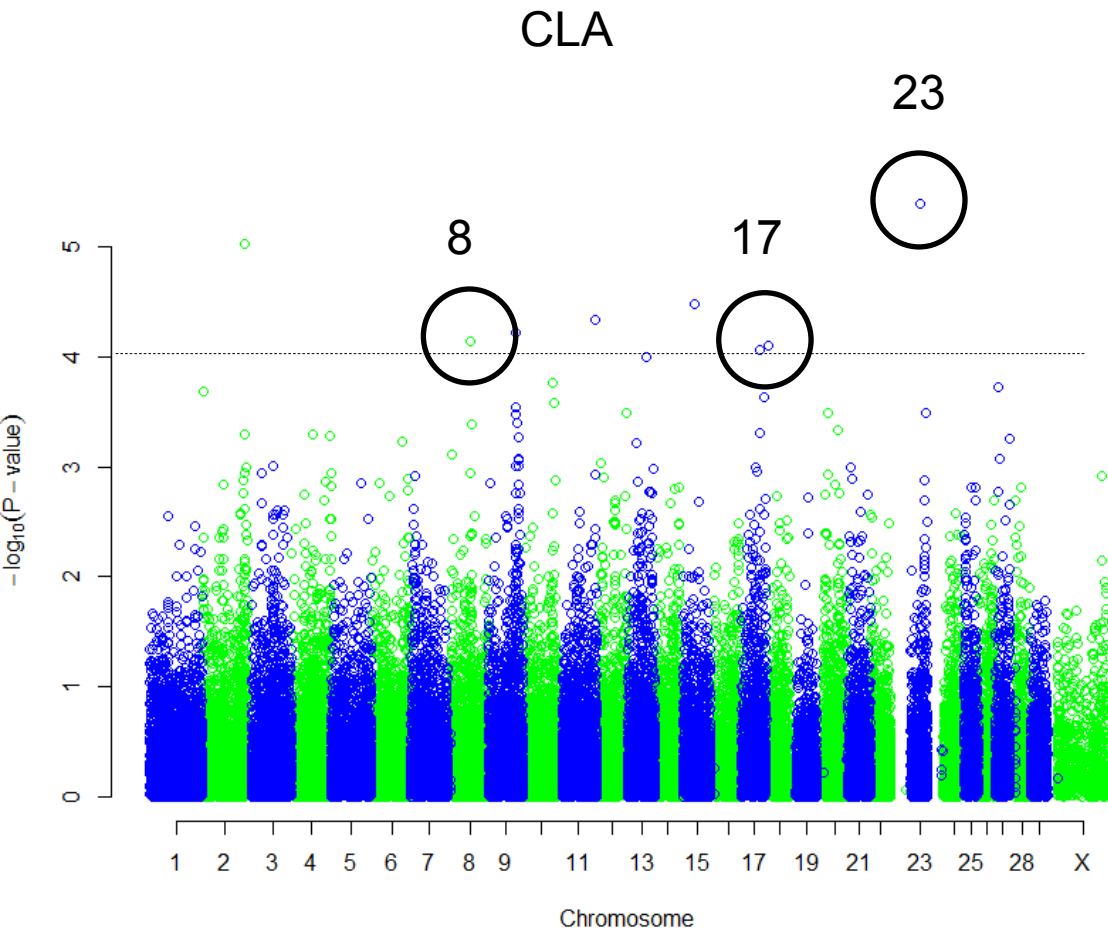
# RESULTS

Delayed cyclicity



Cessation of cyclicity





Traditional fertility traits:

- CFS at chromosome 8
- CFH at chromosome 8
- FLS chromosome 23



# ANALYSIS

## Whole genome sequencing (**WGS**)

- Beagle version 4.1
- All polymorphic variants with accuracy (**AR2**)  $\geq 0.2$  and AR  $\geq 0.7$

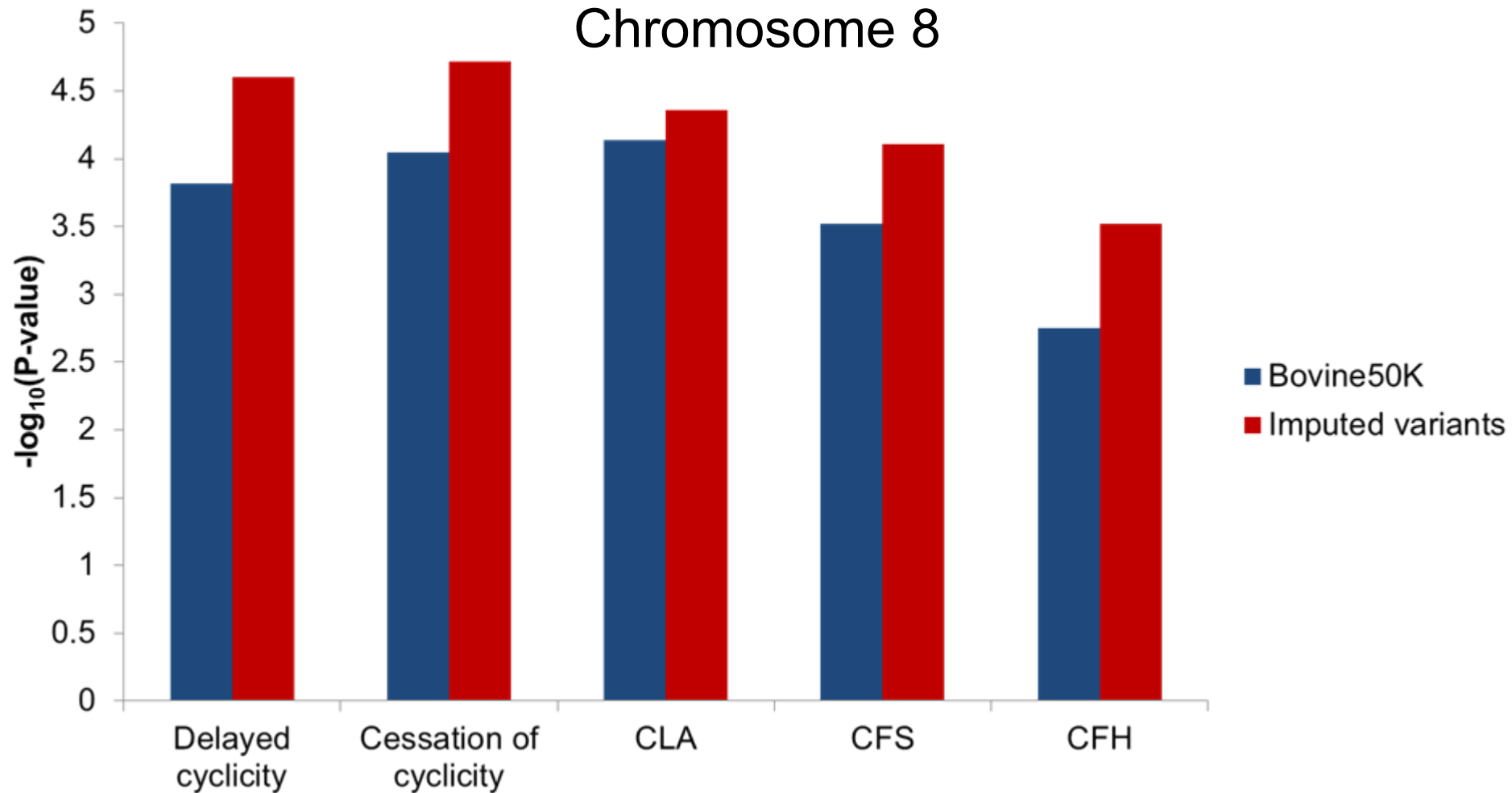
were considered for further studies  
1000 Bull Genome Consortium

