ETH zürich

Unraveling the genetic background of α_{s1}- and α_{s2}-casein phosphorylation in Dutch Holstein Friesian

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nederlandse zuivel organisatie

Acknowledgements

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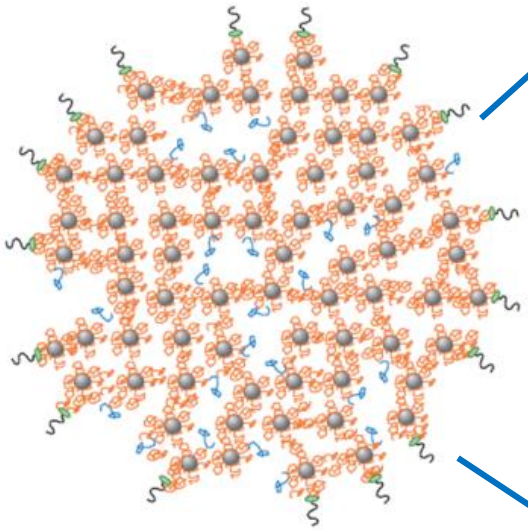
α_{s1}- and α_{s2}-casein

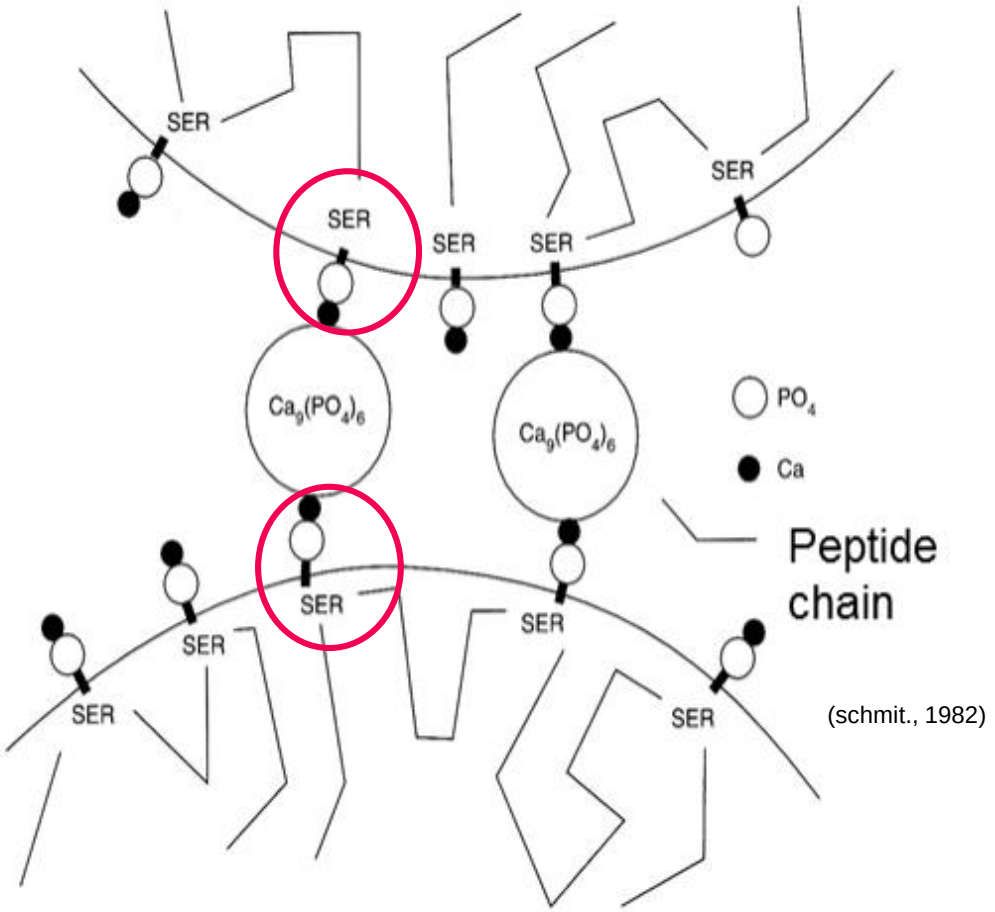
- Proportion in cow's milk protein (%wt/wt):
  α_{s1}-CN: ~40%, α_{s2}-CN: ~10%

