A genomic region on chromosome 17 has a major impact on litter size traits in rabbits

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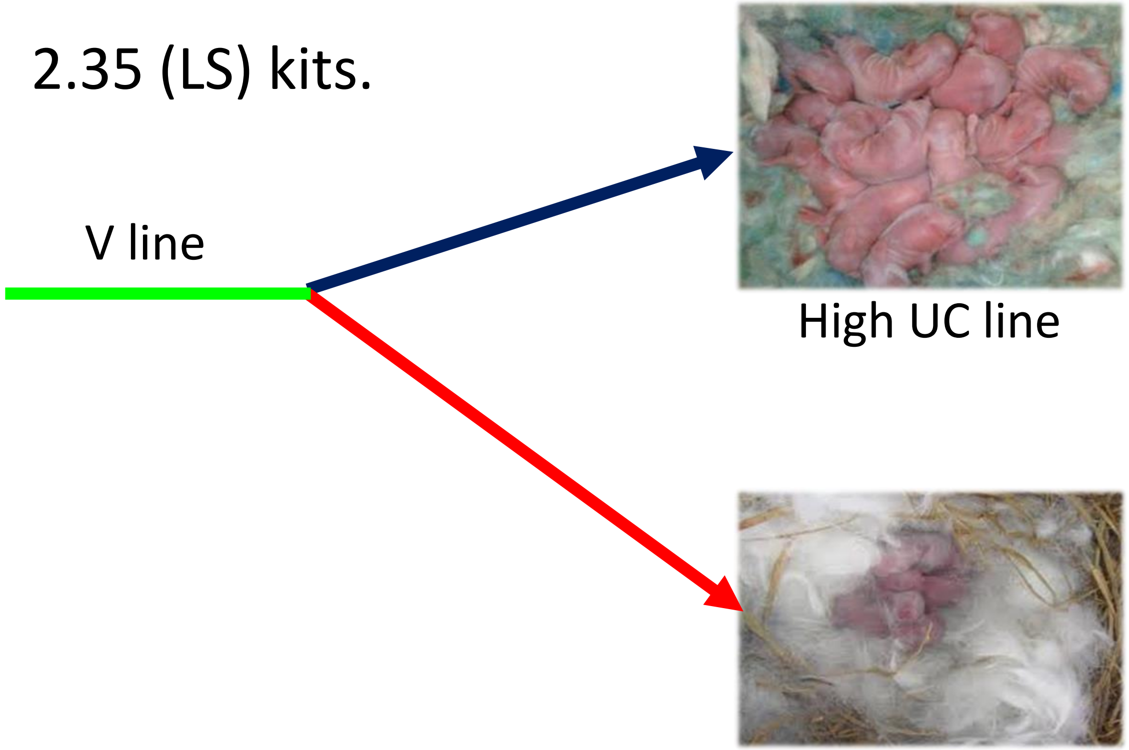
INTRODUCTION

- Genetic improvement of litter size (LS).
- Divergent selection for uterine capacity (UC).
- Selection response 1.50 (UC) and 2.35 (LS) kits.

Ovariectomy



V line

High UC line

Low UC line

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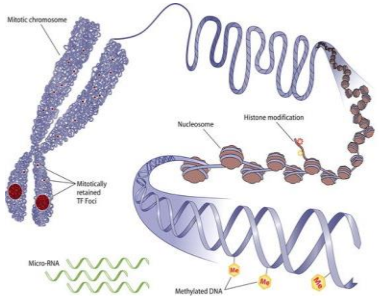
INTRODUCTION

- Candidate genes association study for UC experiment.
- Genome whole asso

SNP-ARRAY
Available

PGR
HSD17B4
OVGP1
EROL
SGB1A1
TIMP1
uteroglobin



```
ATCTCTTGGCTCCAGCATCGATGAAGAACGCA
TCATTTAGAGGAAGTAAAAGTCGTAACAAGGT
GAACTGTCAAAACTTTTAACAACGGATCTCTT
TGTTGCTTCGGCGGCGCCCGCAAGGGTGCCCG
GGCCTGCCGTGGCAGATCCCCAACGCCGGGCC
TCTCTTGGCTCCAGCATCGATGAAGAACGCAG
CAGCATCGATGAAGAACGCAGCGAAACGCGAT
CGATACTTCTGAGTGTTCTTAGCGAACTGTCA
CGGATCTCTTGGCTCCAGCATCGATGAAGAAC
ACAACGGATCTCTTGGCTCCAGCATCGATGAA
CGGATCTCTTGGCTCCAGCATCGATGAAGAAC
GATGAAGAACGCAGCGAAACGCGATATGTAAT
```

