

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

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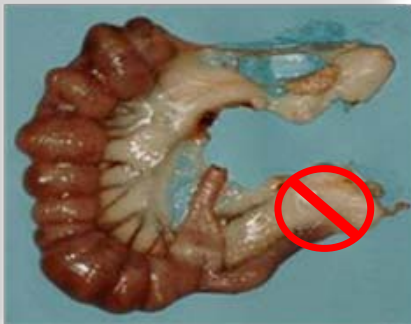
**ICTA**



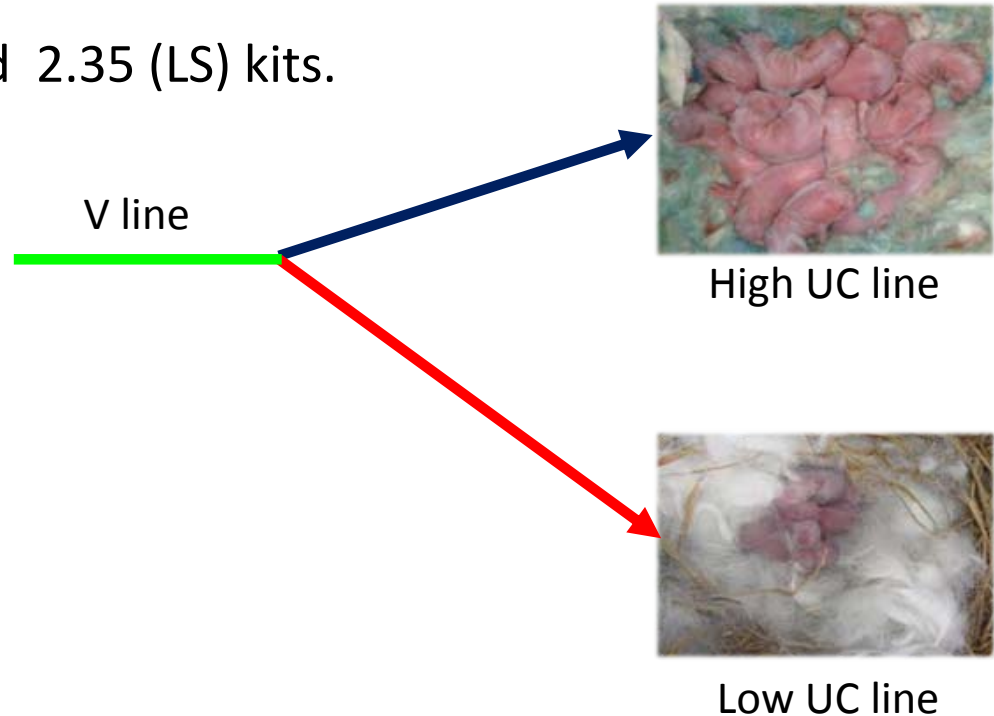
**UPV**

# INTRODUCTION

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



Ovariectomy

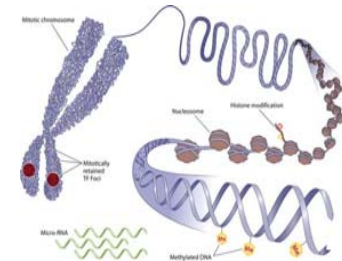
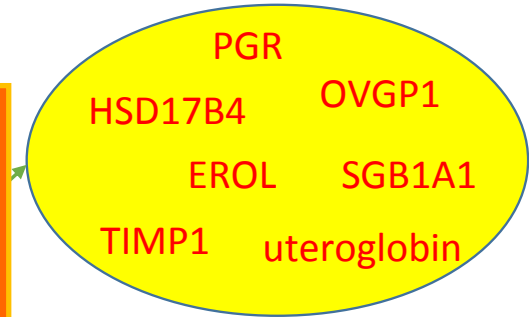


# INTRODUCTION

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



SNP-ARRAY  
Available



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

```
ATCTCTTGGCTCCAGCATCGATGAAGAACGCA  
TCATTAGAGGAAGTAAAAGTCGTAACAAGGT  
GAACGTCAAACTTTTAAACACGGATCTCTT  
TGTGCTTGGCGGCGCCGCAAGGTTGCCCG  
GGCCTGCCGTGGCAGATCCCCAACGCCGGCC  
TCTCTGGCTCCAGCATCGATGAAGAACGAG  
CAGCATCGATGAAGAACGAGCGAAACCGCAT  
CGATACTCTGAGTGTCTTAGCGAAGCTCA  
CGGATCTCTTGGCTCCAGCATCGATGAAGAAC  
ACAACGGATCTCTTGGCTCCAGCATCGATGAA  
CGGATCTCTTGGCTCCAGCATCGATGAAGAAC  
GATGAAGAACGAGCGAAACCGGATGTAAT
```

