

Supplementary Material:

Additive and Dominant genomic analysis for litter size in pure and crossbred Iberian pigs.

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Table S1. REML estimates \pm standard error (SE) of the additive genotypic (co)variances for Number Born Alive (NBA).

	Entrepelado	Crossbred	Retinto
Entrepelado	0.147 \pm 0.156	0.202 \pm 0.169	0.184 \pm 0.150
Crossbred	-	0.477 \pm 0.241	0.410 \pm 0.172
Retinto	-	-	0.359 \pm 0.183

Table S2. REML estimates \pm standard error (SE) of the dominance genotypic (co)variances for Number Born Alive (NBA).

	Entrepelado	Crossbred	Retinto
Entrepelado	0.293 \pm 0.216	0.286 \pm 0.182	0.204 \pm 0.173
Crossbred	-	0.282 \pm 0.188	0.202 \pm 0.177
Retinto	-	-	0.155 \pm 0.205

Table S3. REML estimates \pm standard error (SE) of the permanent environmental and residual variances for Number Born Alive (NBA).

Variances ¹	Entrepelado	Crossbred	Retinto
σ_S^2	0.111 \pm 0.111	0.004 \pm 0.022	0.252 \pm 0.126
σ_E^2	2.820 \pm 0.099	4.385 \pm 0.152	3.468 \pm 0.125

¹ σ_S^2 : Sow permanent environment variance; σ_E^2 : Residual variance.

Table S4. GO (Gene Ontology) terms for biological process of the proposed candidate genes.

Gene	Name	Biological process	
<i>BCO1</i>	<i>Beta-carotene oxygenase 1</i>	GO:0001523 GO:0042574 GO:1901810	- retinoid metabolic process - retinal metabolic process - beta-carotene metabolic process
<i>GCSH</i>	<i>Glycine cleavage system protein H</i>	GO:0019464	- glycine decarboxylation via glycine cleavage system
<i>ATMIN</i>	<i>ATM interactor</i>	GO:0010628 GO:0044458 GO:0045893 GO:0045944 GO:1902857	- positive regulation of gene expression - motile cilium assembly - positive regulation of transcription, DNA-templated - positive regulation of transcription by RNA polymerase II - positive regulation of non-motile cilium assembly
<i>CENPN</i>	<i>Centromere protein N</i>	GO:0007059 GO:0051382	- chromosome segregation - kinetochore assembly
<i>DYNLRB2</i>	<i>Dynein light chain roadblock-type 2</i>	GO:0007018	- microtubule-based movement
<i>CD38</i>	<i>CD38 molecule</i>	GO:0050794	- regulation of cellular process
<i>FGFBP1</i>	<i>Fibroblast growth factor binding protein 1</i>	GO:0090050 GO:1903589	- positive regulation of cell migration involved in sprouting angiogenesis - positive regulation of cell migration involved in sprouting angiogenesis
<i>PROM1</i>	<i>Prominin 1</i>	GO:0045494 GO:0060042 GO:0060219 GO:0072112 GO:0072139 GO:2000768	- Photoreceptor cell maintenance - retina morphogenesis in camera-type eye - camera-type eye photoreceptor cell differentiation - glomerular visceral epithelial cell differentiation - glomerular parietal epithelial cell differentiation - positive regulation of nephron tubule epithelial cell differentiation
<i>TAPT1</i>	<i>Transmembrane anterior posterior transformation 1</i>	GO:0045724 GO:0048706 GO:0048856	- positive regulation of cilium assembly - embryonic skeletal system development - anatomical structure development
<i>LDB2</i>	<i>LIM domain binding 2</i>	GO:0045944 GO:0044089 GO:0043549 GO:0035019 GO:0030334 GO:0010669 GO:0006357 GO:0001942	- positive regulation of transcription by RNA polymerase II - positive regulation of cellular component biogenesis - regulation of kinase activity - somatic stem cell population maintenance - regulation of cell migration - epithelial structure maintenance - regulation of transcription by RNA polymerase II - hair follicle development
<i>FGF5</i>	<i>Fibroblast growth factor 5</i>	GO:0023019 GO:0010001 GO:0008543 GO:0008284	- signal transduction involved in regulation of gene expression - glial cell differentiation - fibroblast growth factor receptor signaling pathway - positive regulation of cell population proliferation
<i>TAOK1</i>	<i>TAO kinase 1</i>	GO:1901985 GO:0097194 GO:0070050 GO:0046330 GO:0032874 GO:0016310 GO:0007095 GO:0007026 GO:0006974	- positive regulation of protein acetylation - execution phase of apoptosis - neuron cellular homeostasis - positive regulation of JNK cascade - positive regulation of stress-activated MAPK cascade - phosphorylation - mitotic G2 DNA damage checkpoint signaling - negative regulation of microtubule depolymerization - cellular response to DNA damage stimulus