Peiro et al. (2010); Argente et al. (2010), Ballester et al. (2013); Merchán et al. (2009)

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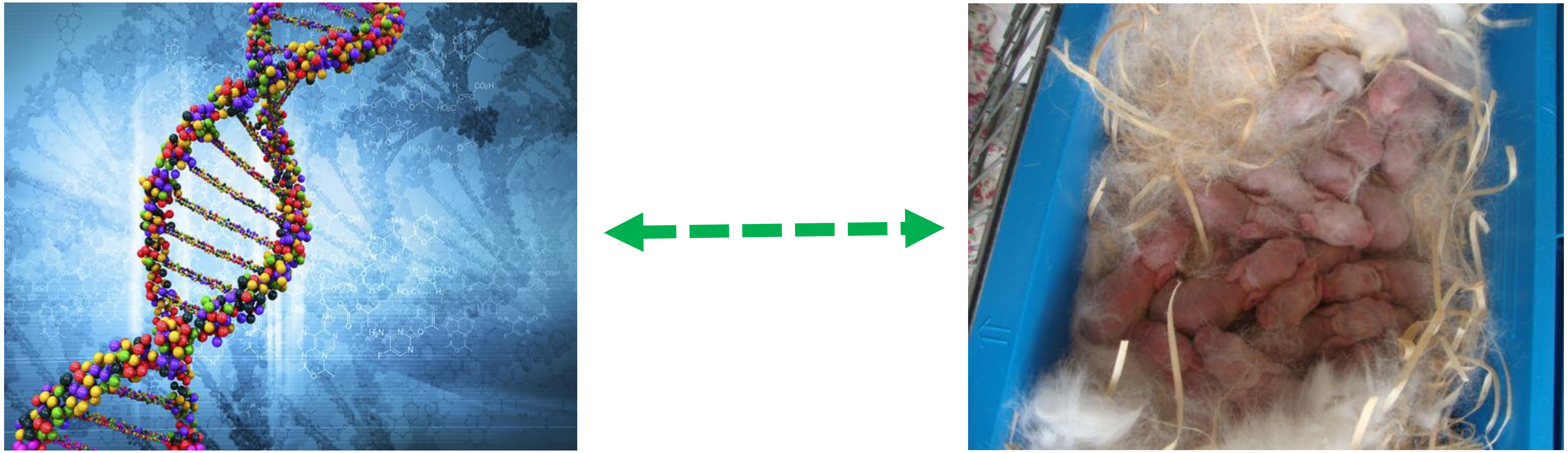
PURPOSE

- To identify genomic regions and candidate genes associated with litter size traits in rabbits



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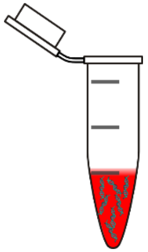
Material and Methods

V line
30 animals

High UC line
90 animals

Low UC line
69 animals



DNA Isolation

200,000 SNPs - Affymetrix

Genotyping and
Quality Control

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Material and Methods

Reproductive Trait	Abbreviation	Number of records
Total number born	TNB	183
Number born alive	NBA	183
Number born dead	NBD	183
Ovulation rate	OR	157
Implanted embryos	IE	158
Embryo survival	ES	154
Fetal survival	FS	158
Prenatal survival	PS	157

