ANNEX 3

The porcine 2, 4-dienoyl-CoA reductase gene (DECR) maps to chromosome 4 and lies within the confidence interval of the FAT1 locus.

Manuscrit enviat a Mammalian Genome

El gen de la dienoil CoA reductasa *DECR* intervé en la β-oxidació dels àcids grassos insaturats (Kunau i Dommes, 1978). Hi ha descrit un cas en humà d'un individu que presentava un defecte en l'activitat de l'enzim *DECR* que provocava una degradació incompleta de l'àcid linoleic, i la producció d'un metabòlit desconegut anteriorment (Roe *et al.*, 1990). Aquest gen fou caracteritzat i mapejat en humà per Helander *et al*. (1997), i el varen posicionar en la banda citogenètica del cromosoma 8 (Hsa8) q21.3.

Com l'annex 1 i 2 descriuen, es va trobar un QTL al cromosoma 4 porcí amb importants efectes sobre la deposició de greix dorsal i el percentatge d'àcid linoleic en aquest teixit. La posició del QTL, segons la localització citogenètica dels microsatèl·lits que el flanquejaven (S0001 i S0214), va ser determinada en la banda cromosòmica Ssc4p1.3-q2.1. En realitzar la comparació entre els mapes físics d'humà i de porc, amb la intenció de detectar gens candidats que poguessin explicar els efectes del QTL es va observar que la posició del gen *DECR* era perfectament compatible amb la del QTL porcí. Així, tant la posició genètica com la funció fisiològica d'aquest gen en el metabolisme lipídic varen perfilar-lo com un clar gen candidat.

Inicialment, era necessari dissenyar uns *primers* que permetessin l'amplificació d'una regió polimòrfica d'aquest gen en porcí. La millor aproximació per a obtenir-los fou la comparació de les seqüències del gen en humà i en ratolí per a determinar quines regions presentaven identitat en la seqüència i per tant es podia considerar que estaria conservada en el porc. Així, es va aconseguir amplificar un fragment que incloï a la major part de l'exó dos del gen, el qual presentava una substitució nucleotídica (G→T) en la posició 76 bp del fragment amplificat que implicava un canvi aminoacídic (Val→Leu) en la posició 61 de la proteïna madura. Aquest polimorfisme fou identificat i caracteritzat en la població del pedigree utilitzat en la present Tesi mitjançant l'enzim de restricció *Bfa*I.

Posteriorment, es va realitzar el mapa de lligament del pedigree amb els microsatèl·lits analitzats prèviament i el gen *DECR* mitjançant l'opció *build* del programa CRI-MAP. Segons el mapa de lligament obtingut, el gen *DECR* podia estar localitzat en dues posicions probables, a 68,3 cM, (*LOD score* = -836,02) entre els microsatèl·lits S0001 i SW839, o a 79,5 cM, (*LOD score* = -835,46) entre SW839 i S0214.

Per a confirmar la posició obtinguda en el mapa de lligament es van realitzar les reaccions d'amplificació amb uns *primers* específics de l'exó dos del gen *DECR* de porc, en un pannell de cèl· lules híbrides irradiades de hàmster/porc. Els resultats obtinguts van posicionar el gen entre els microsatèl· lits S0001 i SW839, confirmant la posició 68,3 cM com a la més probable d'albergar al gen.

Així, a més d'haver posicionat aquest gen en l'espècie porcina per primera vegada, es confirmava que el gen *DECR* és un candidat per al QTL amb efecte sobre el percentatge d'àcid linoleic del cromosoma 4 descrit en l'annex 2, ja que la posició més probable del gen es trobava inclosa en l'interval de confiança d'aquest (67-87 cM).

The porcine *2, 4-dienoyl-CoA reductase* gene *(DECR)* maps to chromosome 4 and lies within the confidence interval of the *FAT1* locus

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Keywords: pig, restriction fragment length polymorphism, 2, 4-dienoyl-CoA reductase, β-oxidation of fatty acids, somatic cell hybrid mapping

The organoleptic properties of meat are greatly affected by the kind and percentage of intramuscular fat. For instance, the addition of conjugated linoleic acids to the diet modify carcass composition in pigs by diminishing fat deposition and the proportion of fat to lean tissue (Ostrowska et al. 1999). Moreover, the activity of several lipogenic enzymes, such as acetyl-coenzyme A carboxylase, malic enzyme and glucose-6-phosphate dehydrogenase, increases when linoleic acid is supplied in the feed (Mourot et al. 1994). Recently, a QTL with a significant effect on the percentage of linoleic acid in subcutaneous adipose tissue was mapped to pig chromosome 4 in an Iberian x Landrace cross (Pérez-Enciso et al. 2000). The Iberian allele was associated to a 1.5% decrease in linoleic acid content and the QTL explained as much as 25% of the phenotypic differences observed between these two commercial breeds. The coincidence between the chromosomal location of this QTL and the FAT1 QTL (Andersson et al. 1994, Marklund et al. 1999), which has a major effect on fat deposition, was very suggestive and prompted the characterization of candidate genes mapping to this region and being involved in lipid metabolism.

The 2,4-dienoyl-CoA-reductase (*DECR*) gene encodes an enzyme which participates in the β-oxidation pathway by catalyzing the reduction of *trans*-2-*cis*-4-dienoyl-CoA to 3 -enoyl-CoA (Kunau and Dommes, 1978). DECR has a homotetrameric structure and it is mostly expressed in liver, heart, pancreas and kidney. The deficiency of this enzyme causes a lethal syndrome characterized by hypocarnitinemia, hyperlysinemia and the presence of 2-trans-4-cis-decadienoylcarnitine in urine and blood of the affected patients (Roe et al. 1990). The presence of this metabolite is due to the incomplete oxidation of the linoleic fatty acid. In human, the transcription unit of the *DECR* gene includes 10 exons and 9 introns of variable size which span 30 Kb and maps to 8q21.3 (Helander et al. 1997). Interestingly, comparative mapping between pig and human predicts that this gene should map to the porcine chromosomal region which contains the linoleic QTL (Goureau et al. 1996).

The chromosomal location of the human *DECR* gene and its crucial role in linoleic fatty acid metabolism made evident the need of characterizing with more detail the molecular features of this gene in pig. Our work had two main objectives (1) Search polymorphisms which may be helpful in linkage mapping and which might be associated to variations in fatty acid linoleic content; and (2) Determine the precise location of this gene in the porcine genome by physical and linkage mapping. We designed two primers complementary to the 5' and 3' ends of exon 2 by aligning the human (accession number U94981) and rat (accession number D00569) *DECR* sequences and finding conserved regions. We obtained a 190 bp amplified product encompassing 2bp intron 1 and 188 bp exon 2. This amplicon was cloned and sequenced forward and reverse in seven different individuals corresponding to four Iberian and three Landrace pigs (see Figure 1). A Blast search of the GenBank revealed that the porcine sequence had a 85% nucleotide similarity with respect to its human ortholog. Further, we detected the existence of one polymorphic *Bfa*I restriction site generated by a nucleotide substitution (GTAG, allele 1 ⇒ CTAG, allele 2) at position 114 of the PCR product (allele 1: 190 bp, allele 2: 114-76 bp). This mutation causes a Val (allele 1) ⇒ Leu (allele 2) amino acid substitution at position 61 of the mature protein (see Figure 2). The segregation of this polymorphism in a previously described three generation Iberian x Landrace pedigree (Pérez-Enciso et al. 2000) was consistent with autosomal codominant inheritance. In addition, we demonstrated that this polymorphism segregates in several pig breeds (see Figure 2).