		GO:0006468 GO:0000226	- protein phosphorylation - microtubule cytoskeleton organization
<i>GIT1</i>	<i>GIT ArfGAP 1</i>	GO:2000300 GO:0106015 GO:0099171 GO:0090063 GO:0071222 GO:0061743 GO:0048666 GO:0048013 GO:0045820 GO:0045454 GO:0032691 GO:0032465 GO:0007626 GO:0007420 GO:0001957	- regulation of synaptic vesicle exocytosis - negative regulation of inflammatory response to wounding - presynaptic modulation of chemical synaptic transmission - positive regulation of microtubule nucleation - cellular response to lipopolysaccharide - motor learning - neuron development - ephrin receptor signaling pathway - negative regulation of glycolytic process - cell redox homeostasis - negative regulation of interleukin-1 beta production - regulation of cytokinesis - locomotory behavior - brain development - intramembranous ossification
<i>ANKRD13B</i>	<i>ankyrin repeat domain 13B</i>	GO:0002091	- negative regulation of receptor internalization

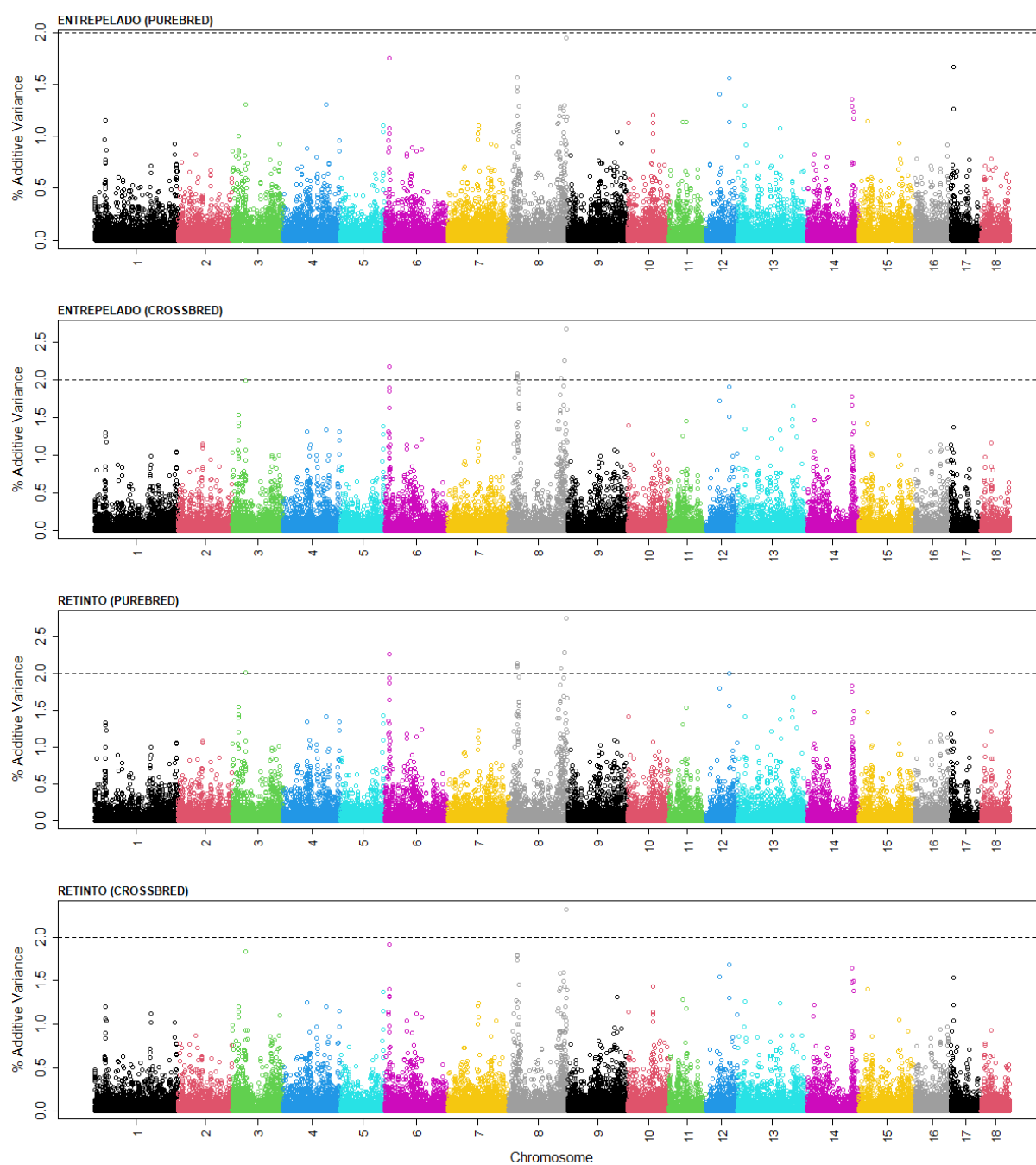


Figure S1. Distribution of the percentage of the additive genetic variance explained by genomic segments of 30 SNPs within the autosomal genome of purebred and crossbred performance for Number Born Alive (NBA) in the Entrepelado and Retinto varieties.

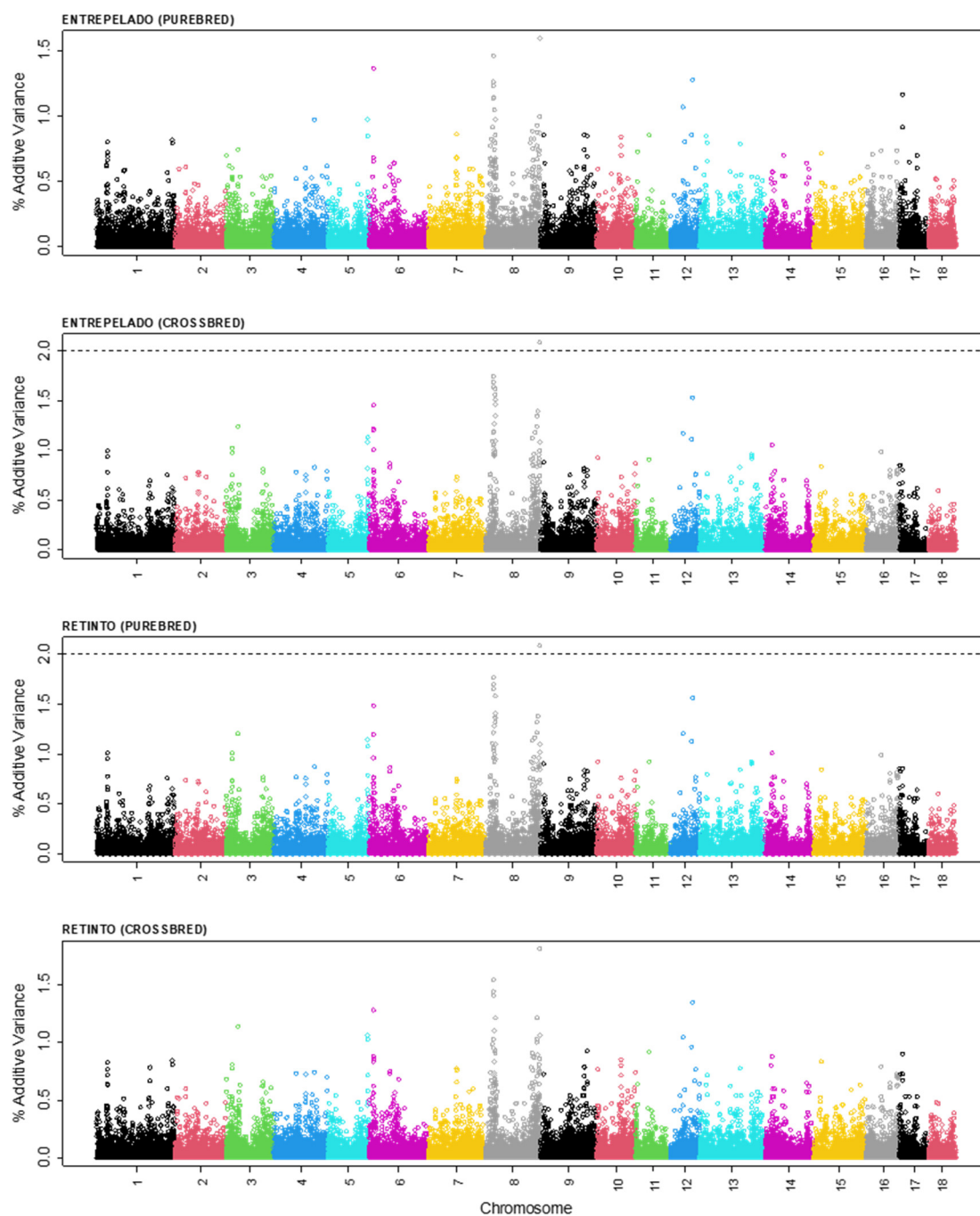


Figure S2. Distribution of the percentage of the additive genetic variance explained by genomic segments of 20 SNPs within the autosomal genome of purebred and crossbred performance for Total Number Born (TNB) in the Entrepelado and Retinto varieties.