- Variation in phosphorylation levels (P)
- α_{s1}-CN: 8P and 9P
- α_{s2}-CN: from 10P to 15P

Casein micelle structure



(Dalgleish *et al*., 2012)



(schmit., 1982)

α_{s1}- and α_{s2}-casein

J. Dairy Sci. 101:1–11

Genetic parameters for α_{S1}-casein and α_{S2}-casein phosphorylation isoforms in Dutch Holstein Friesian

Z. H. Fang,*† H. Bovenhuis,† H. J. F. van Valenberg,‡ P. Martin,* T. Huppertz,§ and M. H. P. W. Visker†

Trait		Mean	h^2
α_{s1}-CN	total	33.64	0.52 (0.11)
	8P	21.26	0.48 (0.10)
	9P	7.42	0.76 (0.12)
α_{s2}-CN	total	6.67	0.94 (0.12)
	10P	0.99	0.54 (0.11)
	11P	3.44	0.89 (0.12)
	12P	2.24	0.71 (0.12)
α_{s1}-CN PD		25.79	0.78 (0.12)
α_{s2}-CN PD		34.01	0.64 (0.11)

α_{s1}- and α_{s2}-casein

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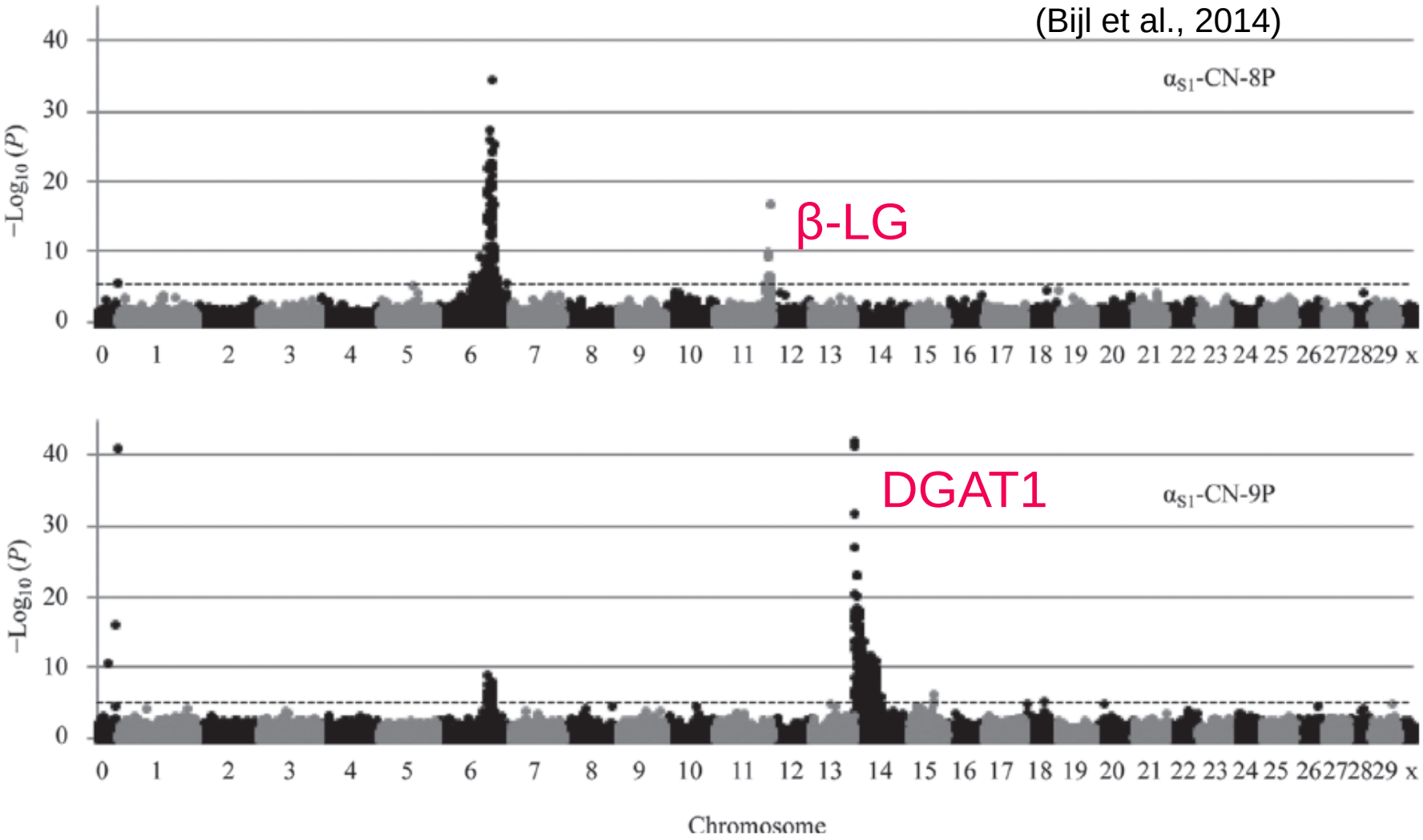
Phosphorylation degree:

α_{s1}-CN PD = α_{s1}-CN-9P/ total α_{s1}-CN X 100%

α_{s2}-CN PD= α_{s2}-CN-12P/ total α_{s2}-CN X 100%

GWAS for α_{s1}-casein phosphoforms

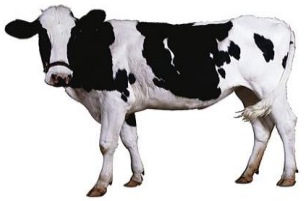
Dutch milk genomics initiative
(Bijl et al., 2014)



Objectives

- Investigate the genetic background of α_{s2}-CN phosphoforms
- Shared genetic control between α_{s1}-CN PD and α_{s2}-CN PD?

Phenotypes



~2000 primiparous, mid-late lactation
from ~400 herds

- Relative concentrations of α_{s2}-CN-10P, α_{s2}-CN-11P and α_{s2}-CN-12P (determined by capillary zone electrophoresis)
- Phosphorylation degree of α_{s1}-CN and α_{s2}-CN (α_{s1}-CN PD and α_{s2}-CN PD)

Genotypes

- 50K SNP chip

Single-SNP associations

$$y = \beta_1 dim + \beta_2 e^{-0.05*dim} + \beta_3 ca + \beta_4 ca^2 + season + scode + SNP + herd + a + e$$