Physical mapping of the *DECR* locus was performed by using the irradiated pig/hamster somatic cell hybrid panel kindly provided by D. Milan and described in the ImpRH *Webpage* (*http://imprh.toulouse.inra.fr*) (Milan et al. 2000). We used pig specific primers to amplify 148 bp of the second exon of the pig DECR gene (FW: 5'-TTGTATCAAAGCACTGAAGCTTTT, REV: 5'-TGGACAGATGAGTTGTCATTCTT). The final PCR volume was 15 µl and contained 1 x PCR buffer, 2mM $MgCl_2$, 100 µM dNTPs, 0.5 µM of each primer and 25 ng of genomic DNA.

The cycling parameters were 94º G-2 min and 32 cycles of 94º C-1 min, 63º C-1 min and 72º G-1 min plus a final extension step of 72º C-5 min. The PCR analysis were performed in duplicate to avoid false positive/negative results and the double-checked data were analysed with the ImpRH mapping tool (Milan et al. 2000). Our results indicated that the *DECR* gene maps to the *SW1003* microsatellite, near the centromere of pig chromosome 4. We confirmed this chromosomal location by linkage mapping. The typing of the 32 F_0, 65 F_1 and 343 F_2 individuals produced in the Iberian x Landrace cross was achieved by amplifying the second exon of the *DECR* gene and digesting the amplicon with *Bfa*I. Previously, these pigs had been typed for seven microsatellites (*SW2404, S0301, S0001, SW839, S0214, SW445* and *S0097*) which were highly polymorphic and evenly spaced along pig chromosome 4 (Pérez-Enciso et al. 2000). *DECR* was mapped by using CRIMAP and the two most likely positions turned out to be 68.3 cM and 79.5 cM with likelihoods -836.022 and -835.46, respectively. The ambiguity in the linkage analysis was attributable to the low informativity of this polymorphism in this cross. Nevertheless, the first position was compatible with the RH map and thus we conclude that the position of the *DECR* gene lies between microsatellites S0001 and SW839 (see Figure 3). Interestingly, this location coincides well with the confidence interval of the QTL detected in our cross affecting the linoleic percentage in backfat (67-85 cM) (Clop et al., manuscript in preparation). Moreover, the position of the *DECR* gene lies within the interval of the *FAT1* QTL (Andersson et al. 1994, Marklund et al. 1999) which may contain one pleiotropic gene or several genes strongly involved in lipid metabolism and fat deposition.

In conclusion, our results confirm the *DECR* gene as a strong positional candidate gene for explaining the variation of linoleic acid in the subcutaneous adipose tissue. A high content of linoleic fatty acid in backfat tissue (above 150 g linoleic acid/kg fat) has a deep impact in meat quality since fat becomes softer and more susceptible to oxidative rancidity (Whittemore 1993). These features highlight the interest of dissecting the genetic architecture of this trait. Currently,

we are refining the mapping of this gene with additional microsatellites and characterizing a panel of exonic and intronic polymorphisms which may assist us in the search of mutations closely related to the function of this enzyme.

Acknowledgments

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Figure legends

Figure 1. Nucleotide and amino acid sequence of the amplified second exon of the porcine 2, 4-dienoyl-CoA reductase gene (*DECR*, allele 2) (accession number AF335499). The primers (indicated in italics) were FW: 5'-AGTTTTTCAGTTATGGGACAAAAA-3' and REV: 5'-CACTGAGCACCTAGGCTG GA-3'. The amplification of the 190 bp fragment was performed in an MJ Research PTC device. The PCR reactions contained 1x PCR buffer, 1.5 mM $MgCl_2$, 100 µM dNTPs, 0.5 µM of each primer, 200 ng of genomic DNA and 1.25 U of Taq DNA polymerase (Ecogen) in a 50 µl final volume. The thermal profile was 94ºC/1.5 min - 55ºC/2 min - 72ºC/2.5 min for cycles. Seven amplified products were cloned in the pCR2.1-TOPO vector (Invitrogen) and sequenced forward and reverse with the ABI Prism cycle sequencing kit (Applied Biosystems). The polymorphic G/C position corresponds to codon 61 and it is indicated in bold. The *Bfa*I restriction site is underlined.

Figure 2. *Bfa*I restriction polymorphism in the porcine *DECR* gene and allelic frequencies in several pig breeds. Eleven µl of the PCR were digested with 22.5 U of *Bfa*I restriction enzyme (New England Biolabs) at 37º C overnight and electrophoresed in 2% high resolution agarose gels stained with ethidium bromide. Alternatively, we used the *Snapshot* kit (Perkin-Elmer) for typing this polymorphism

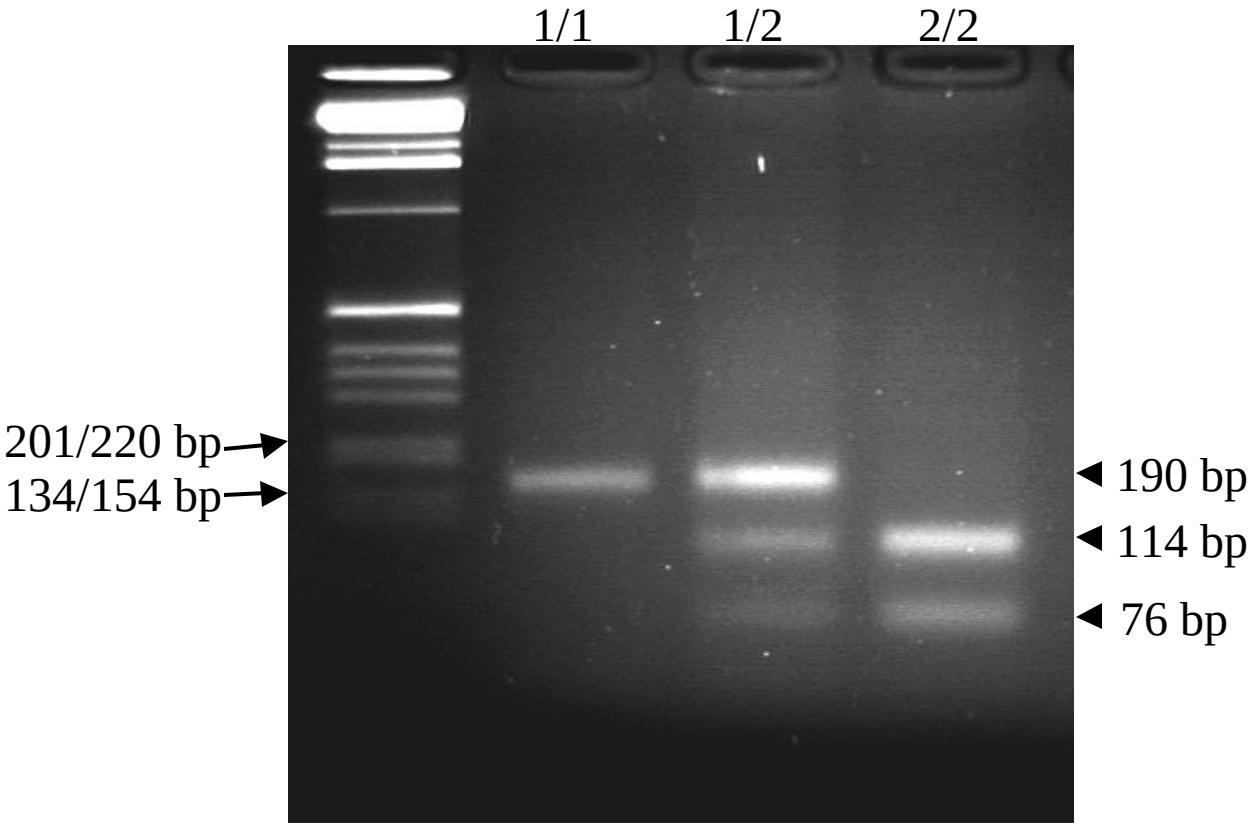
Figure 3. Linkage mapping of the *DECR* gene. The *DECR* gene lies between microsatellites *S0001* and *SW839* on pig chromosome 4 (68.3 cM), close to the position (75 cM) where the highest effect of the linoleic QTL was found.

