

Table S1. Genes located within the genomic regions with an average F_{ST} over the 99.9th percentile between Entrepelado and Retinto.

SSC	Base pairs	Genes
8	56983392-60232132	-
15	80515676-86990138	<i>OLA1, SP9, CIR1, SCRN3, GPR155, CHRNA1, CHN1, ATF2, ATP5MC3, LNPB, EVX2, HOXD13, HOXD12, HOXD11, HOXD10, HOXD9, HOXD8, MIR10B, HOXD4, HOXD3, HOXD1, MTX2, HNRNPA3, NFE2L2, AGPS, RBM45, OSBPL6, PRKRA, PJKK, FKBP7, PLEKHA3, SESTD1, ZNF385B, CWC22, UBE2E3, ITGA4, CERKL, NEUROD1</i>
17	42130987-42480736	<i>RALGAPB, ADIG, SLC32A1, ACTR5, PPP1R16B, DHX35</i>

Table S2. Genes located within the genomic regions with an average F_{ST} over the 99.9th percentile between Entrepelado and Torbiscal.

SSC	Base pairs	Genes
2	60177754-61303666	<i>COLGALT1, PGLS, SLC27A1, NXNL1, MVB12A, BST2, CCDC194, PLVAP, GTPBP3, ANO8, DDA1, MRPL34, ABHD8, ANKLE1, BABAM1, USHBP1, OCEL1, USE1, MYO9B, HAUS8, F2RL3, SIN3B, NWD1, SMIM7, SLC35E1, CHERP, CALR3, EPS15L1, KLF2, APIM1, CIB3, HSH2D, RAB8A, TMP4</i>
2	71588075	<i>CERS4, FBN3, ELAVL1, TIMM44, CTXN1, SNAPC2, TGFBF3L, MAP2K7, LRRC8E, EVI5L, CD209, FCER2, TRAPPC5, PCP2, RETN, STXBP2, PET100, XAB2, CAMSAP3, PNPLA6, MCOLN1, ZNF358, TEX45, PEX11G, INSR</i>
2	92958395-93175114	<i>EDIL3</i>
6	104376948-105459825	<i>NDC80, METTL4, ADCYAP1, YES1, ENOSF1, TYMS, CLUL1, CETN1, COLEC12</i>
10	36887963-37186755	-
14	45509383	<i>MN1, PITPNB, TTC28, CHEK2, HSCB, CCDC117</i>

Table S3. Genes located within the genomic regions with an average F_{ST} over the 99.9th percentile between Retinto and Torbiscal.

SSC	Base pairs	Genes
1	77056462-77472299	<i>CDK19, AMD1, GTF3C6, RPF2, SLC16A10, MFSD4B, REV3L, TRAF3IP2, FYN</i>
1	90748703-90896710	<i>SENP6, FILIP1, TMEM30A, COX7A2, COL12A1</i>
1	141989498-142042139	<i>UBE3A, SNORD115</i>
6	104376948-105459825	<i>NDC80, METTL4, ADCYAP1, YES1, ENOSF1, TYMS, CLUL1, CETN1, COLEC12</i>
8	89447995-89679243	<i>PCDH18</i>
12	28731262-28831639	<i>CA10</i>