Second Parity

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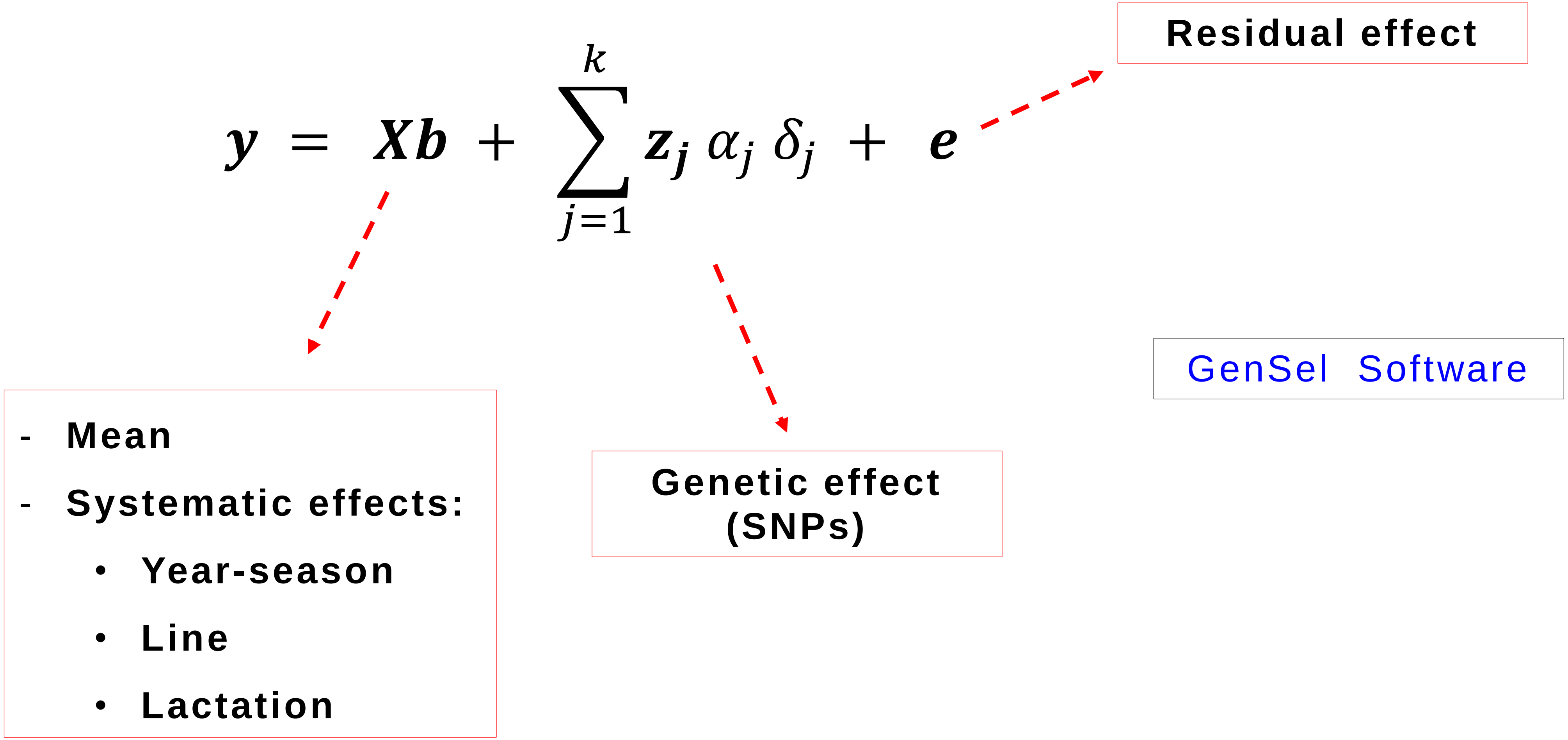
Material and Methods: GWAS

- Bayes B Method.



$$\boldsymbol{y} = \boldsymbol{X}\boldsymbol{b} + \sum_{j=1}^{k} \boldsymbol{z}_{\boldsymbol{j}}\, \alpha_j\, \delta_j + \boldsymbol{e}$$

Residual effect

- **Mean**
- **Systematic effects:**
  - **Year-season**
  - **Line**
  - **Lactation**

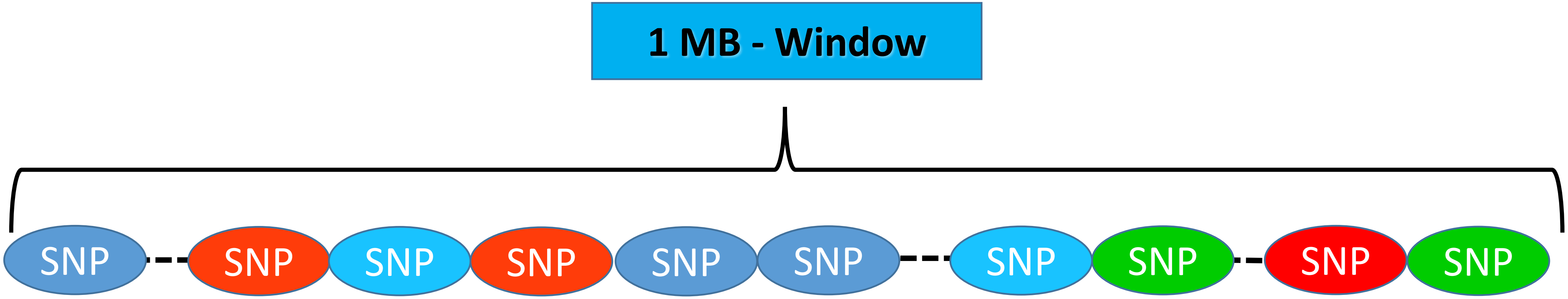
Genetic effect (SNPs)

GenSel Software

Garrick et al. (2013)

Material and Methods: GWAS

- 2,173 genomic regions were analyzed with a 1-Mb window size.
- Relevant windows explained at least 1.0% genetic variance.
- Genes and its biological functions.