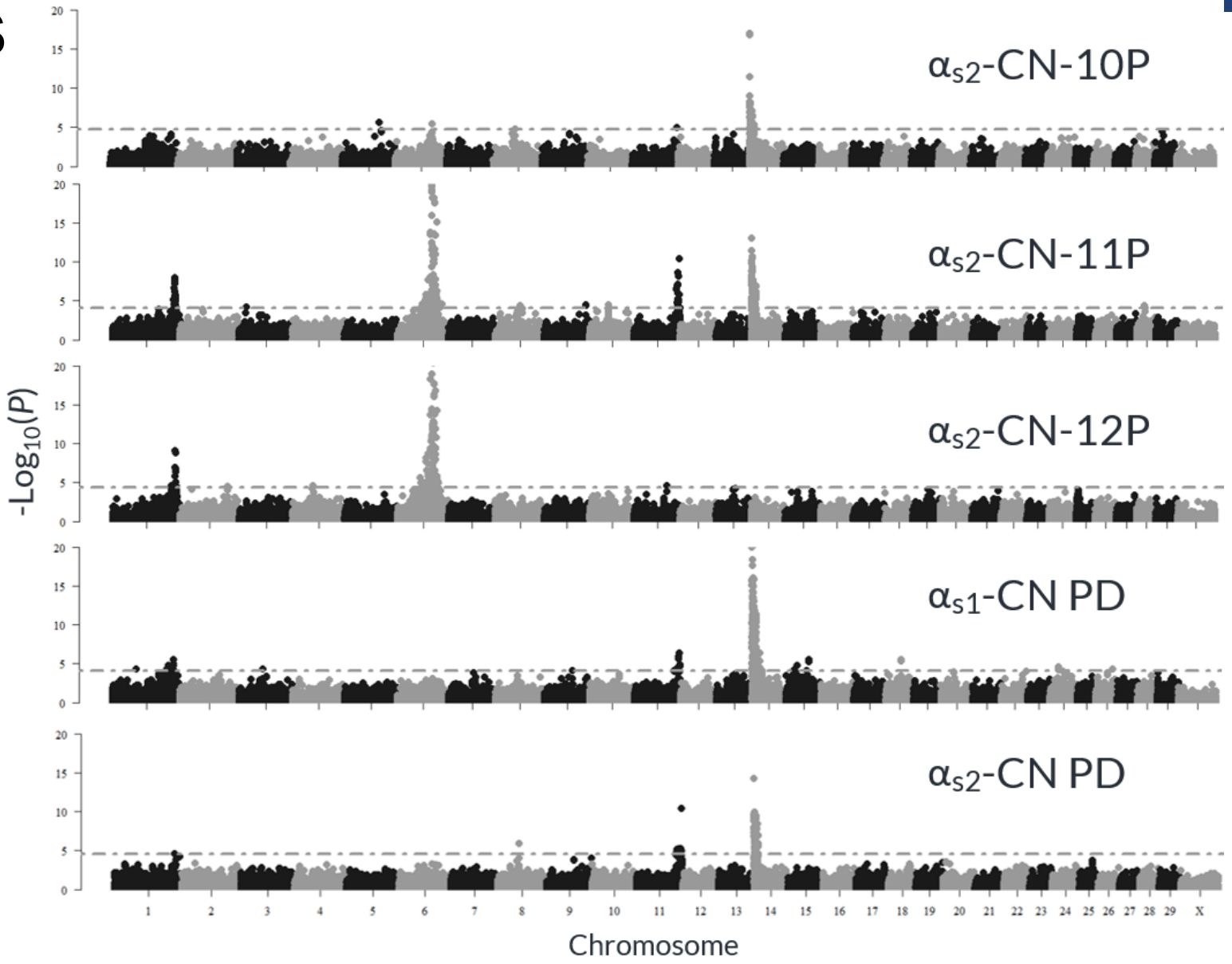
Fixed effects

- **dim**: days in milk
- **ca**: age at the first calving
- **season**: calving season
- **scode**: proven vs young bulls
- **SNP**: effect of SNP genotypes