32 40
*AG TTT TTC AGT TAT GGG ACA AAA A*ATA TTG TAT CAA AGC ACT GAA GCT TTT CCG
L Y Q S T E A F P

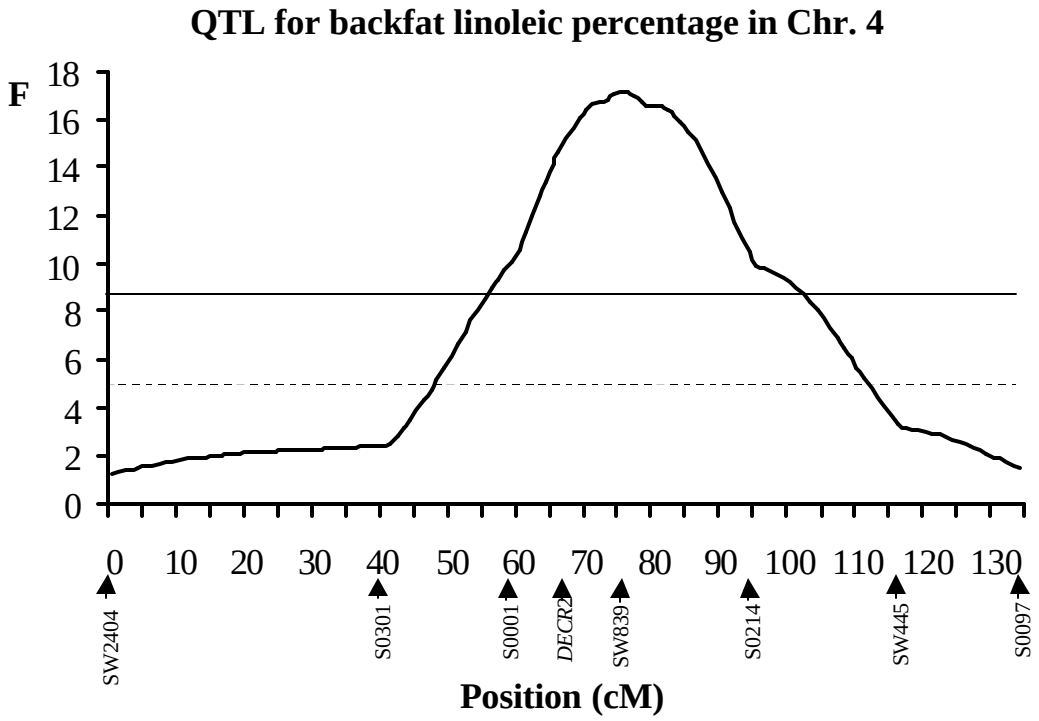
50
TCT AAG TCC TTC CCA CCC TTT CAA AAA GTG ATG CTG CCA CCA AAT ACT TTT CAA
S K S F P P F Q K V M L P P N T F Q

