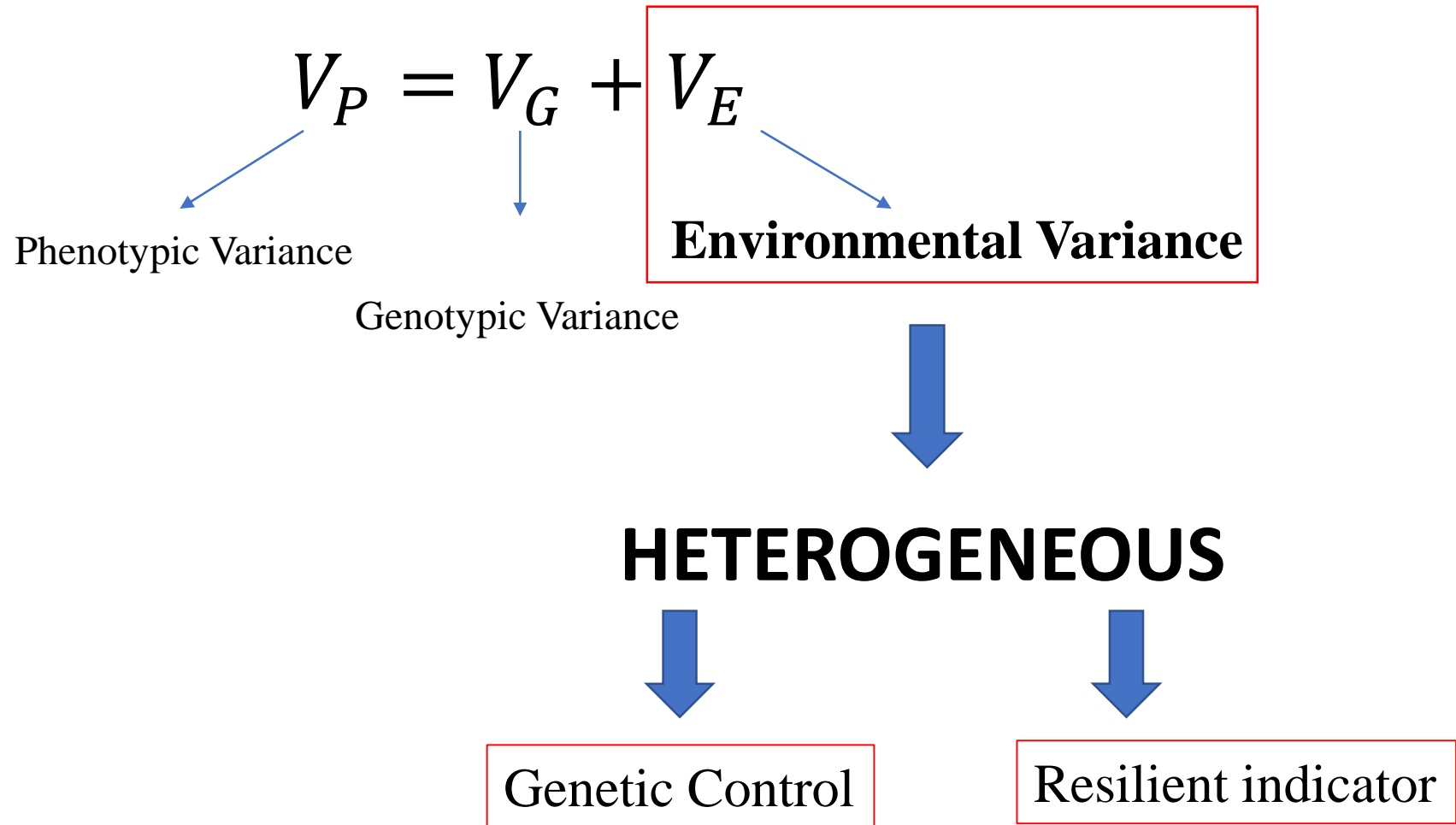


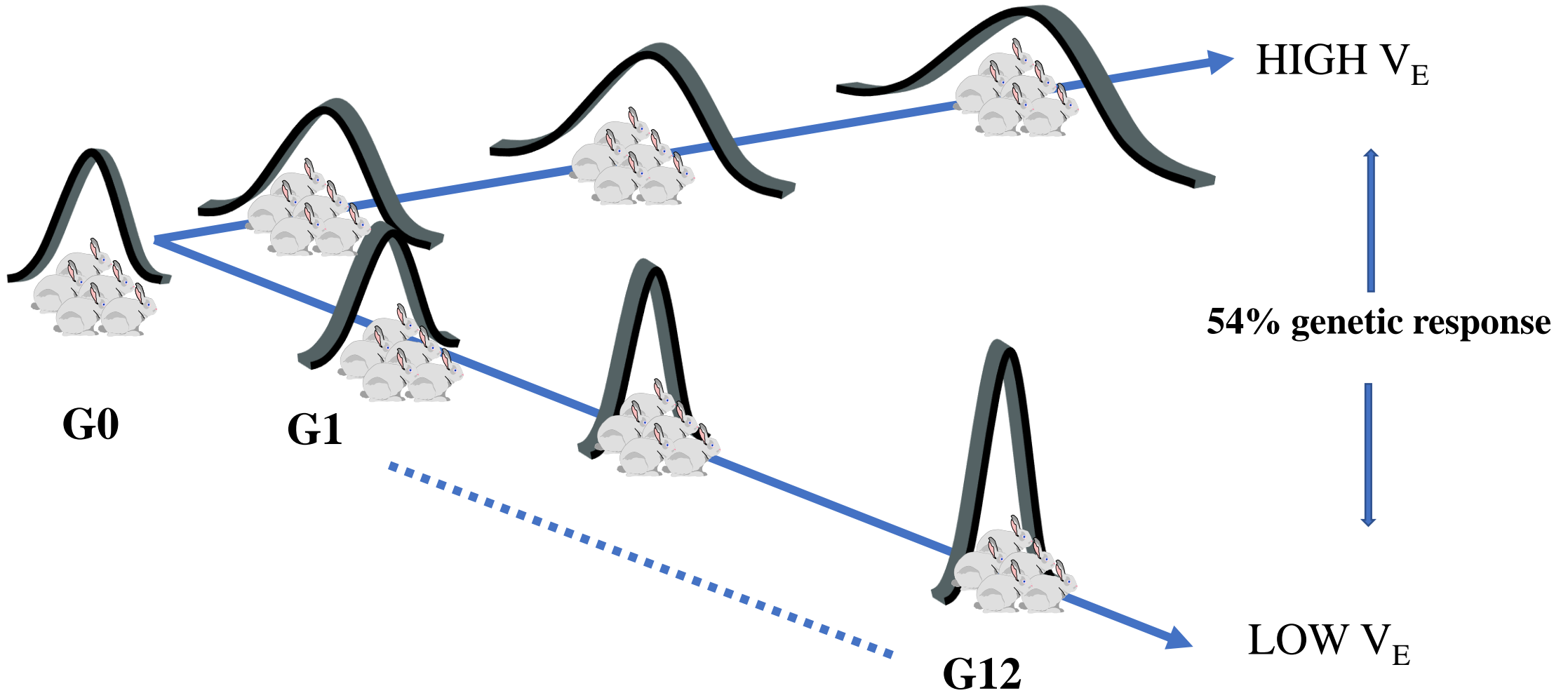


Unraveling genomic regions associated with environmental variance of litter size in rabbits

Casto-Rebollo, C., Argente, M.J., García, M.L., Pena, R., Fontanesi, L., Blasco, A.
& Ibáñez-Escriche, N.