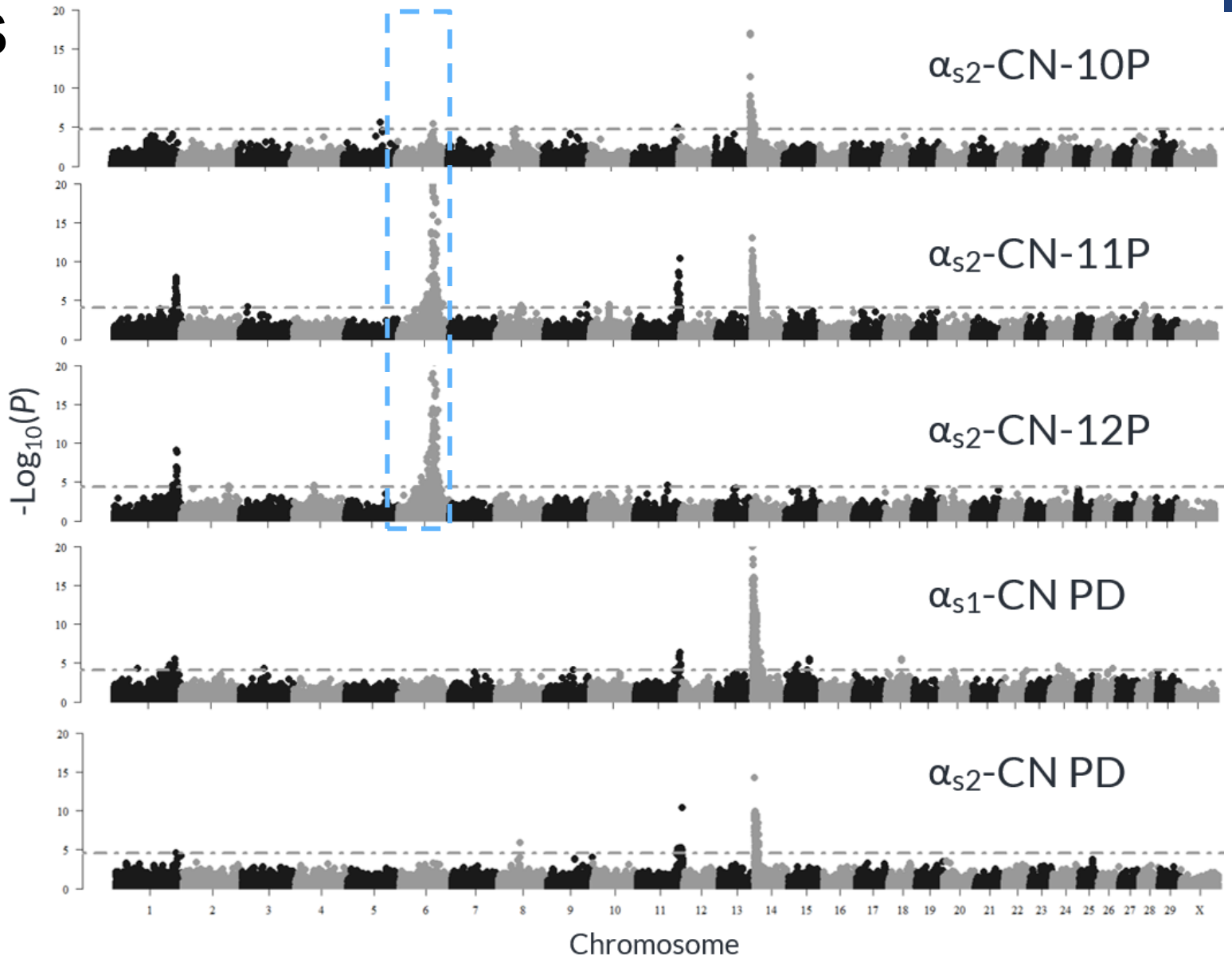
Random effects

- **herd**: effect of herd
- **a**: additive genetic effect
- **e** : residual

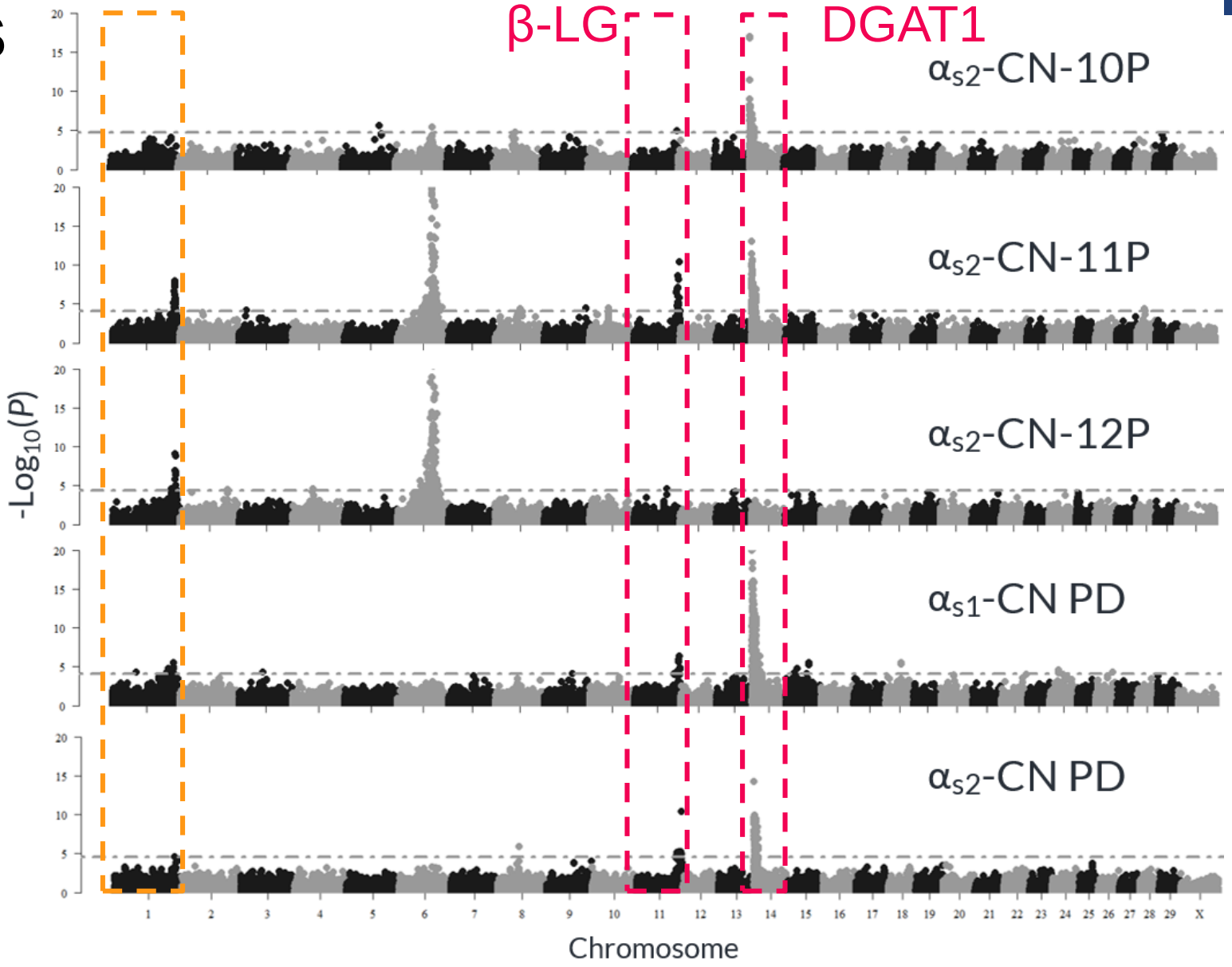
GWAS


αs2-CN-10P
αs2-CN-11P
αs2-CN-12P
αs1-CN PD
αs2-CN PD
-Log10(P)