60 70
GGA AAA **C**↓TA GCA TTC ATT ACC GGG GGA GGA ACT GGC ATT GGT AAA AGA ATG
G K L A F I T G G G T G I G K R M

ACA ACT CAT CTG *TCC AGC CTA GGT GCT CAG TG*
T T H L

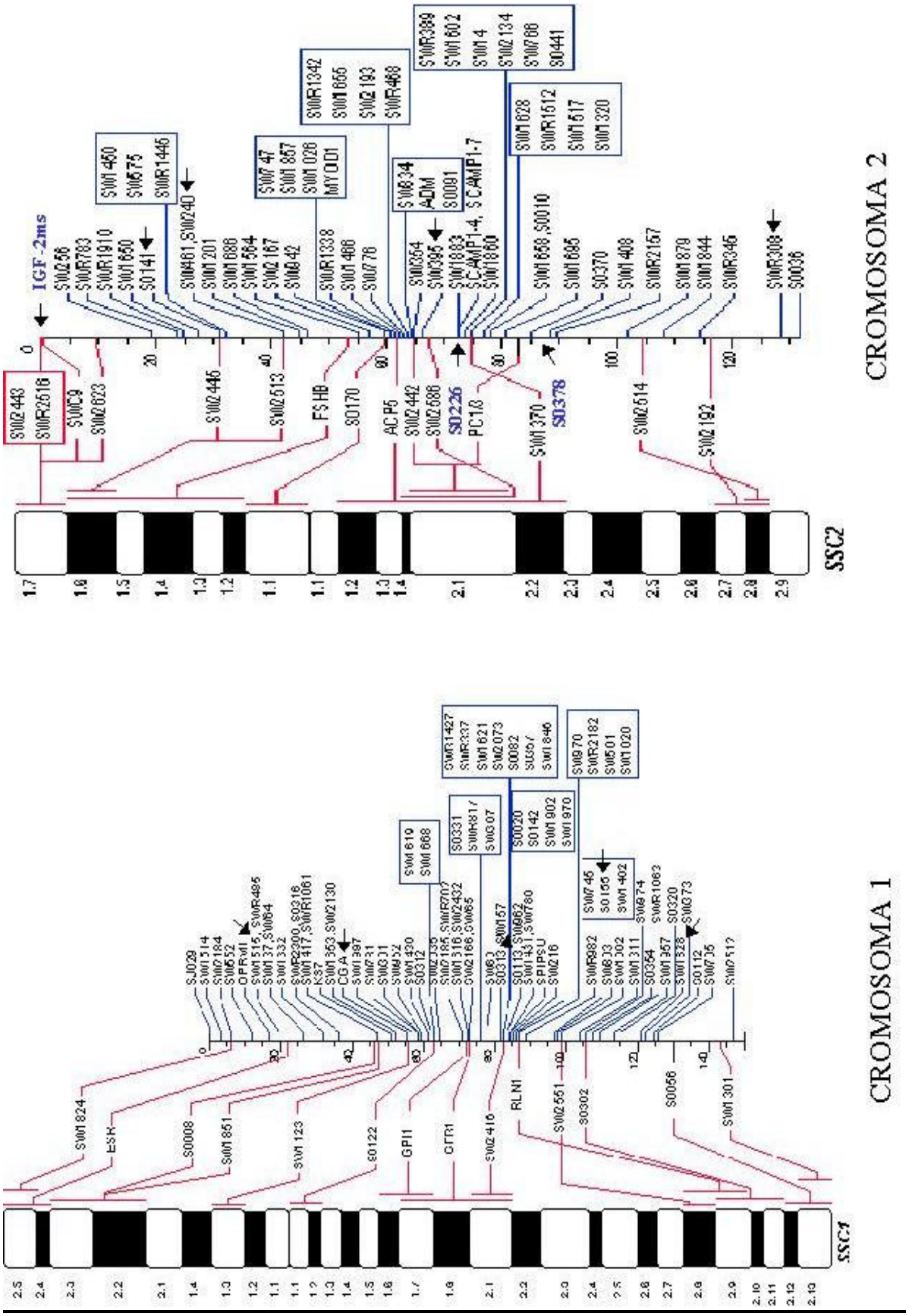


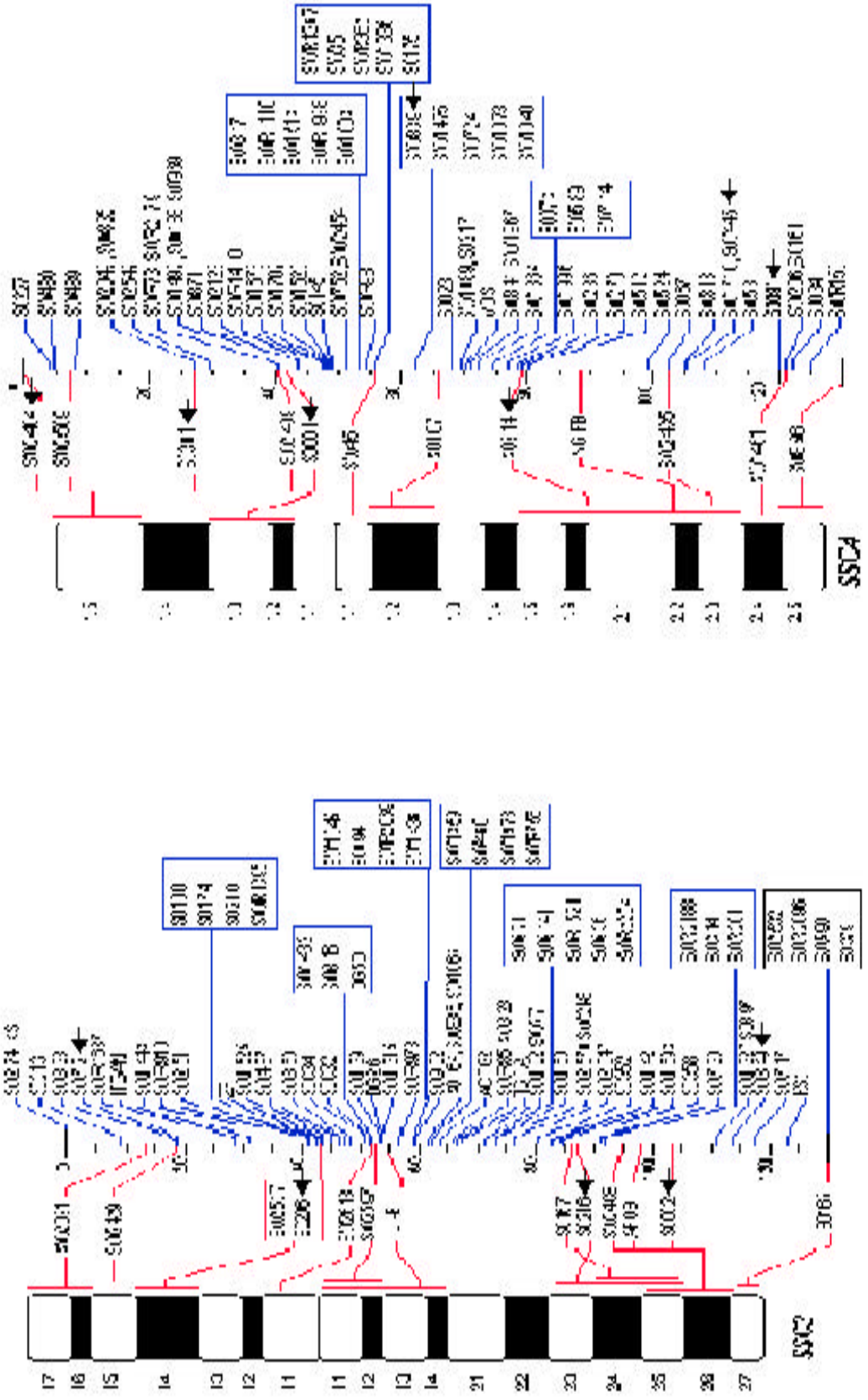
Breed	n	Allele 1	Allele 2
Large White	20	0.10	0.90
Landrace	110	0.74	0.26
Pietrain	20	0.55	0.45
Iberian	49	0.34	0.66