# PURPOSE

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



# Material and Methods



V line  
30 animals

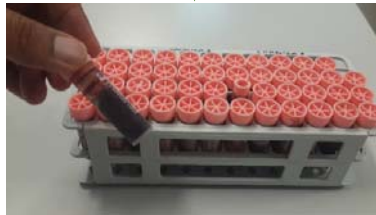


High UC line  
90 animals



Low UC line  
69 animals

DNA Isolation



200,000 SNPs - Affymetrix

Genotyping and  
Quality Control

# 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**

# Material and Methods: GWAS

- Bayes B Method.

$$y = Xb + \sum_{j=1}^k z_j \alpha_j \delta_j + e$$

Residual effect

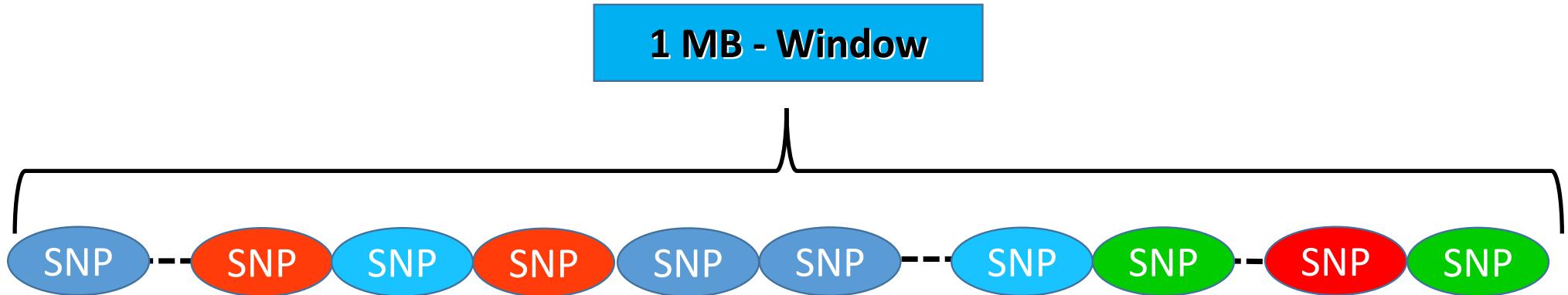
GenSel Software

Genetic effect  
(SNPs)