1 MB - Window

Results

- 11 relevant windows.
- 54 genes (42 coding and 12 noncoding).

Chromosome	Trait (% Genetic Variance by window)	Length (Mb)
17	TNB (**16.3**), NBA (**3.5**), IE (**11.7**)	3.26
17	IE (**3.8**)	0.98
11	IE (**10**)	4.00
9	OR (**1.1**)	0.97
9	OR (**1.0**)	0.96

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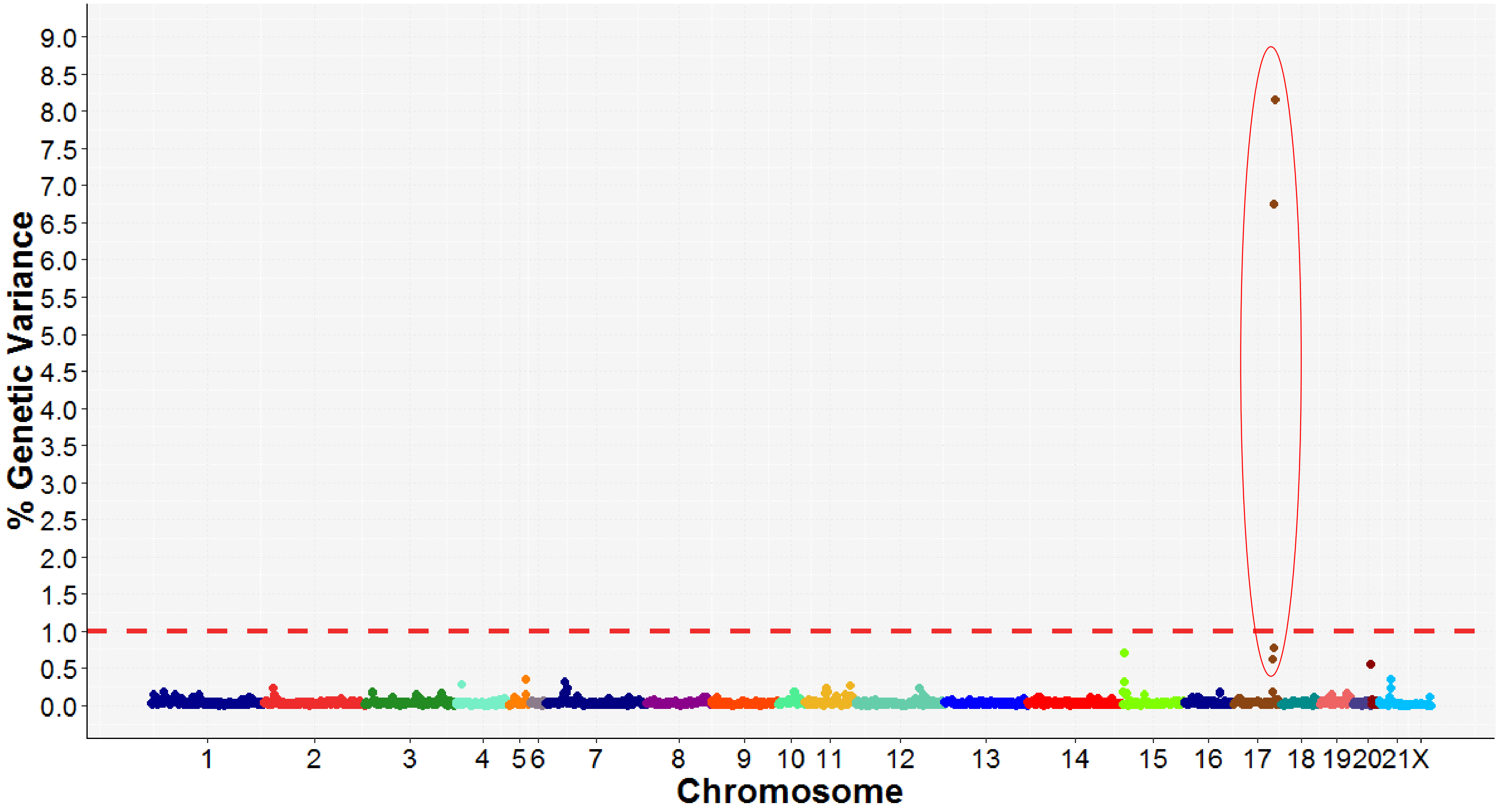
Results