Divergent selection experiment for V_E of litter size



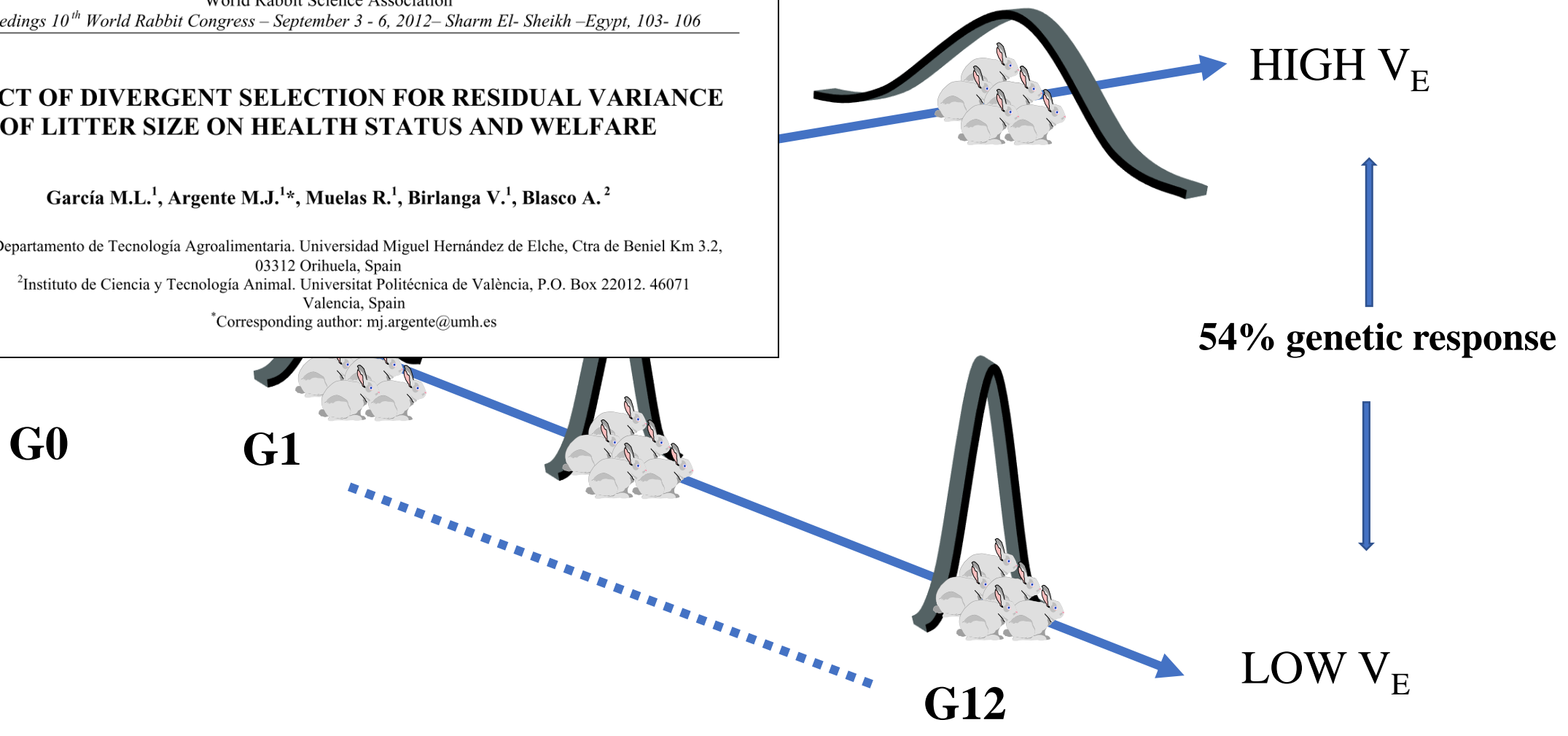
Divergent selection experiment for V_E of litter size

World Rabbit Science Association
 Proceedings 10th World Rabbit Congress – September 3 - 6, 2012– Sharm El- Sheikh –Egypt, 103- 106