Chromosome
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 X

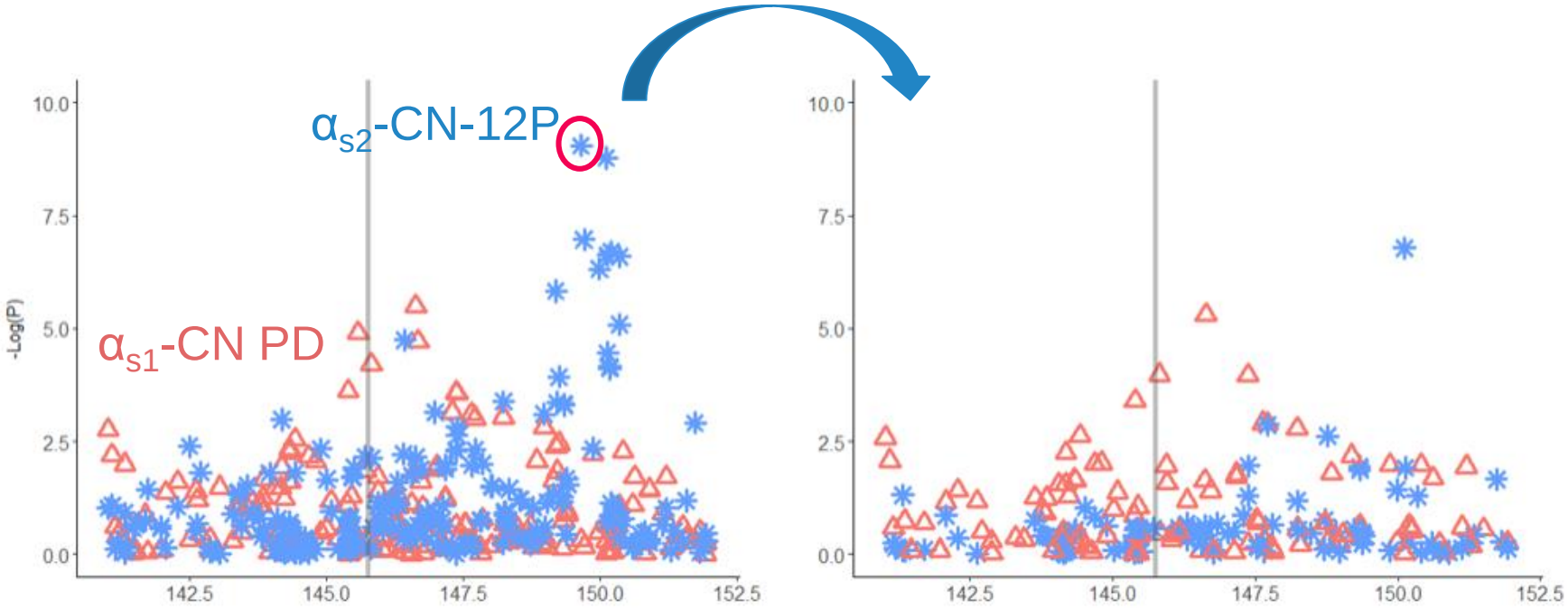
GWAS


αs2-CN-10P
αs2-CN-11P
αs2-CN-12P
αs1-CN PD
αs2-CN PD
-Log10(P)
Chromosome
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 X