- WGS reference population of 547 HF bulls

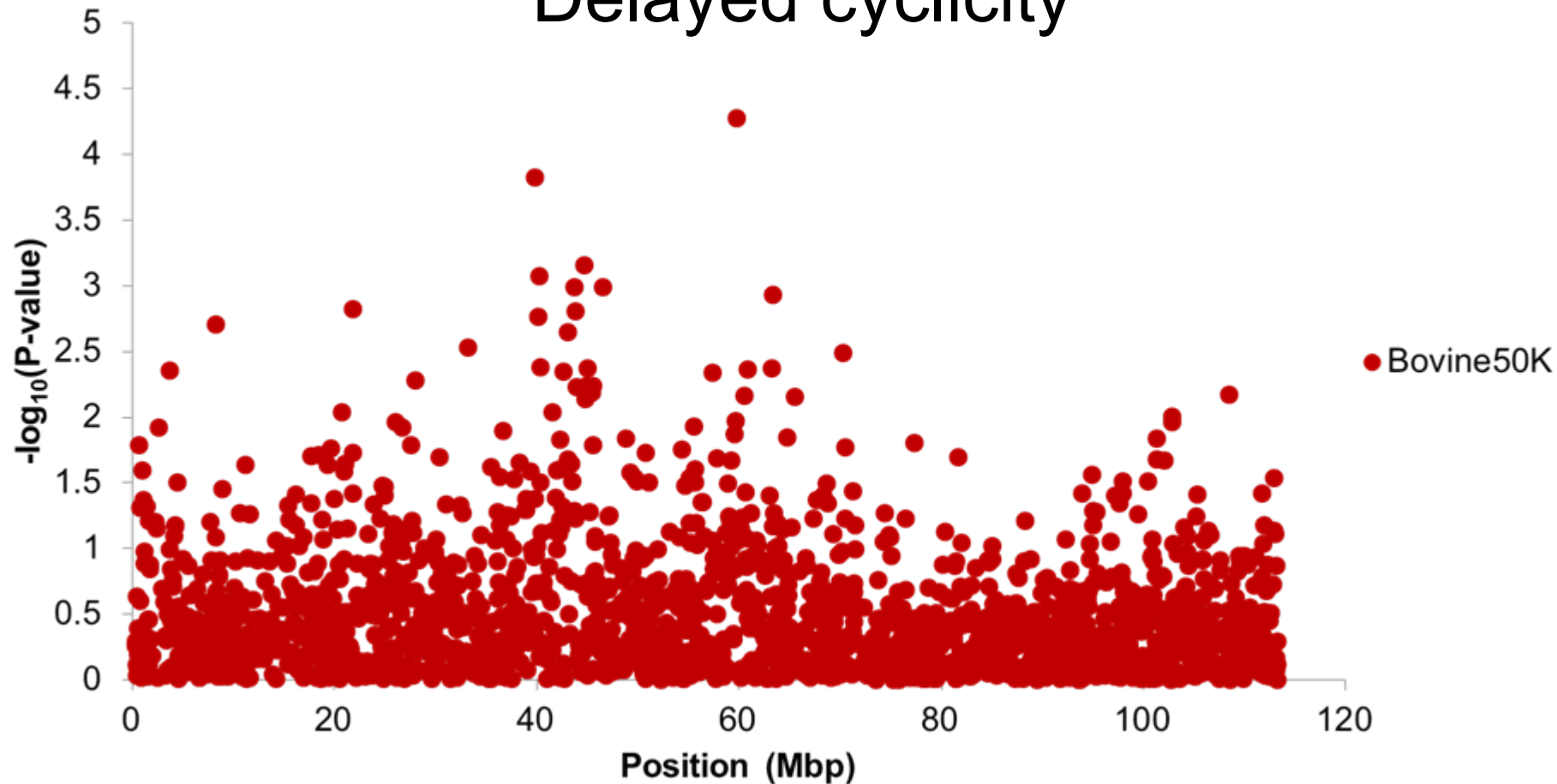
GWAS using sequences was performed with the same model and software as for the Bovine50K