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

# 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.





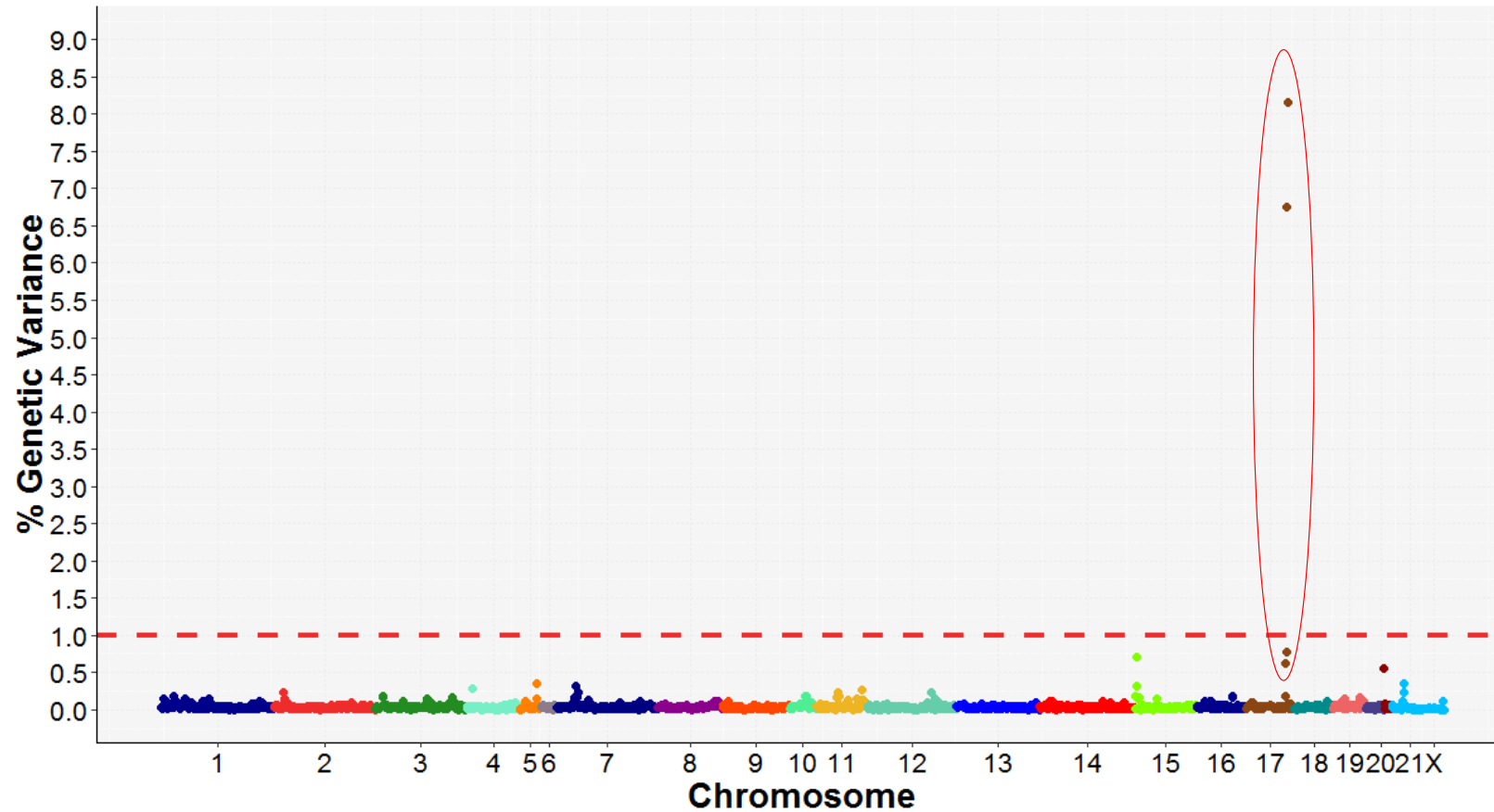
# Results

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

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

# Results

- Manhattan plot for total number born



# Results

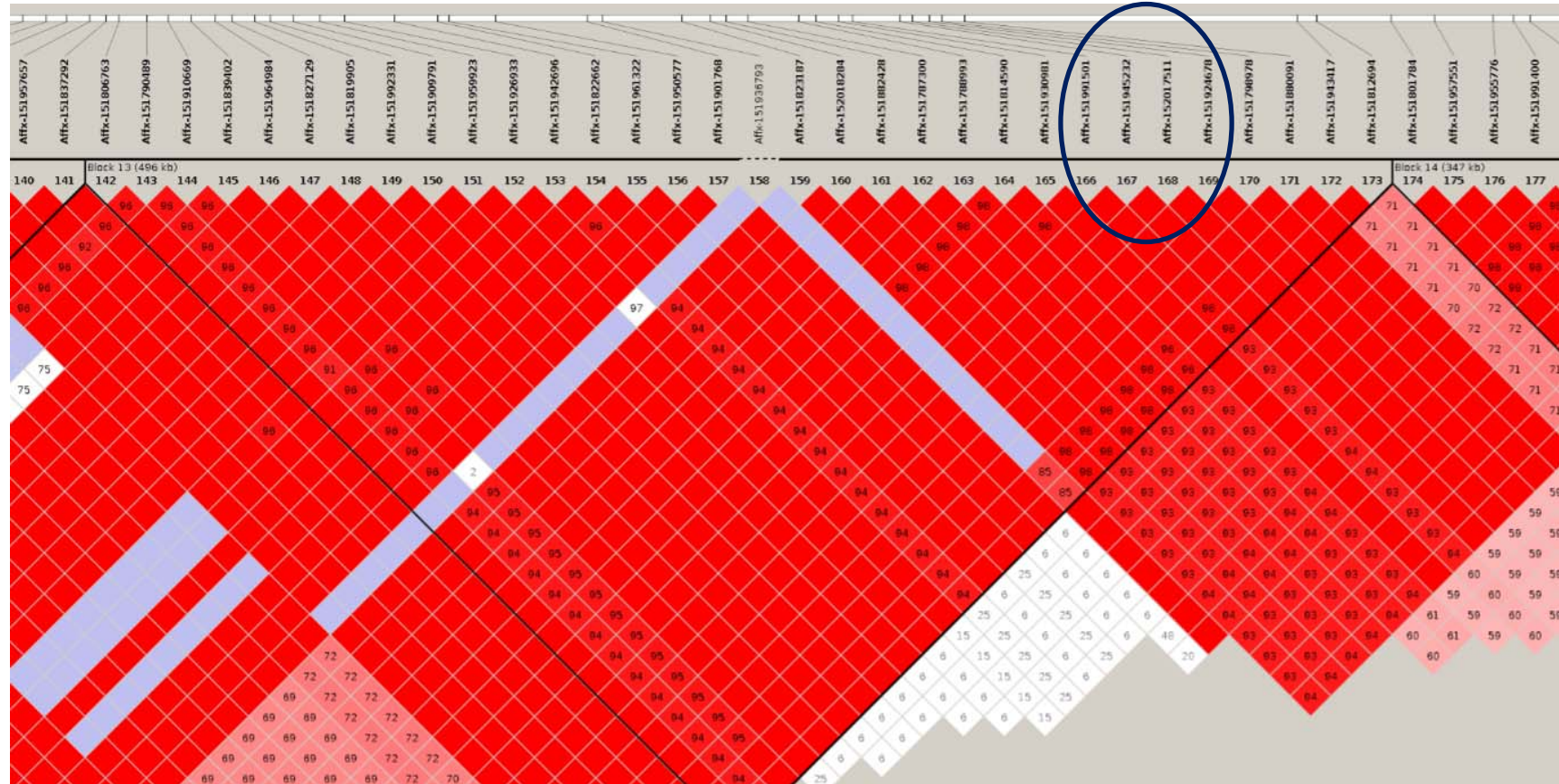
- On chromosome 17

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



# 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.

# Thank you