EFFECT OF DIVERGENT SELECTION FOR RESIDUAL VARIANCE OF LITTER SIZE ON HEALTH STATUS AND WELFARE

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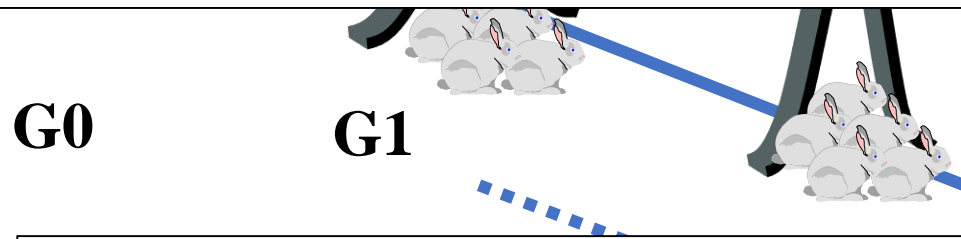
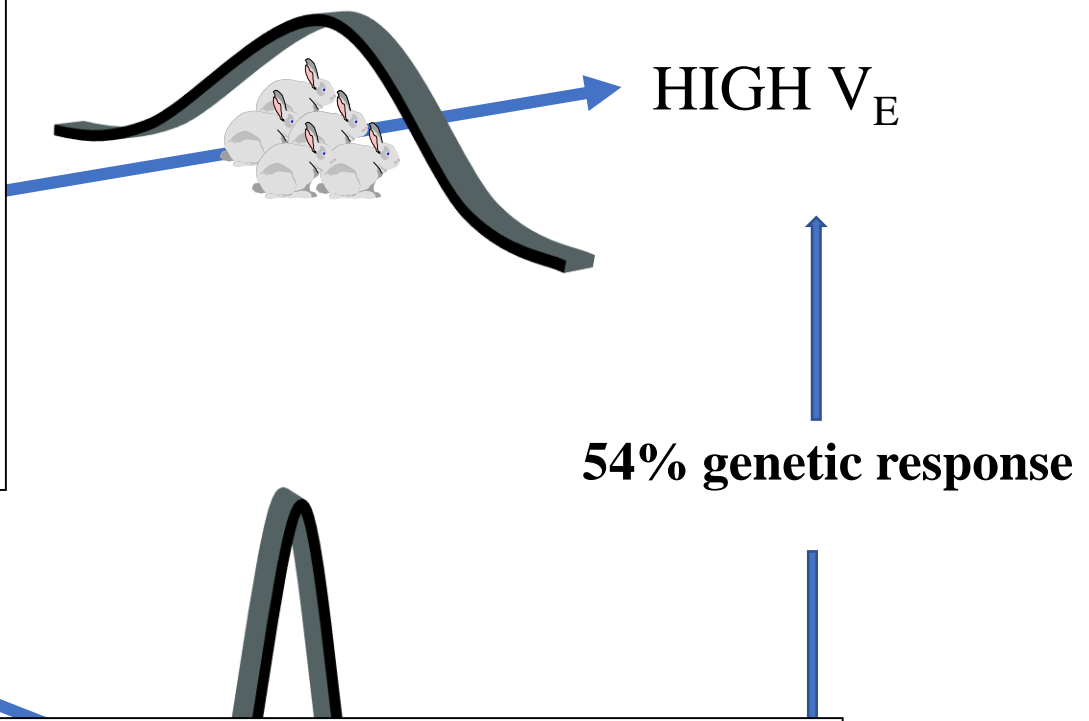
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Proceedings, 10th World Congress of Genetics Applied to Livestock Production