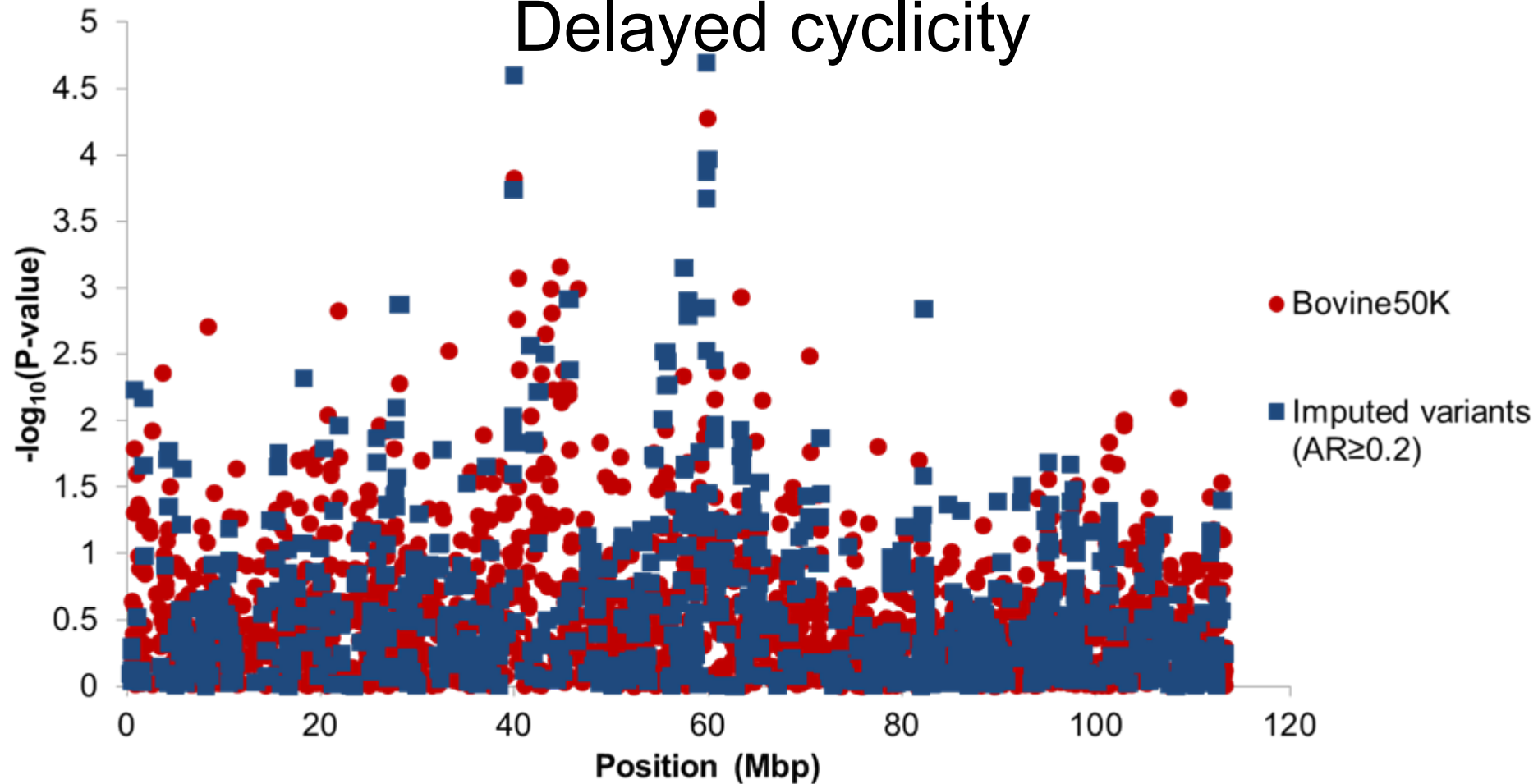
## Chromosome 8



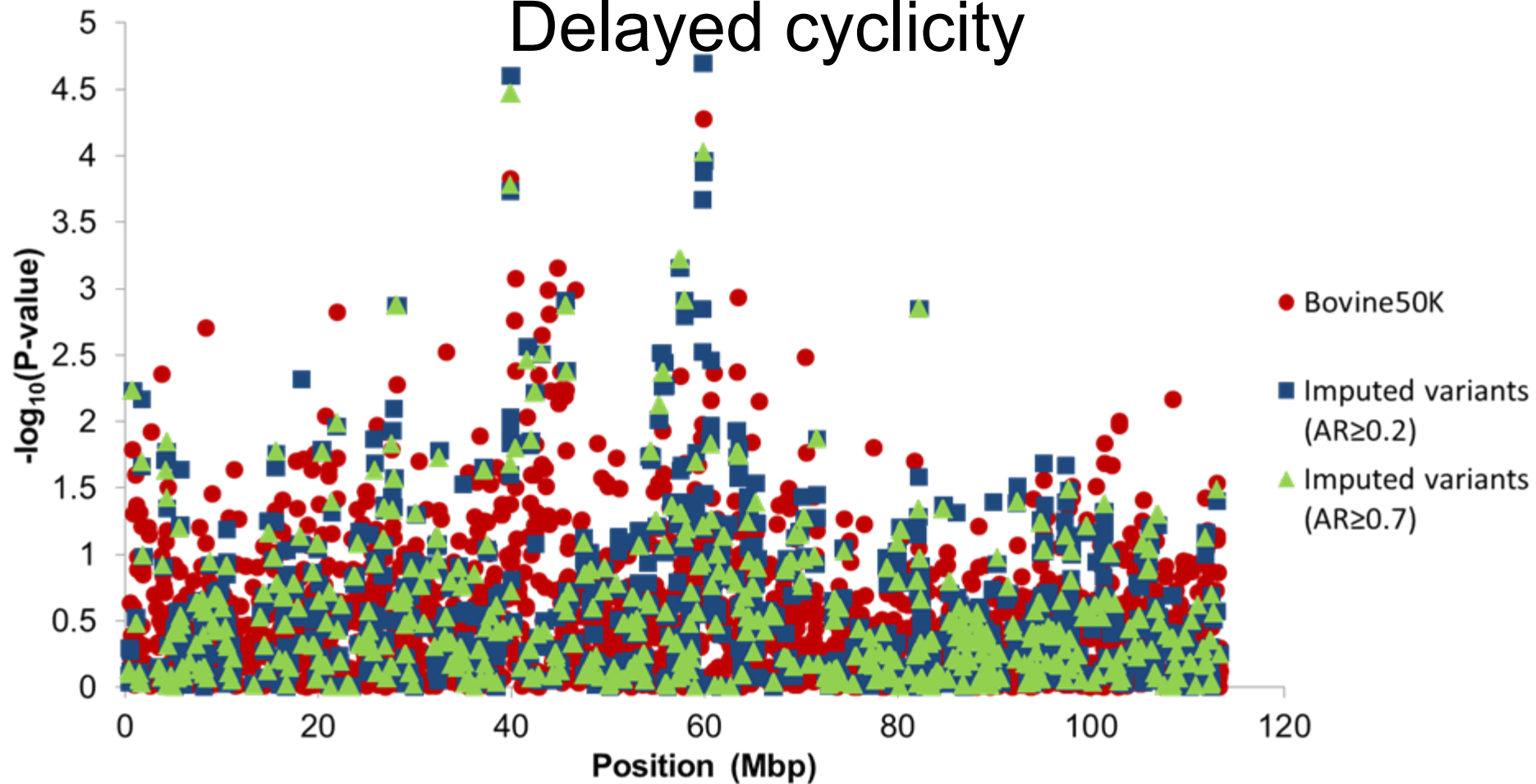
## Delayed cyclicity



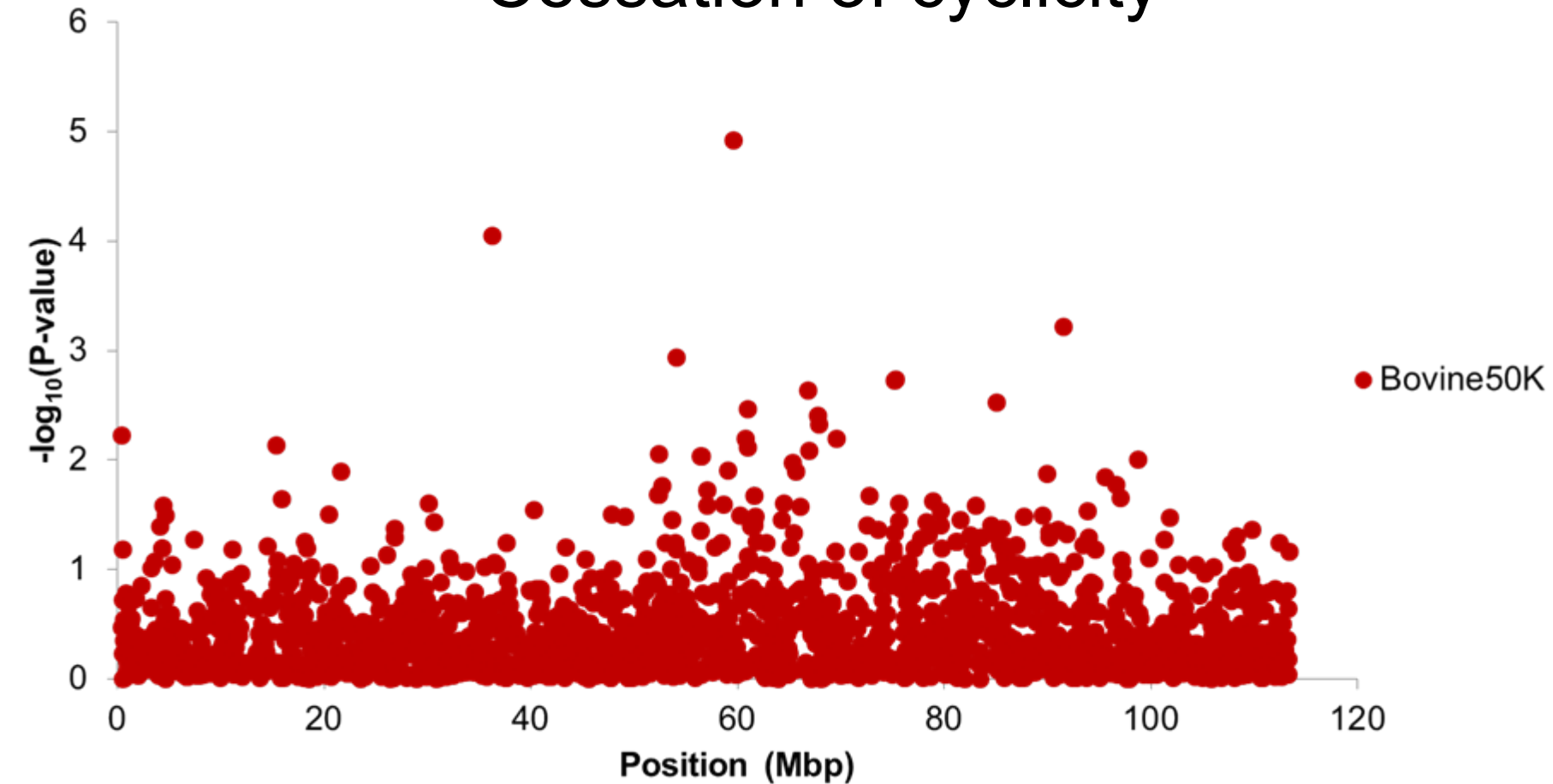