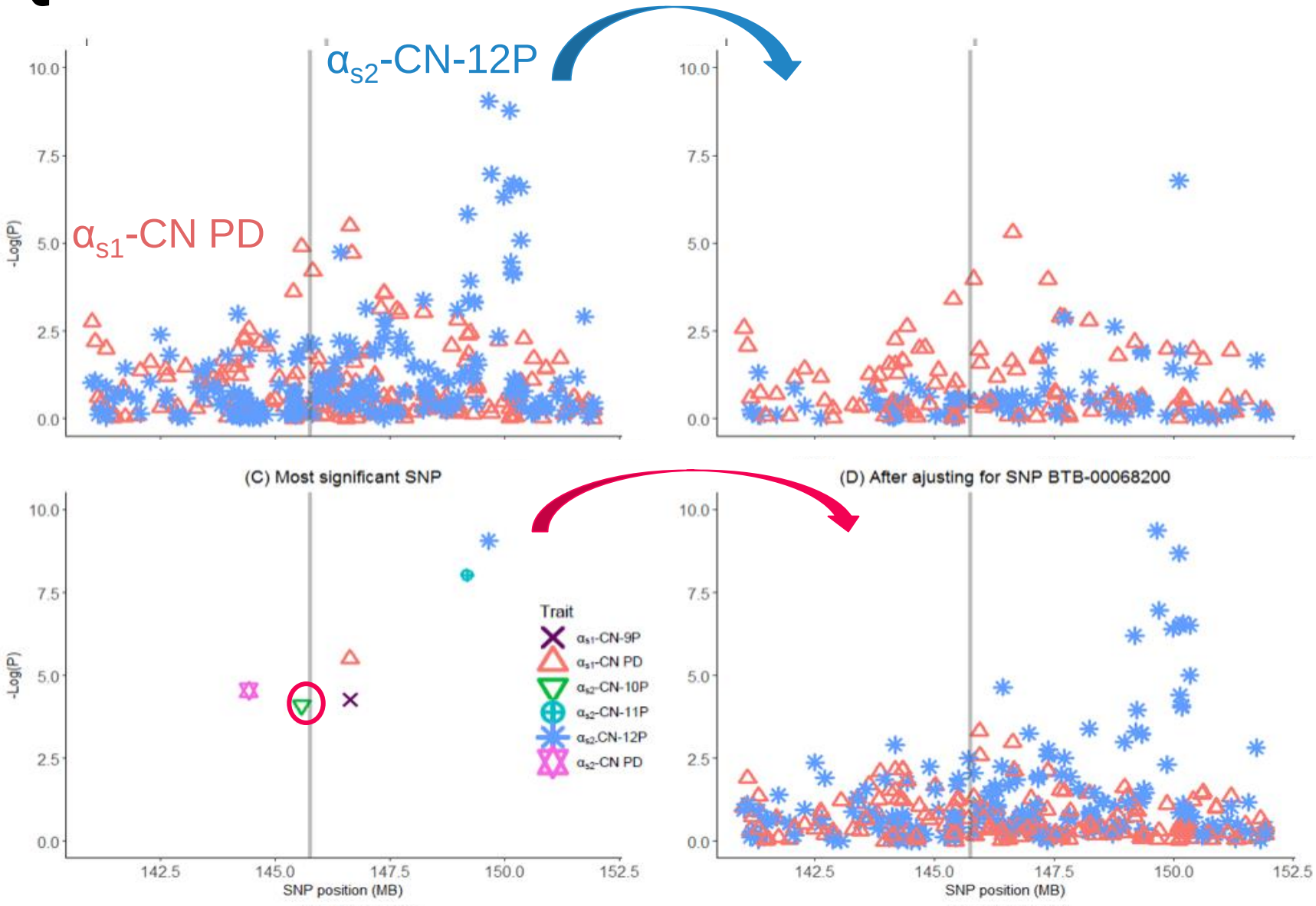
GWAS


β-LG
DGAT1
αs2-CN-10P
αs2-CN-11P
αs2-CN-12P
αs1-CN PD
αs2-CN PD
-Log10(P)
Chromosome