Effect of Selection for Residual Variance of Litter Size on Hematology Parameters as Immunology indicators in Rabbits

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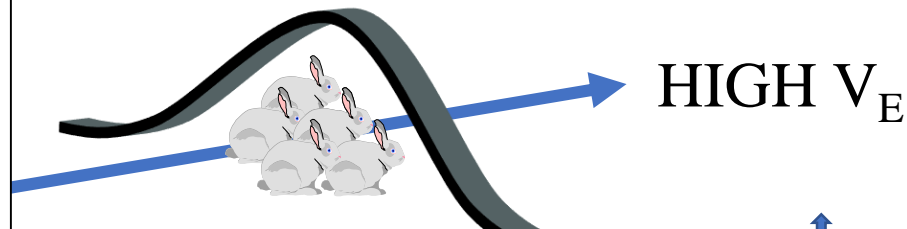
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Selection for Genetic Environmental Sensitivity of Litter Size Changes Resilience in Rabbits

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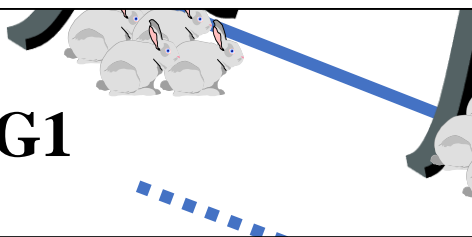
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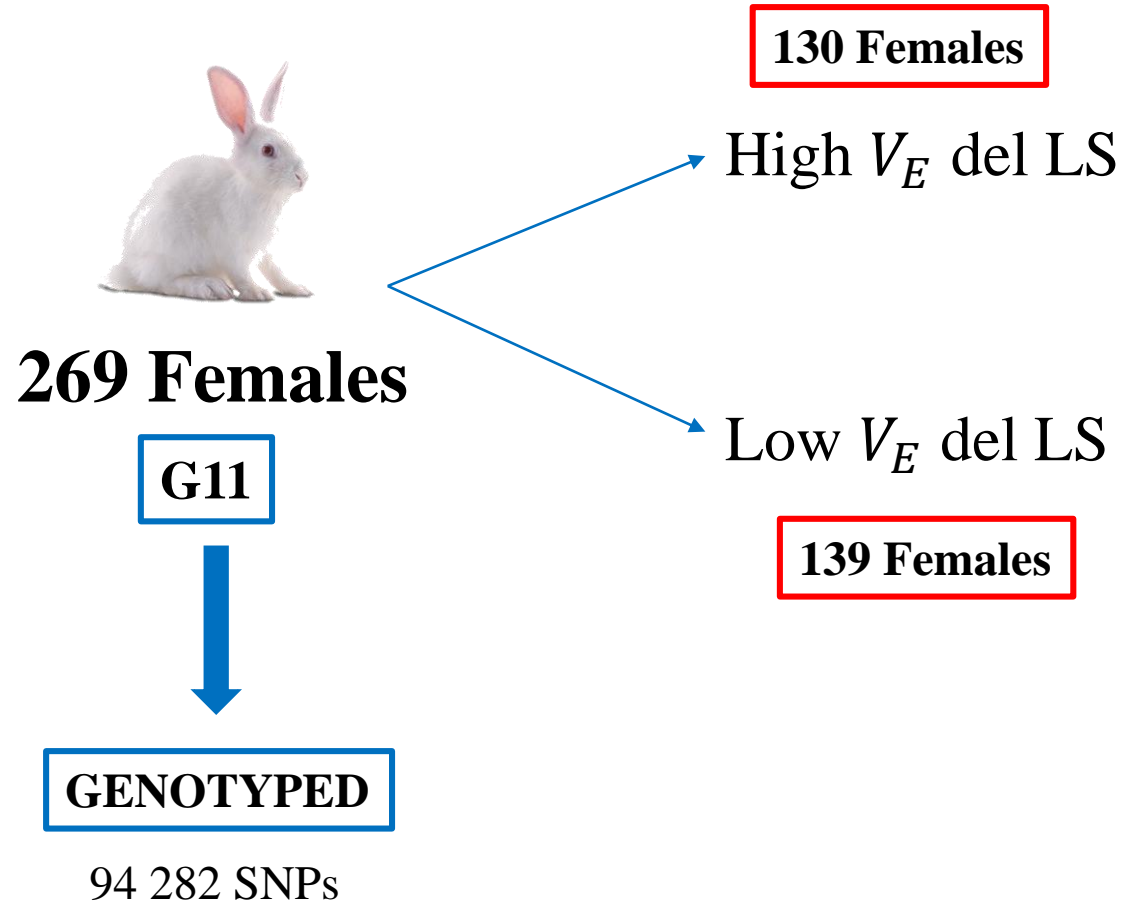
¹Universidad Miguel Hernández de Elche, Orihuela, Spain, ² Slovak University of Agriculture in Nitra, Nitra, Slovak Republic, ³Universitat Politècnica de València, Valencia, Spain.