## Delayed cyclicity



## Delayed cyclicity

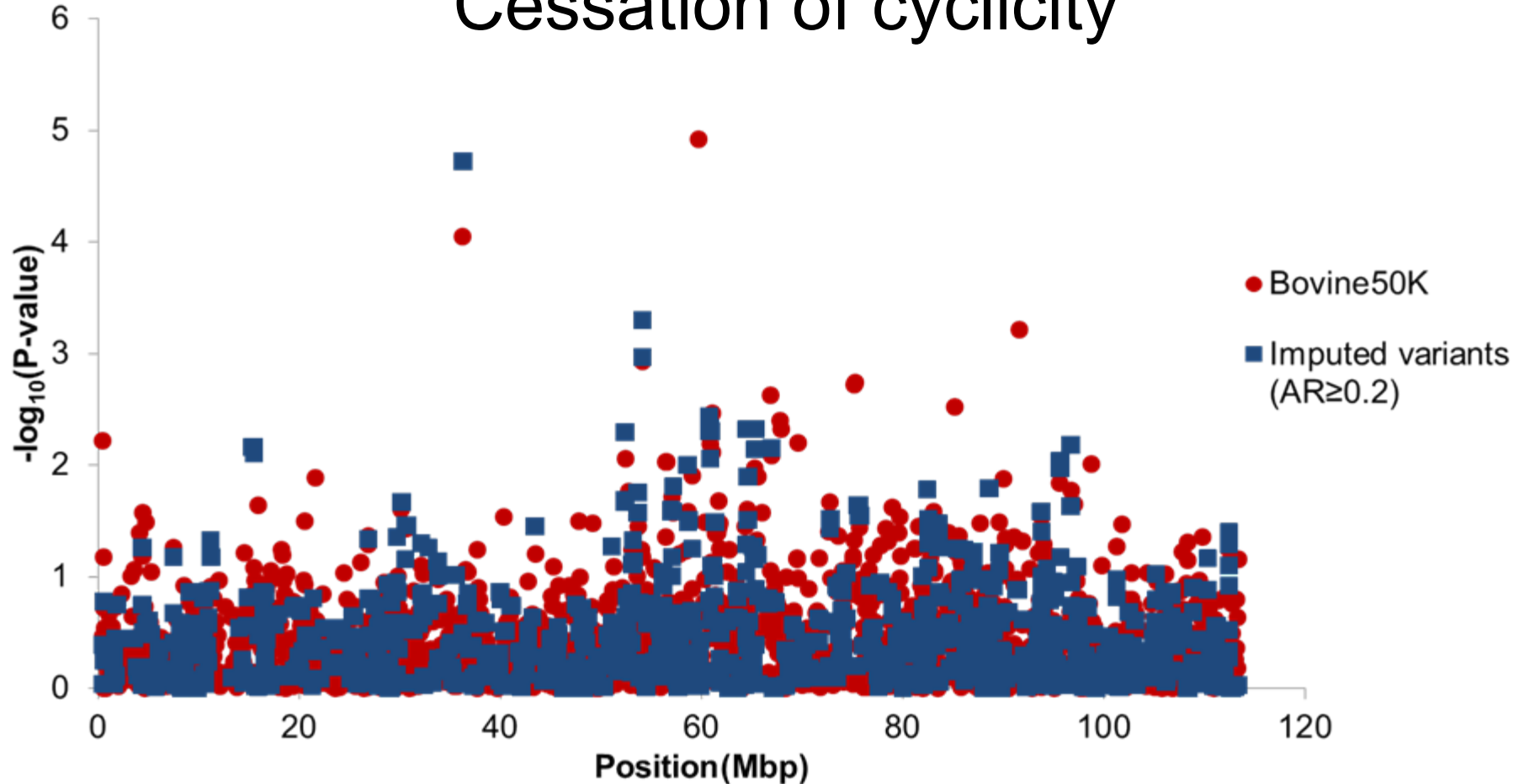


## Cessation of cyclicity

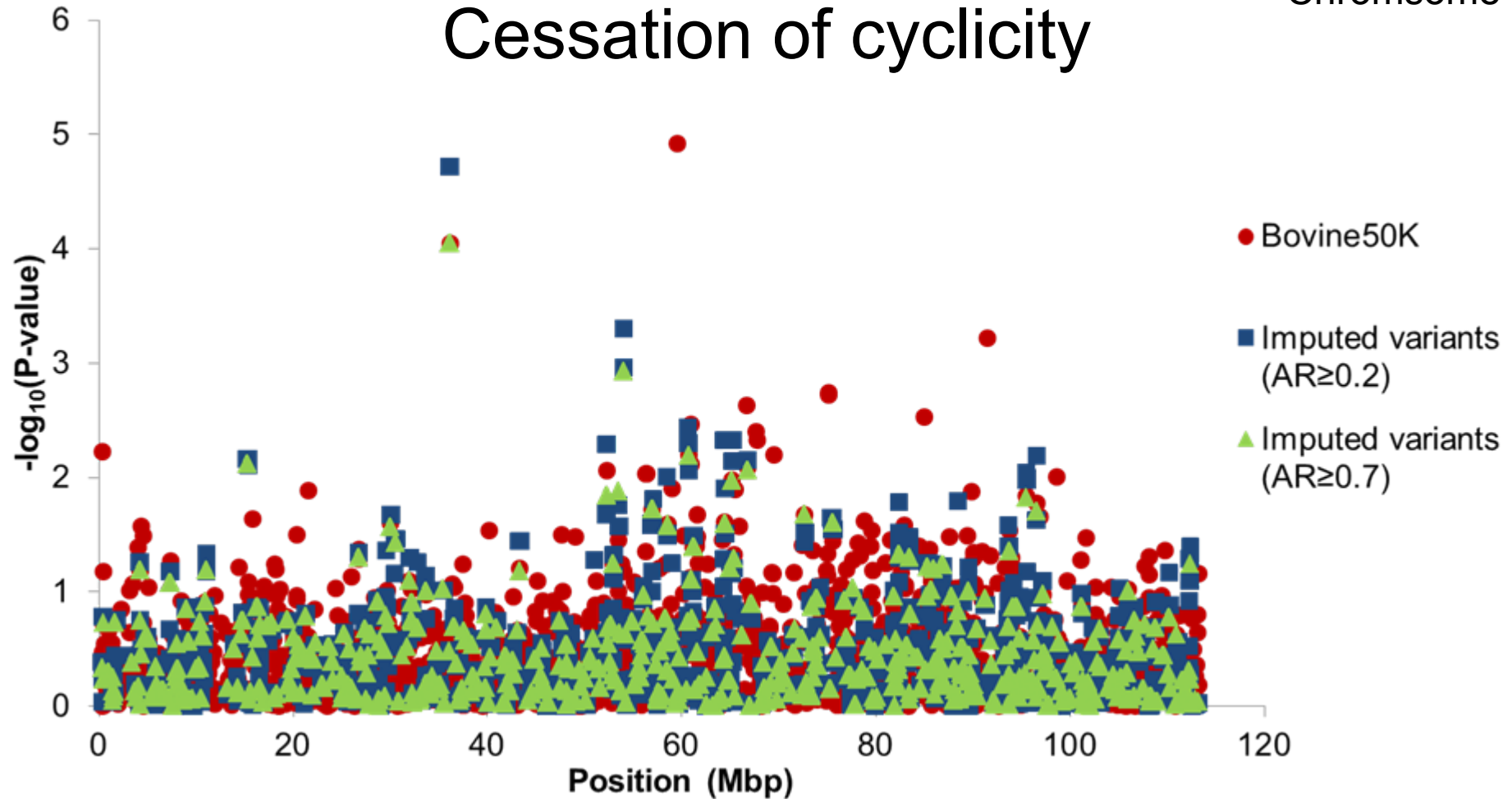