QTL on chromosome 1



QTL on chromosome 1

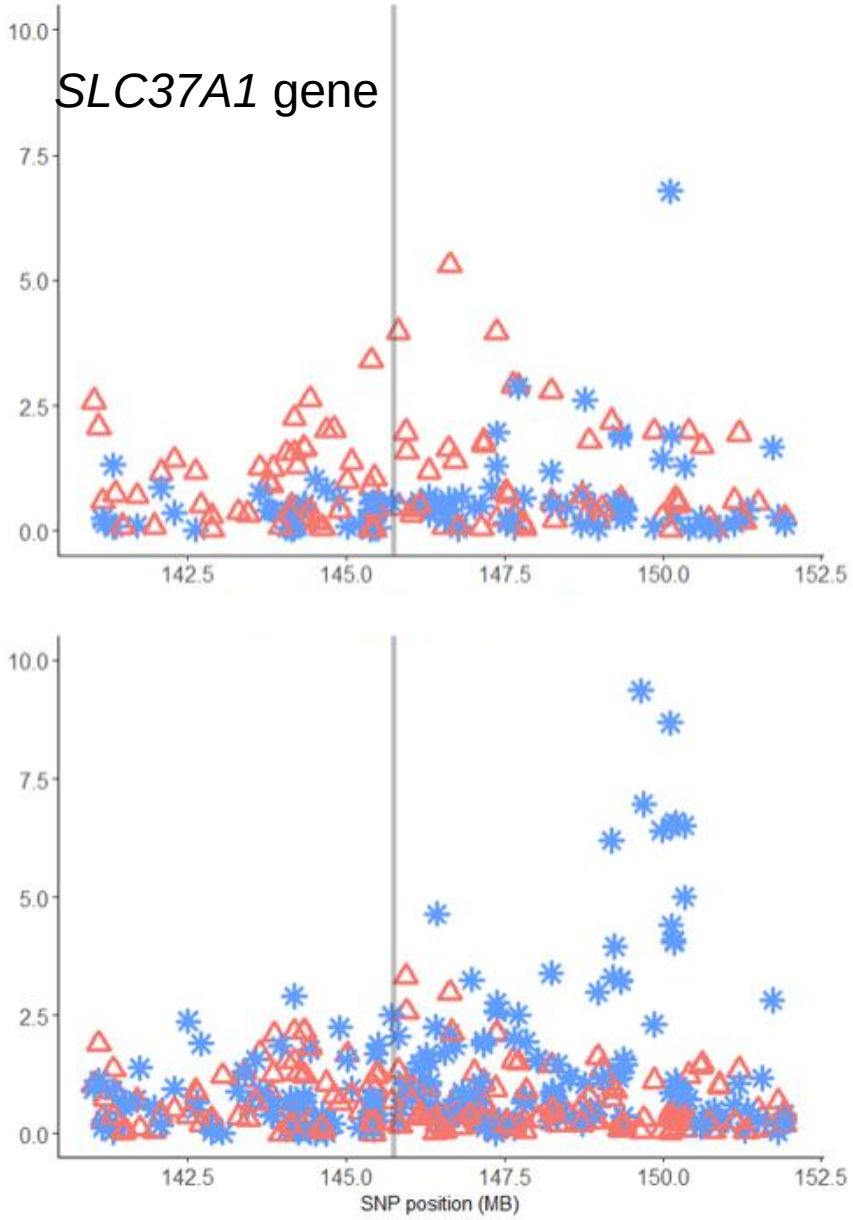


QTL on chromosome 1

α_{s1}-CN PD
&
α_{s2}-CN PD

2 QTL

α_{s2}-CN production



Conclusions

- Three genomic regions affect phosphorylation degree of α_{s1}- and α_{s2}-CN:

chromosome1 : SLC37A1 (translocate phosphorus)

chromosome11 : β-LG

chromosome14 : DGAT1

- Actual roles of these proteins need further investigation