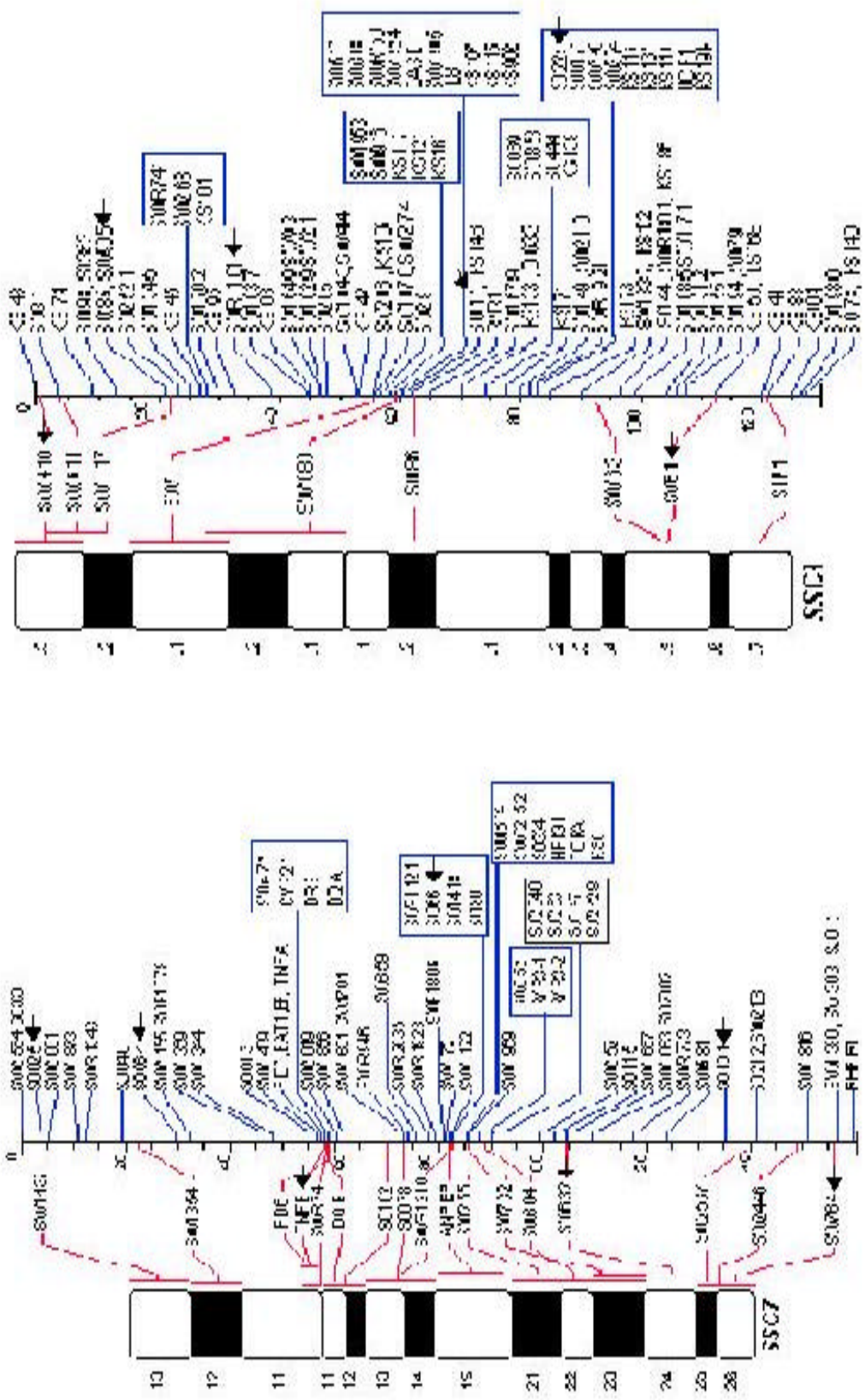

QTL for backfat linoleic percentage in Chr. 4
F
18
16
14
12
10
8
6
4
2
0
0
10
20
30
40
50
60
70
80
90
100
110
120
130
SW2404
S0301
S0001
DECR2
SW839
S0214
SW445
S0097
Position (cM)

ANNEX 4

Mapes de lligament obtinguts segons el USDA-MARC Swine Genome Map (www.genome.iastate.edu/maps/marcmap/html).

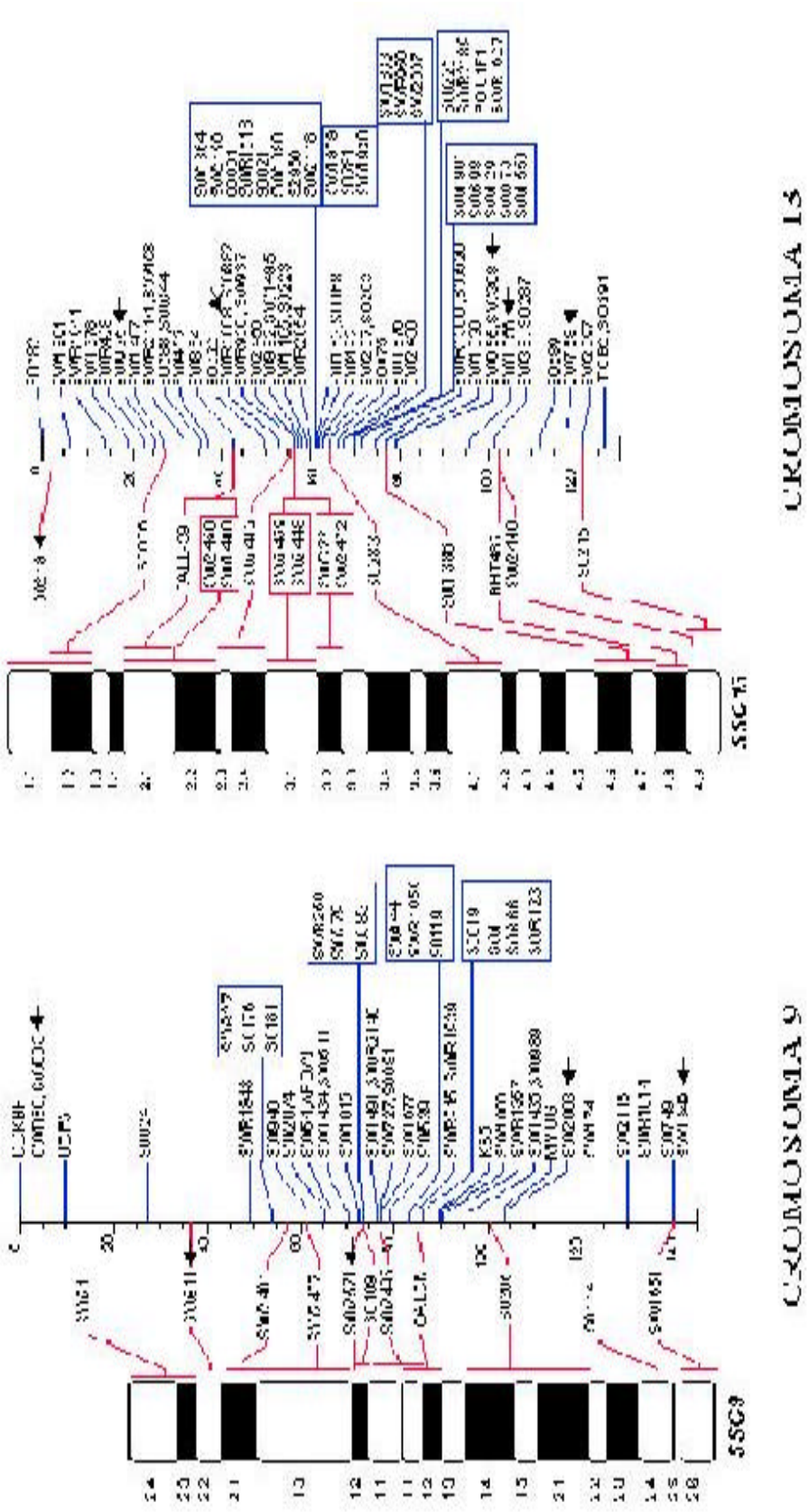

CROMOSOMA 2
SSC2
IGF-2ms
SW2443
SW0R2516
SW0C9
SW2623
SW2445
SW2513
FS HB
SD170
AC P5
SW2442
SW2588
SD226
PC18
SW1370
SD378
SW2514
SW2192
SW1450
SW575
SW0R1446
SW0461,SW0240
SW1201
SW1688
SW1564
SW2167
SW842
SW0R1338
SW1466
SW778
SW747
SW1857
SW1026
MYOD1
SW0R1342
SW1855
SW2193
SW0R468
SW634
ADM
SW354
SW395
SW1883
SCAMP1-4, SCAMP1-7
SW1860
SW0R389
SW1602
SW14
SW2134
SW788
SD441
SW1628
SW0R1612
SW1617
SW1320
SW1658 ,SD010
SW1885
SD370
SW1408
SW0R2157
SW1879
SW1844
SW0R345
SW0R308
SD036
CROMOSOMA 1
SSC1
SW1824
ESR
SD008
SW1851
SW1123
SD122
GPI1
GTR1
SW2416
RLN1
SW2551
SD302
SD056
SW1301
SJ029
SW1514
SW2184
SW652
OPRM1
SW1515 ,SW0R495
SW137 ,SW064
SW1332
SW0R2300, SD316
SW1417 ,SW0R1061
KS7
SW1363 ,SW2130
CGA
SW1397
SW731
SW831
SW852
SW1430
SD312
SW2135
SW2185 ,SW0R702
SW1316 ,SW2432
SW2166 ,SW065
SW619
SW668
SW963
SW157
SD313
SD331
SW0R931 /
SW307
SW0R1427
SW0R337
SW1621
SW2073
SD092
SW1846
SD113 ,SW062
SW1431 ,SW780
SPIPSU
SW216
SD020
SD142
SW1902
SW1970
SW970
SW0R2182
SW501
SW1020
SW0R982
SW833
SW1302
SW1311
SW745
SD155
SW1402
SW974
SD354
SW1357
SW1328
SW0R1063
SD320
SW0G73
SD112
SW735
SW2512