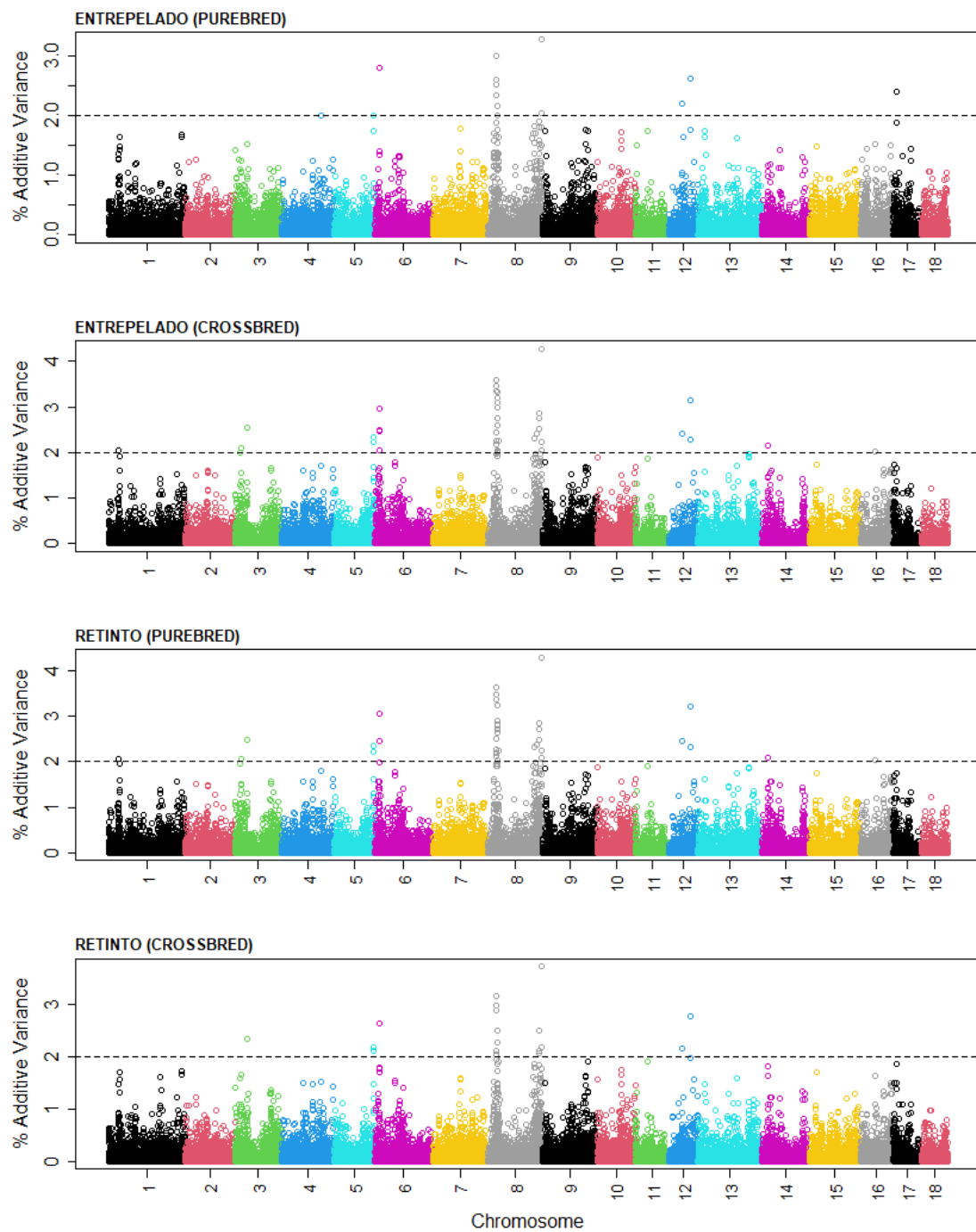


Figure S3. Distribution of the percentage of the additive genetic variance explained by genomic segments of 40 SNPs within the autosomal genome of purebred and crossbred performance for Total Number Born (TNB) in the Entrepelado and Retinto varieties.