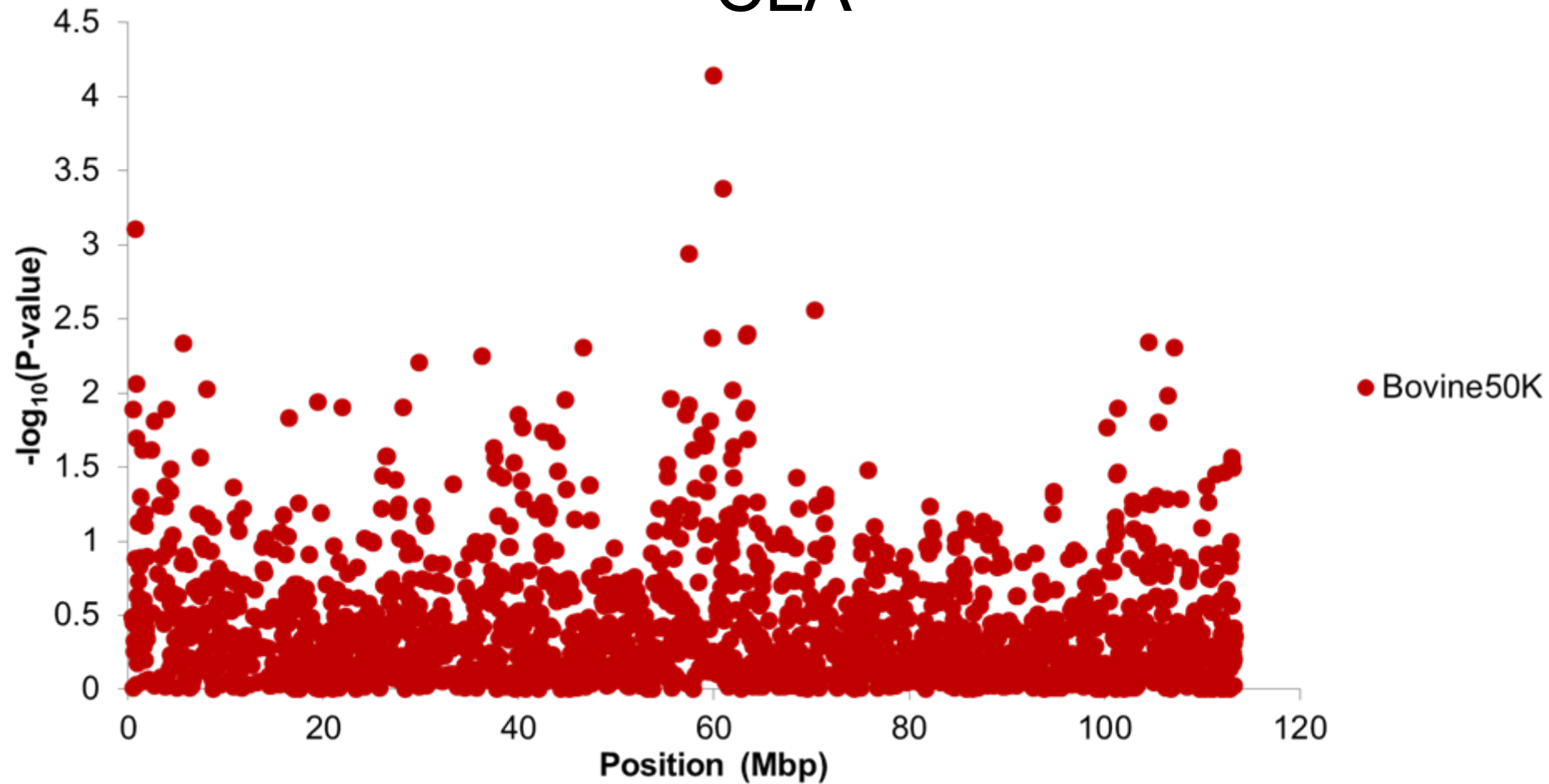
## Cessation of cyclicity



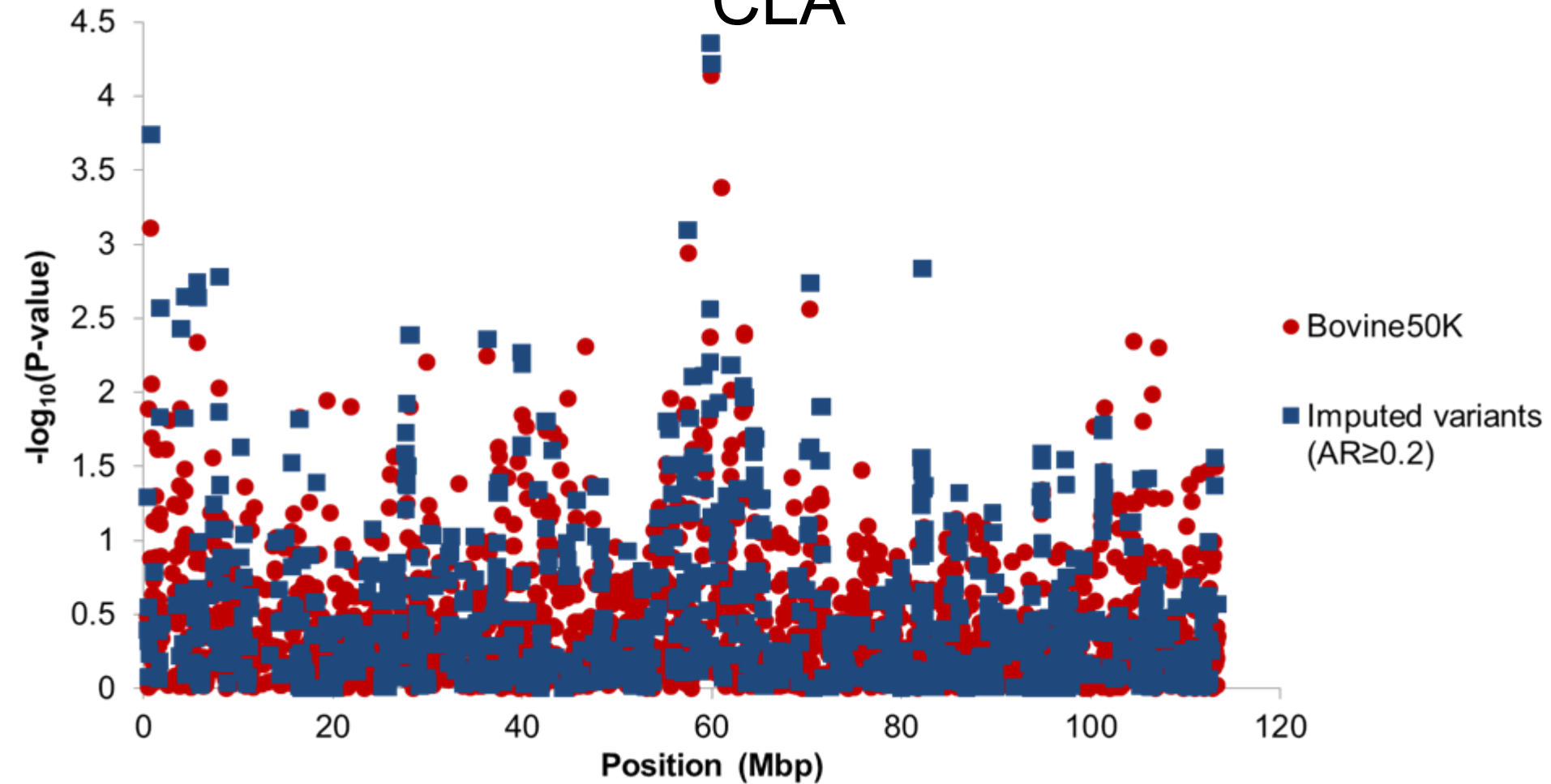
## Cessation of cyclicity