- Manhattan plot for total number born



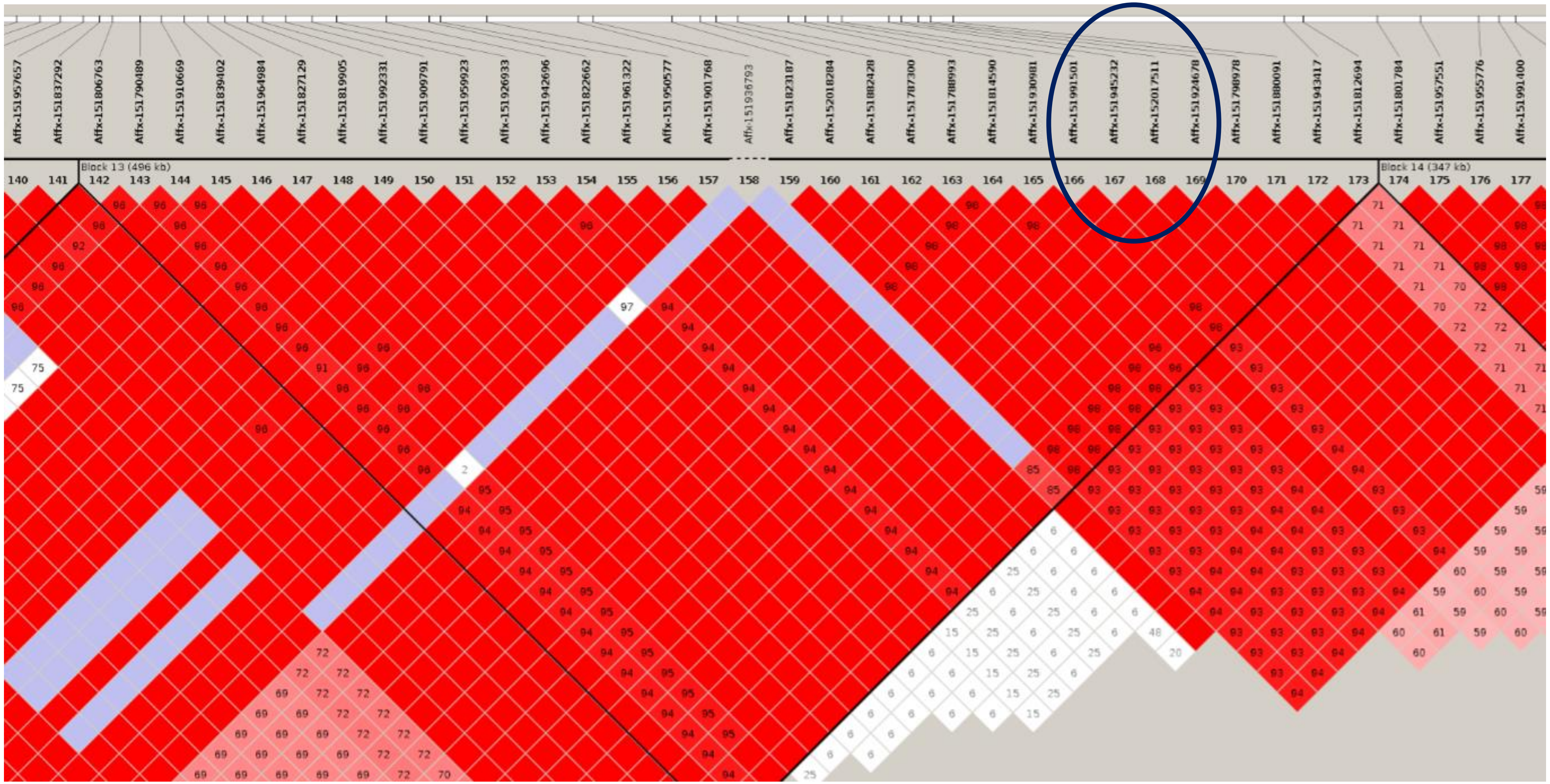
Results

- On chromosome 17

Principal Genes	Traits	Biological Functions
BMP4	TNB, NBA, IE	Involved in follicular growth and embryo development in mammals.
PTGDR & PTGER2	TNB, NBA	Cellular response to prostaglandin stimulus. Differentiation of germ and Sertoli cells .
STYX	TNB, NBA	Disrupts spermatid development
CDKN3	IE	Embryo development processes

Results

- Linkage disequilibrium blocks



BMP4 - Gen

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Conclusions

- The GWAS detected **consecutive genomic regions** associated with **TNB, NBA and IE on chromosome 17**.
- The **BMP4, PTGDR, STYX and CDKN3** genes profile like putative **candidate genes**.
- This GWAS in rabbits is only a **starting point** for further research.

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Thank you

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