CROMOSOMA 4
CROMOSOMA 3



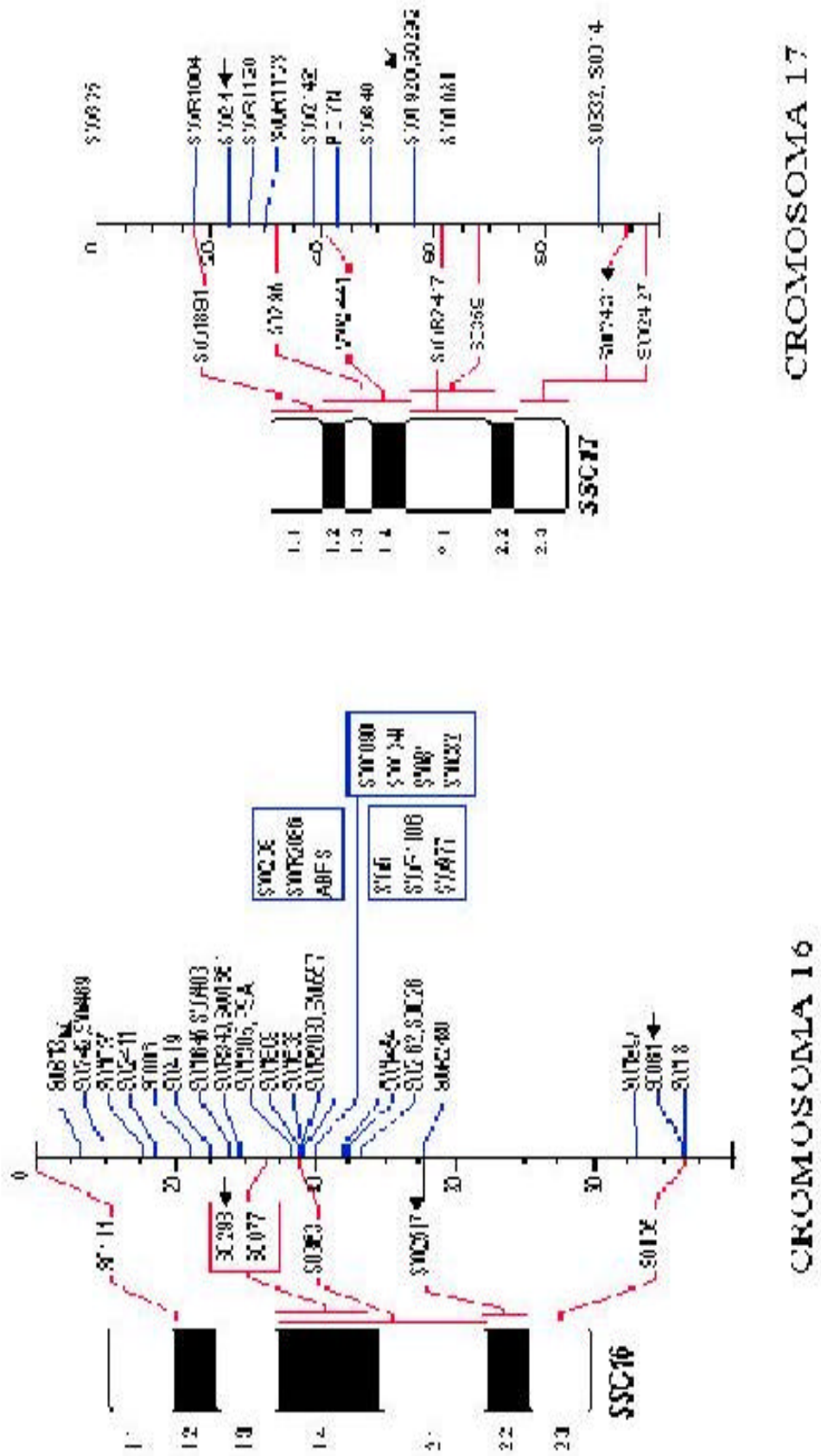
CROMOSOMA 8

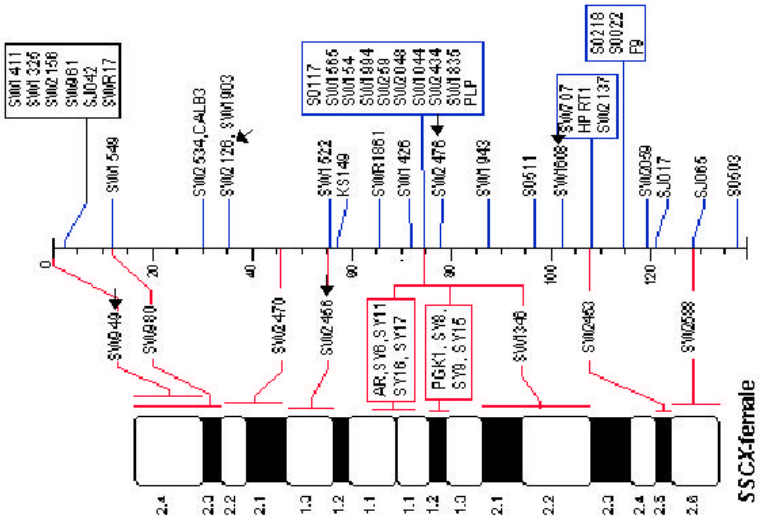
CROMOSOMA 7



CHROMOSOMA 13

CHROMOSOMA 9


CROMOSOMA 17
SSC17
CROMOSOMA 16
SSC16


SWR411
SW1325
SW2156
SW9861
SJD42
SWR17
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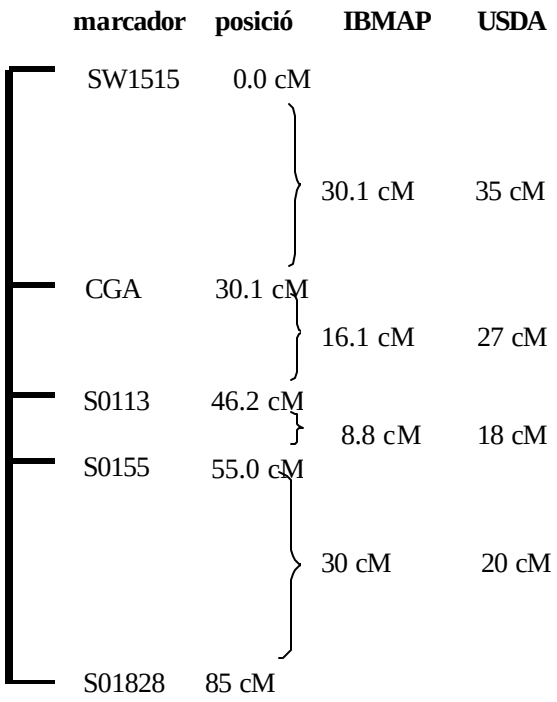
SW2534_CALB3
SW2126, SW1903
SW1522
KS149
SWR1861
SW1426
SW2476
SW1943
S0511
SW1508
SW707
HPRT1
SW2137
S0218
S0022
F9
SW2059
SJD17
SJD65
S0503
S0117
SW1565
S0154
SW1884
SW269
SW2048
SW1044
SW2434
SW1835
PLP
SW949
SW980
SW2470
SW2466
AR, SY8, SY11
SY16, SY17
PGK1, SY9,
SY10, SY15
SW1345
SW2463
SW2598
0
20
40
60
80
100
120
2.4
2.3
2.2
2.1
1.3
1.2
1.1
1.1
1.2
1.3
2.1
2.2
2.3
2.4
2.5
2.6
SSCX-female