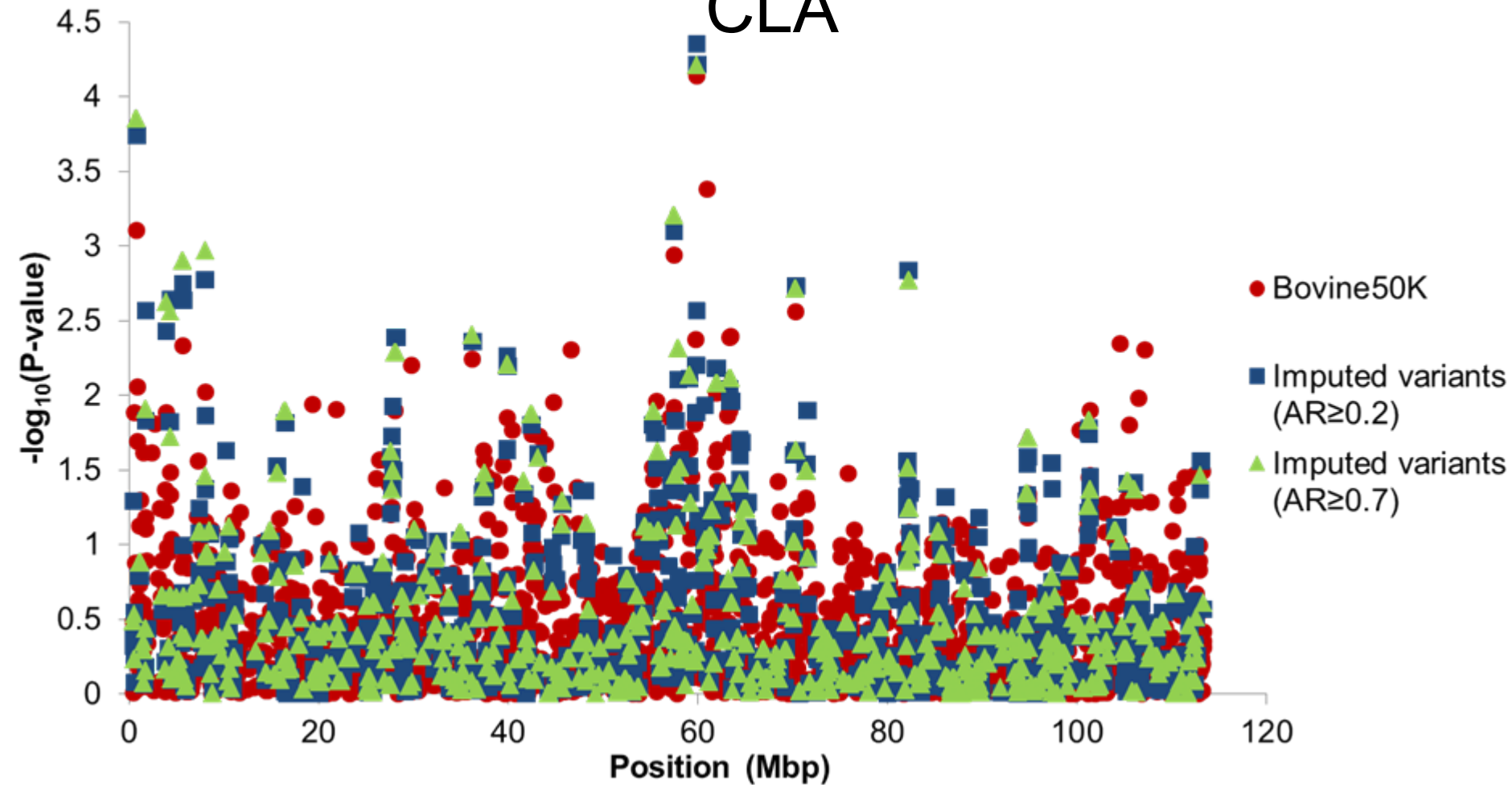
CLA



CLA



CLA



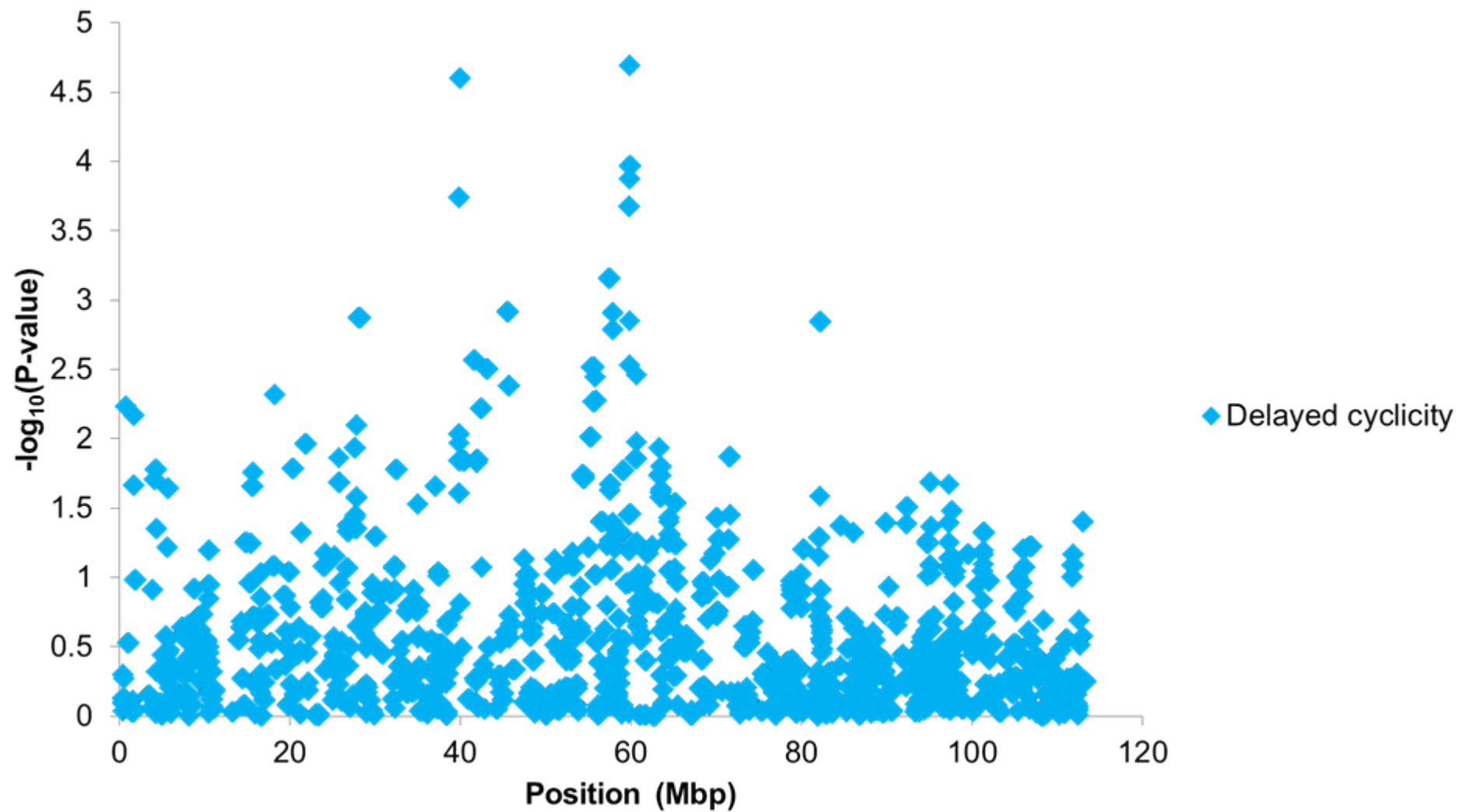
# Overlapping regions

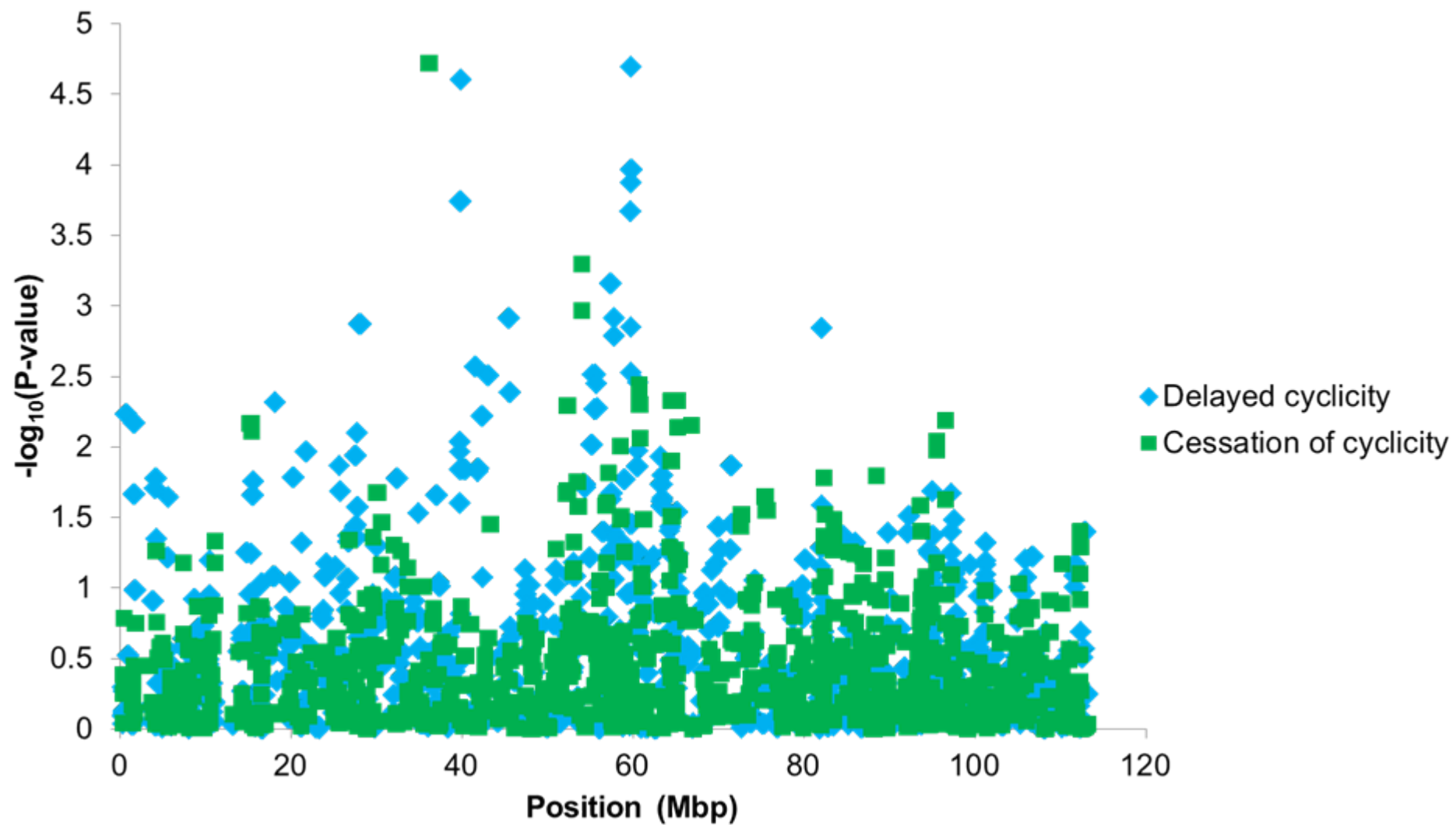