E

Identify genomic regions associated with
 V_E of litter size (LS)

Divergent selection experiment for V_E of litter size

GENOTYPE



Divergent selection experiment for V_E of litter size

1. LITTER SIZE PRE-CORRECTED

$$LS = YS + PL + e$$

2. WITHIN-DOE VARIANCE OF LITTER SIZE

$$V_E = \frac{1}{n+1} \sum_{i=1}^n (x_i - \bar{x})^2$$

SMR

Single Marker Regression

$$y = Xb + z_j\alpha_j + Zg + e$$

Fixed Effect (points to Xb)
Allelic substitution effect (points to α_j)
Genotype (points to z_j)
Genetic effect (points to Zg)
 $N(\mathbf{0}, GRM\sigma_g^2)$

p-value < 1E-5

p-value < 1E-4

**Associated
genomic regions**

MMR

Multiple Marker Regression

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

SNPs

Effect
1- π

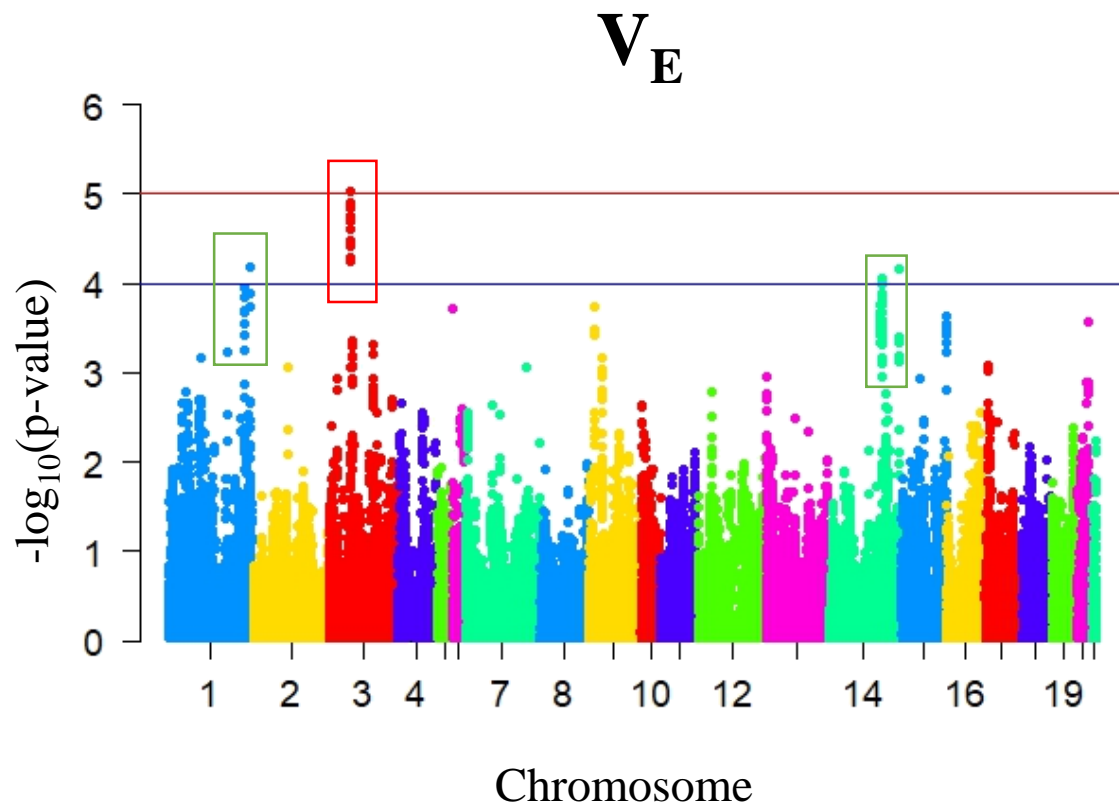
\emptyset Effect
 $\pi=0.9997$