CROMOSOMA X

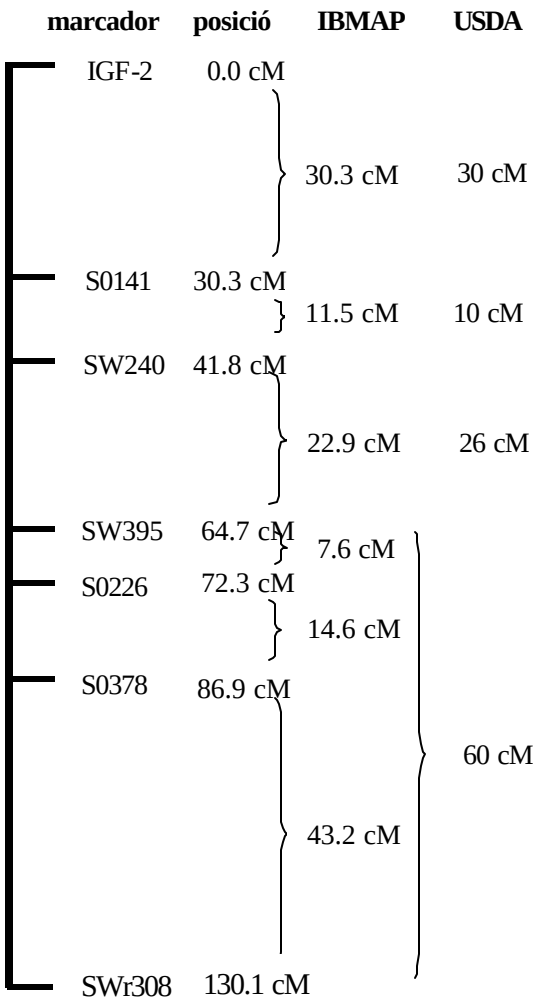
ANNEX 5

Construcció dels mapes de lligament obtinguts en el projecte IbMap, indicant la posició relativa dels marcadors en els cromosomes (posició), la distància de recombinació entre els diferents marcadors (IbMap) i la distància relativa entre loci indicada en el mapa genètic del USDA MARC (USDA). El LOD score de cada grup de lligament es reflexa al peu de cada cromosoma.