Between the endocrine fertility traits

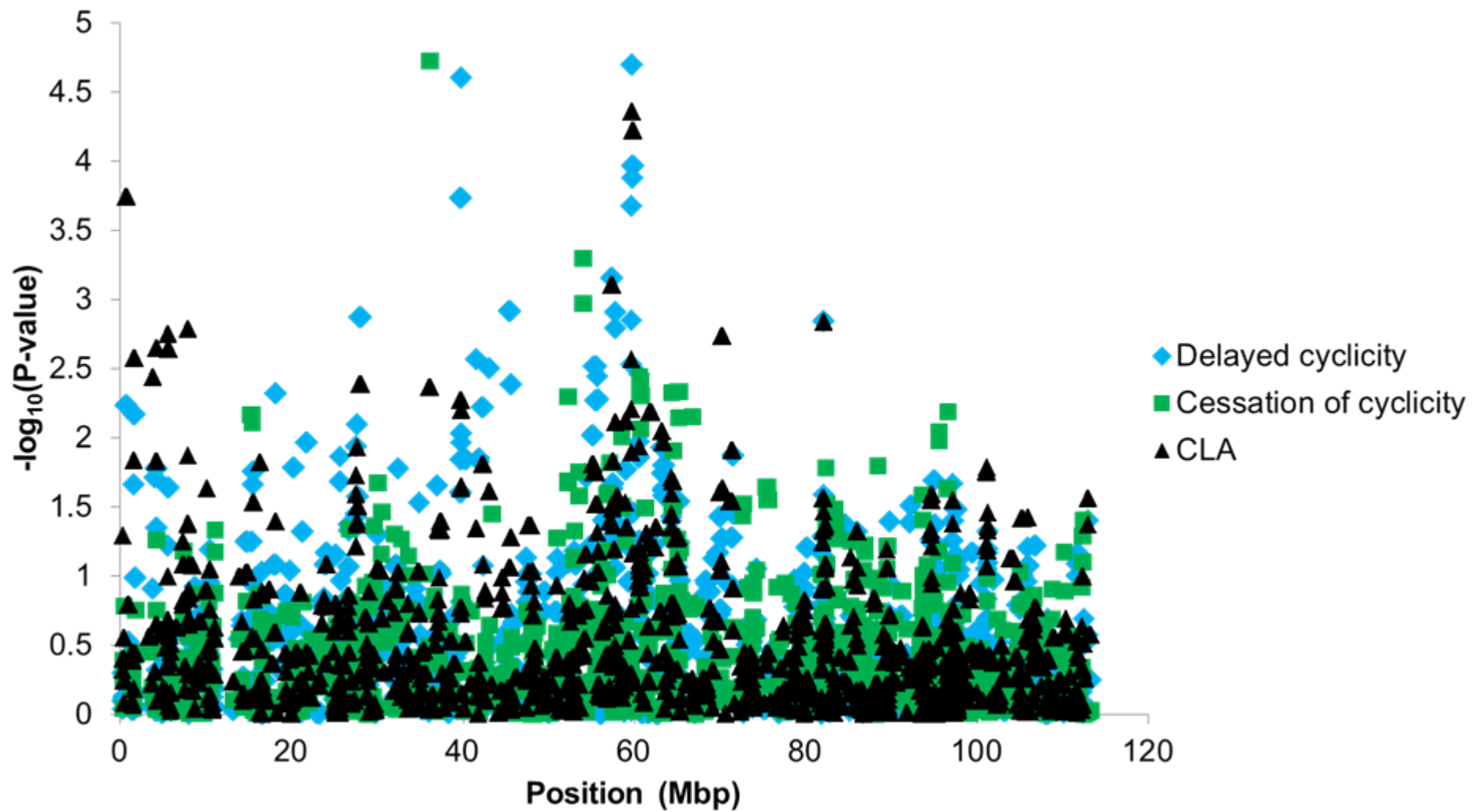
Between the endocrine and traditional fertility traits