BF > 10

V_G windows > 1%

SMR

Single Marker Regression



p-value=9,46E-6

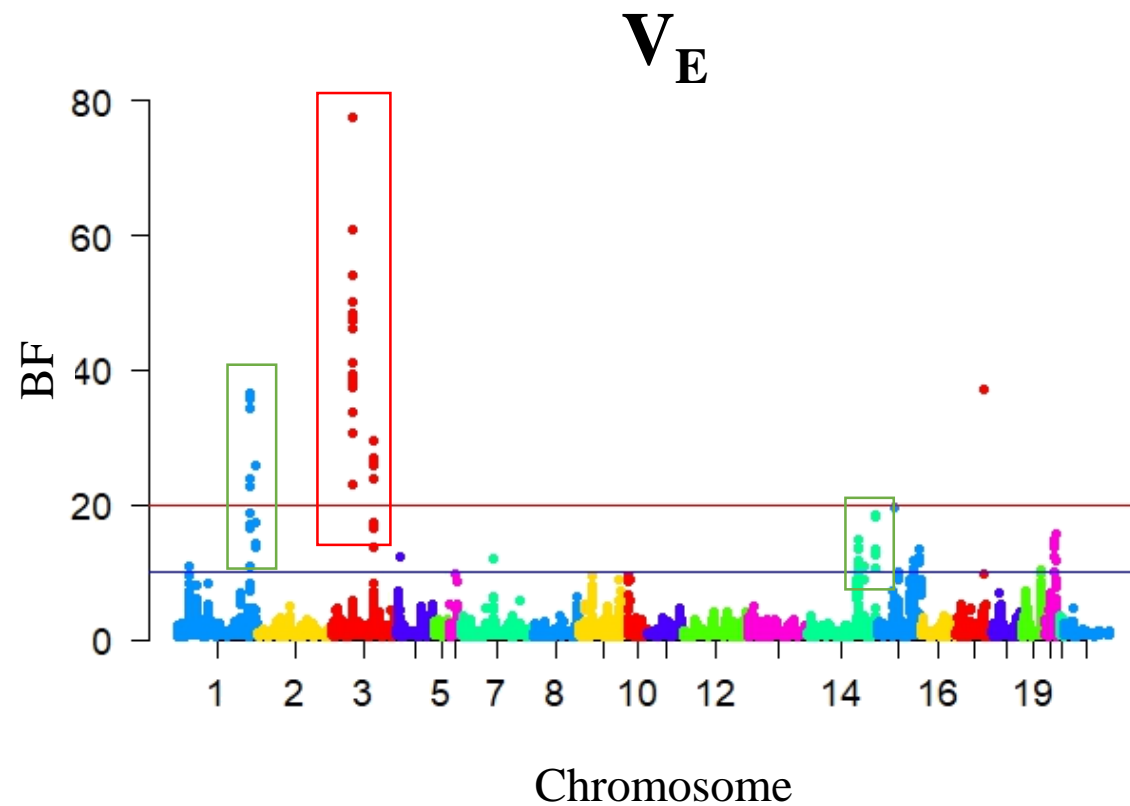
Affx-151984290

MMR

Multiple Marker Regression

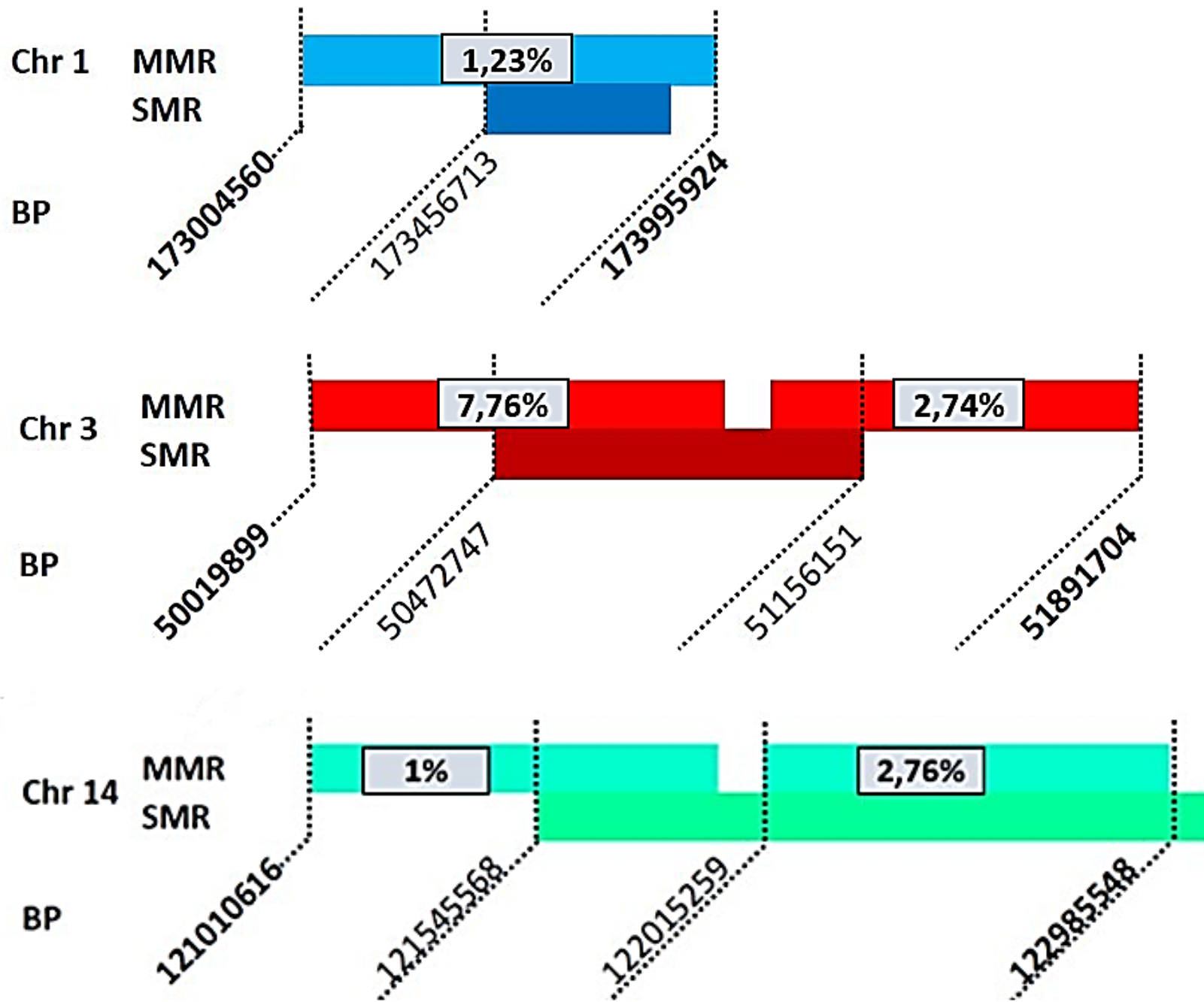


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BF=77,40

RESULTS



CHR	PB	GENES
1	173004560-173995924	<i>KIAA1549L</i> , <i>C11orf91</i> , <i>CD59</i> , <i>LMO2</i> , <i>CAPRIN1</i> , <i>NAT10</i> , <i>ABTB2</i> , <i>CAT</i> , <i>ELF5</i> , <i>EHF</i>
3	50019899-51891704	<i>CPNE3</i> , <i>CNGB3</i> , <i>CNBD1</i> , <i>SLIT3</i> , <i>SPDL1</i> , <i>DOCK2</i> , <i>FAM196B</i> , <i>FOXI1</i> , <i>LCP2</i> , <i>KCNMB1</i> , <i>KCNIP1</i>
14	121545568-122985548	<i>DCBLD2</i> , <i>ST3GAL6</i> , <i>CPOX</i> , <i>GPR15</i> , <i>CLDND1</i> , <i>GABRR3</i> , <i>ARL6</i> , <i>EPHA6</i>