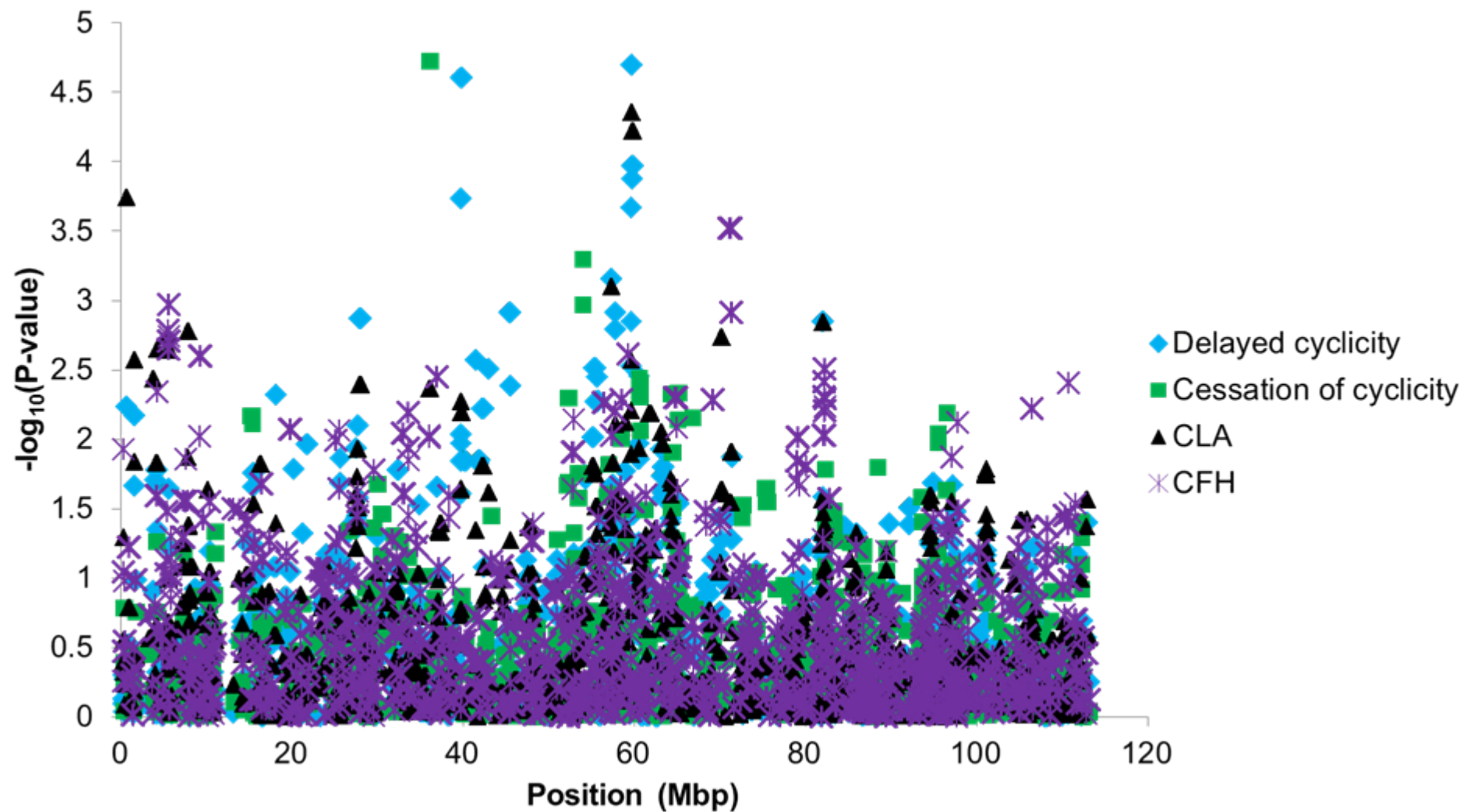


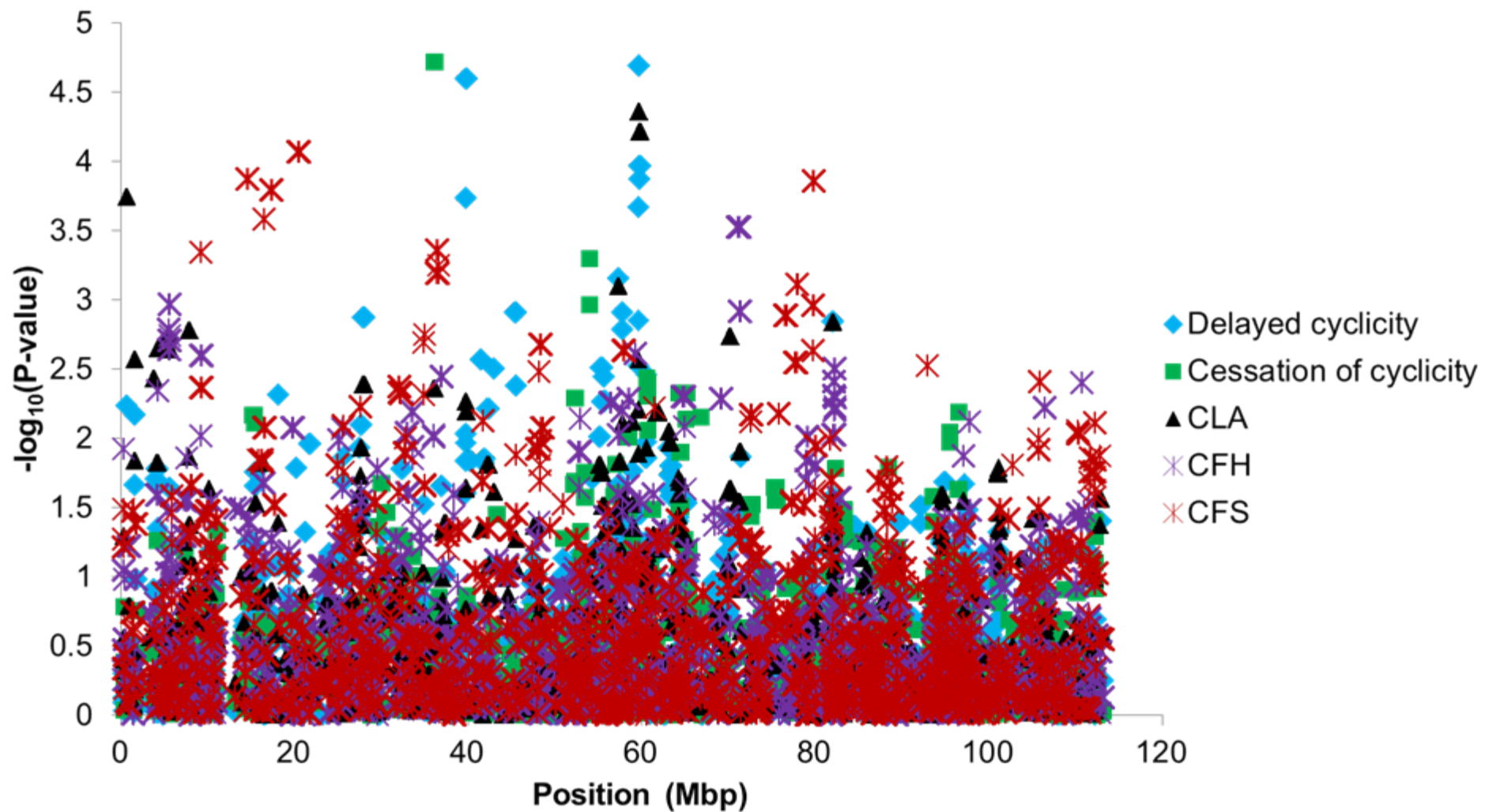


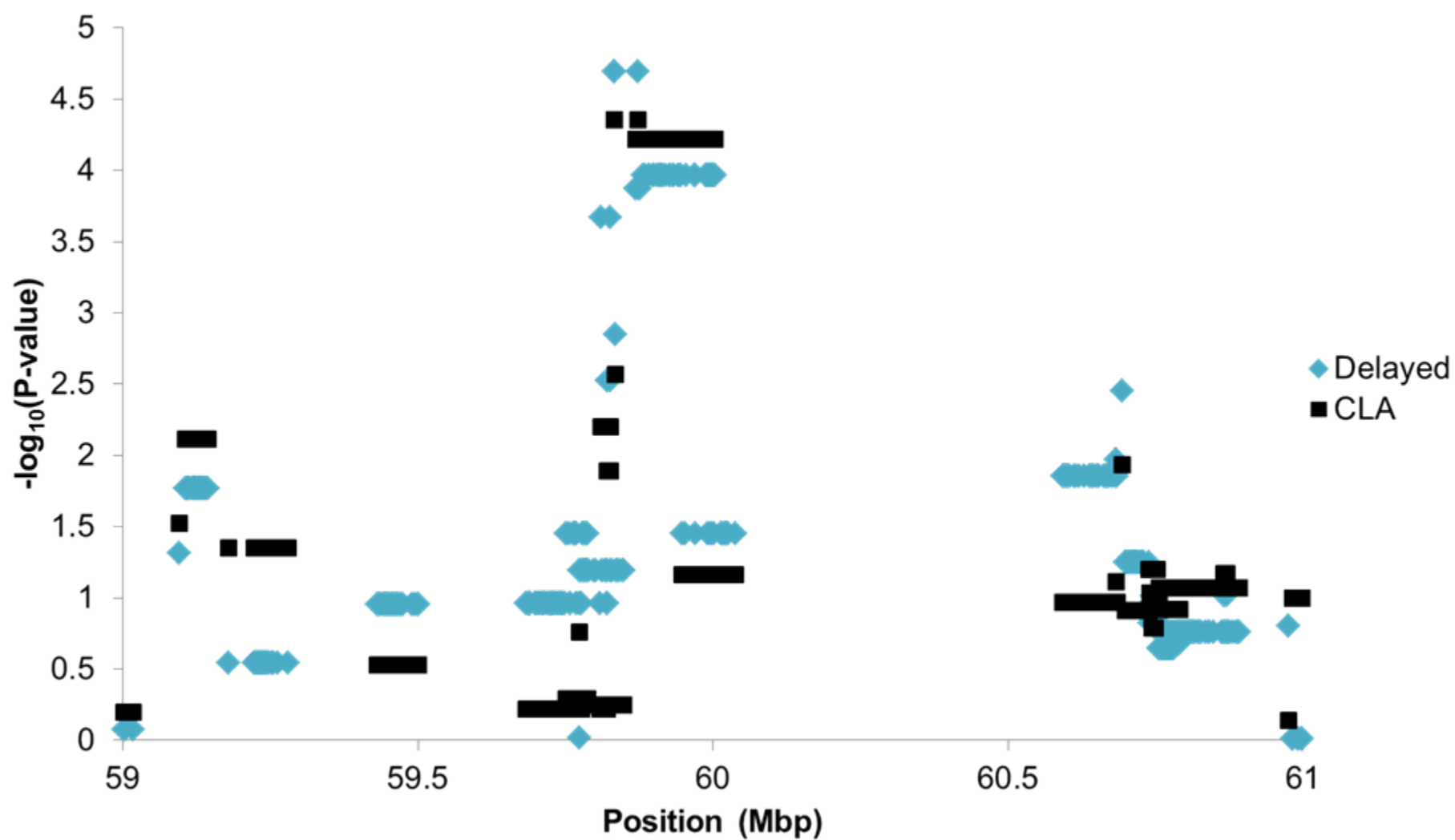














# Candidate genes?

Between 59-61Mbp at chromosome 8

- Endocrine gland morphology/physiology (SIT1, CA9, HINT2, GBA2)
- Embryo development/physiology/morphology (TLN1)
- Abnormalities in the reproductive system (GBA2)



# Conclusions

Region/s at chromosome 8 with interesting genes

Genotype the animals again

Relatively small data set

- imputing from Bovine50K to WGS may increased the chance of finding regions associated to the traits



Supervisors:  
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An increase in the total of variants –more information

➤ Chr8

- 50K 1962 SNP
- $AR \geq 0.2$  66993 variants (34X)
- $AR \geq 0.7$  22506 variants (12X)

➤ Chr17

- 50K 1339 SNPs
- $AR \geq 0.2$  76132 variants (57X)
- $AR \geq 0.7$  66536 variants (20X)

➤ Chr23

- 50K 914 SNPs
- $AR \geq 0.2$  66536 variants (73X)
- $AR \geq 0.7$  20821 variants (23X)

# RESULTS

	Delayed cyclicity	Cessation of cyclicity	CLA	CFS	CFH
Chrom 8					
50K	3.82	4.05	4.14	3.52	2.75
AR $\geq$ 0.2	4.60	4.72	4.36	4.07	3.52
AR $\geq$ 0.7	4.47	4.05	4.21	4.11	3.46
Chrom 17					
50K	4.65	6.19	4.07	1.68	3.87
AR $\geq$ 0.2	4.37	6.03	3.88	4.02	4.21
AR $\geq$ 0.7	4.52	6.20	4.52	4.13	4.23
Chrom 23					
50K	4.56	4.64	5.39	2.12	3.09
AR $\geq$ 0.2	4.92	4.48	5.53	4.07	3.76
AR $\geq$ 0.7	4.82	4.65	5.26	4.66	3.79