Highlighted Genes

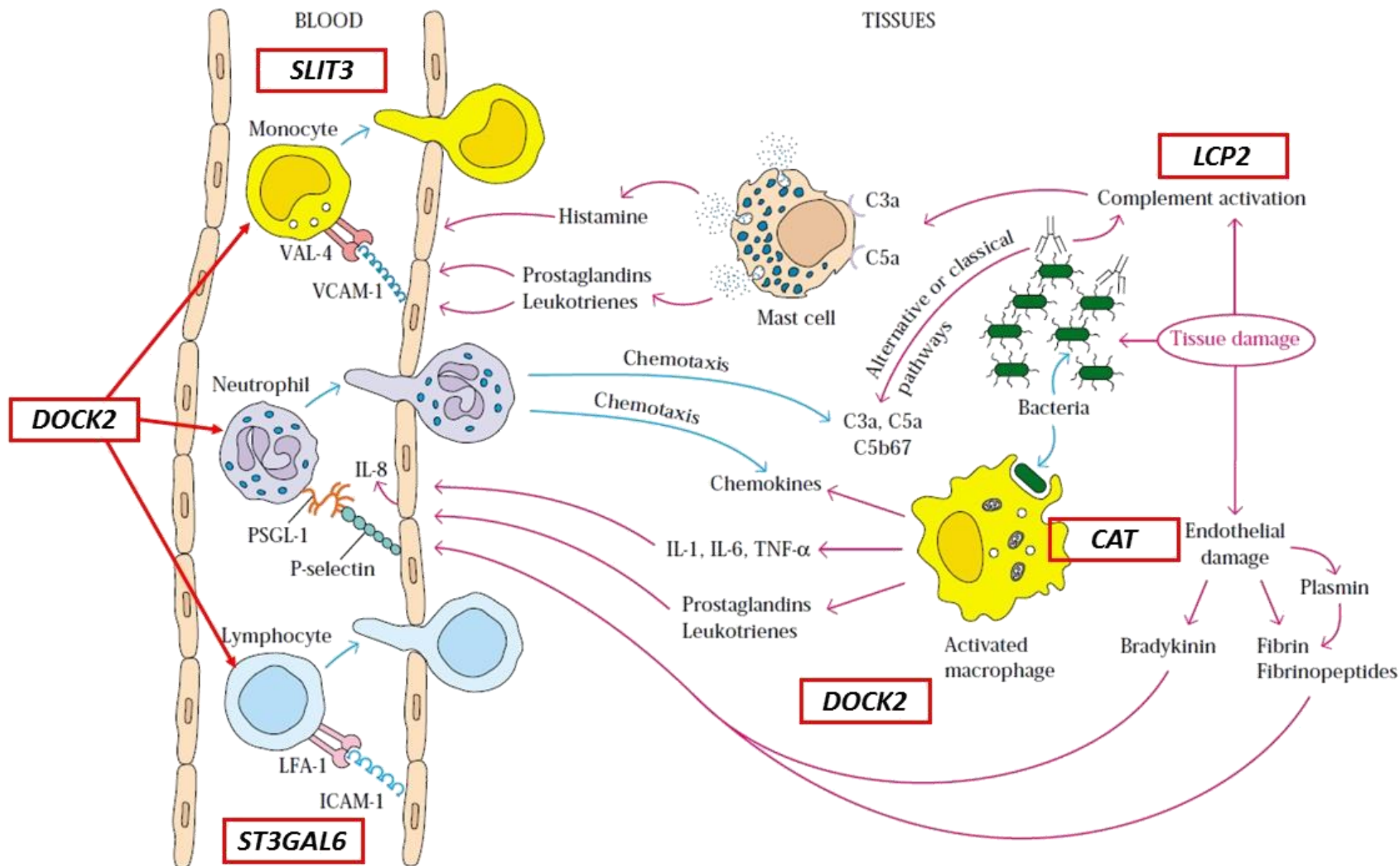


Inflammatory response

Inflammatory Response



First line of Defense



Genomic Regions Associated with V_E of Litter size



DOCK2, CAT, ST3GAL6, SLIT3, LMO2, LCP2 and CD59



Inflammatory response



Resilience of Animals

THANK YOU FOR YOUR ATTENTION



Genomic Regions Associated with V_E of Litter size



DOCK2, CAT, ST3GAL6, SLIT3, LMO2, LCP2 and CD59



Inflammatory response



Resilience of Animals