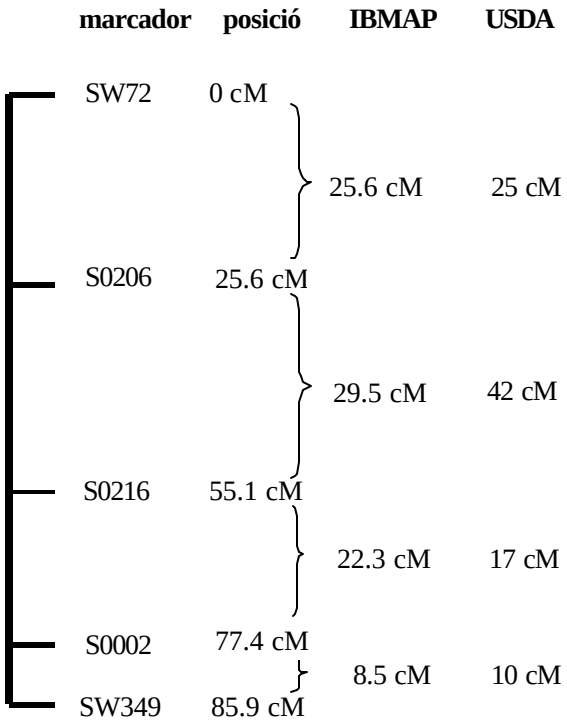
LOD score = -446.97

CROMOSOMA 1



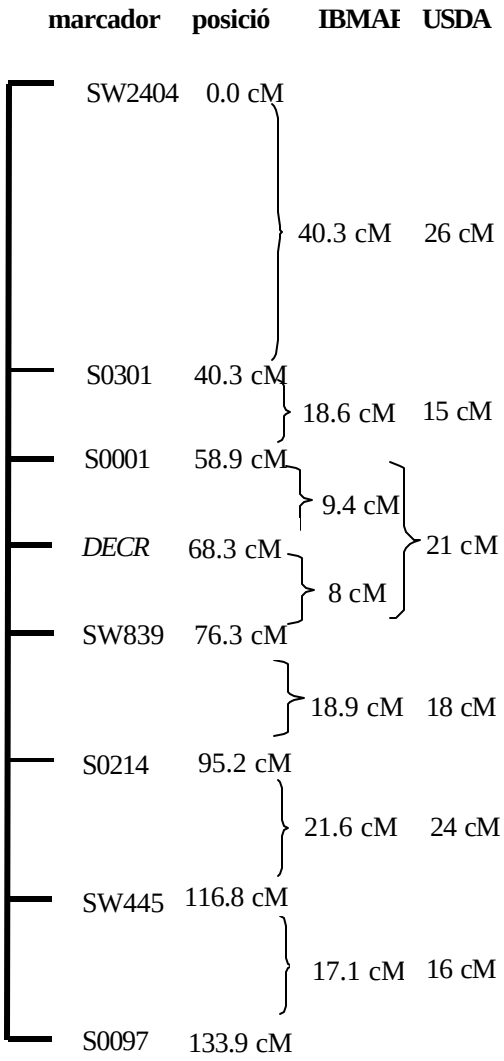
LOD score = -780.82

CROMOSOMA 2



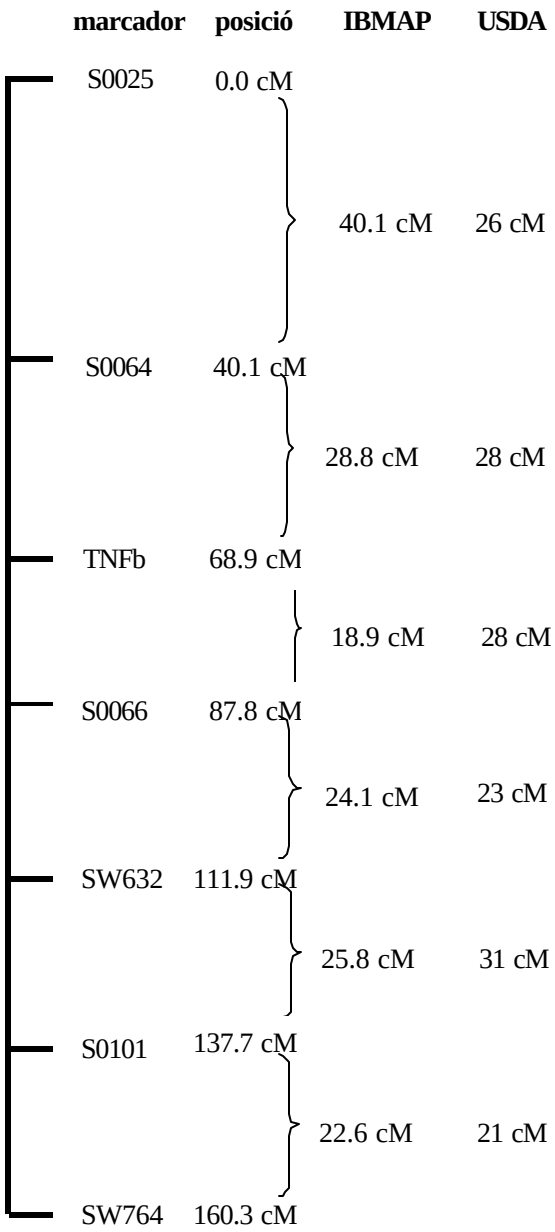
LOD *score* = -474.80

CROMOSOMA 3



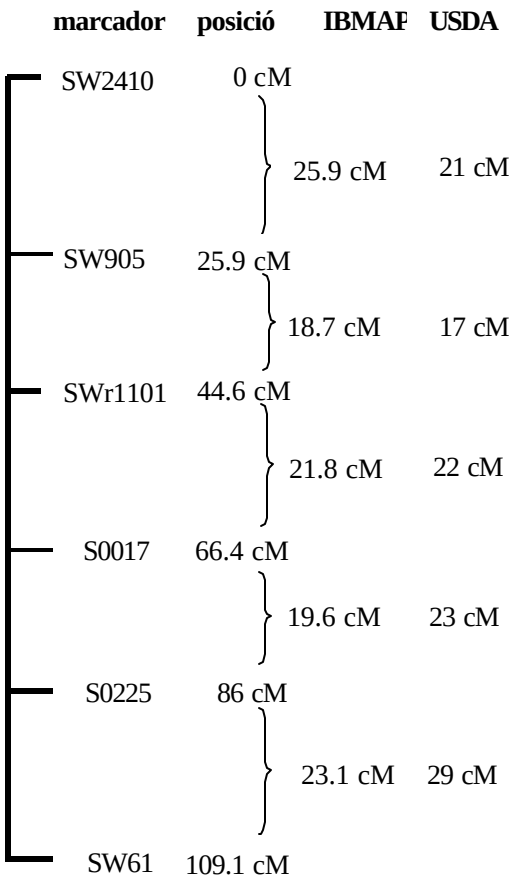
LOD *score* = -836.02

CROMOSOMA 4



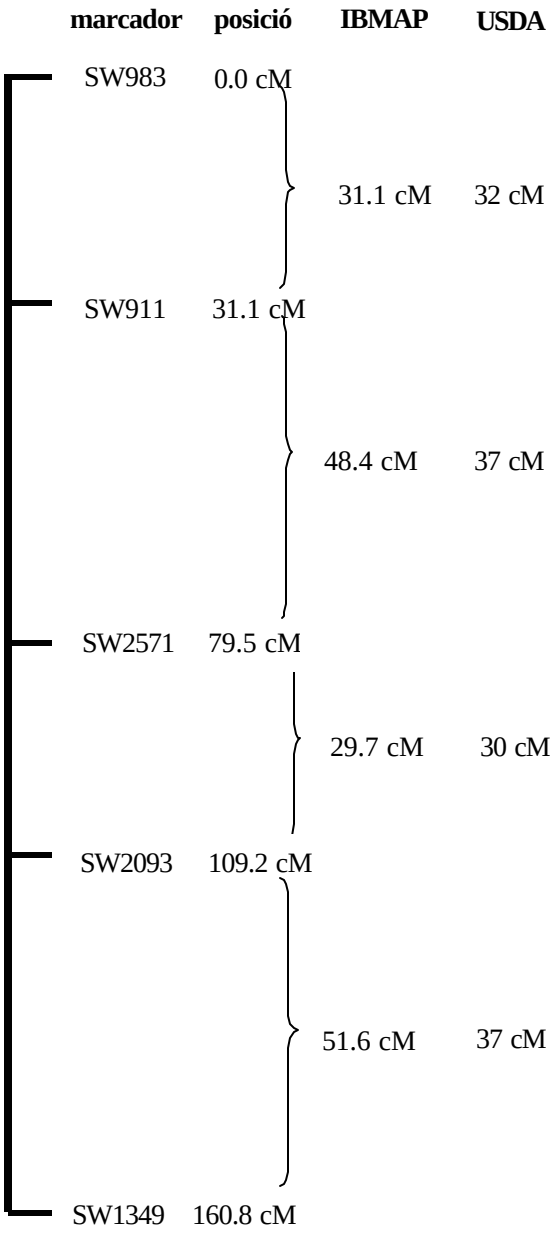
LOD *score* = -870.32

CROMOSOMA 7



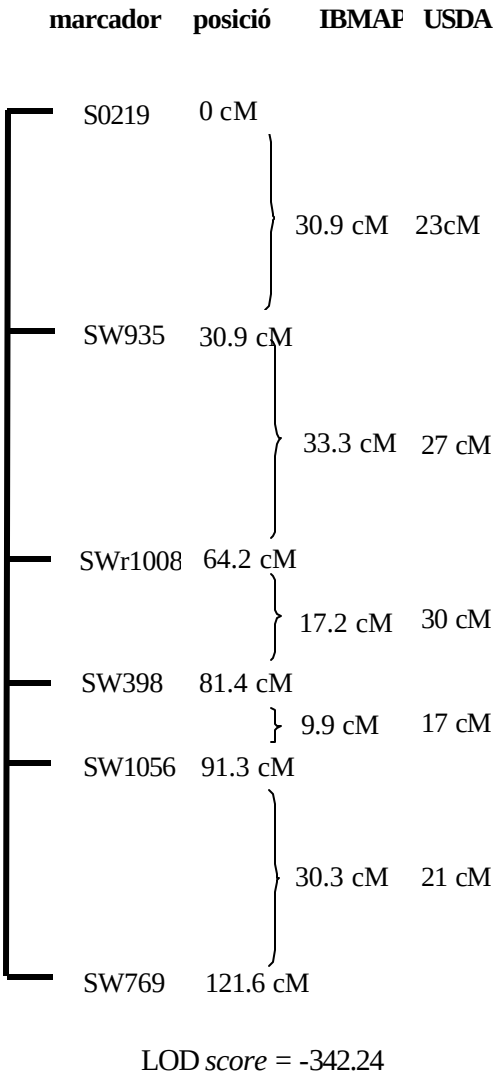
LOD *score* = -447.59

CROMOSOMA 8



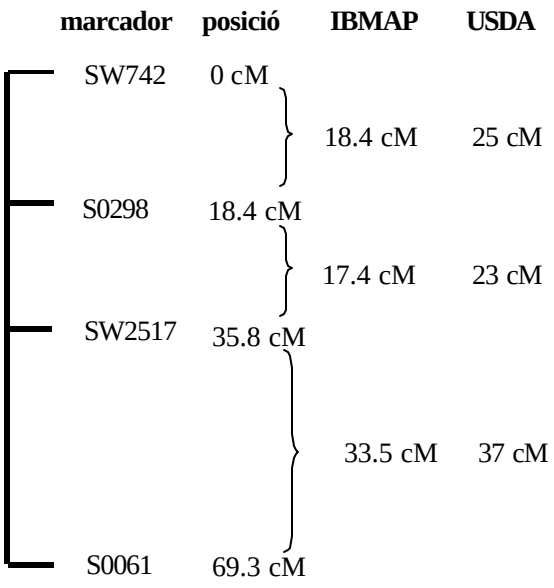
LOD score = -605.29

CROMOSOMA 9



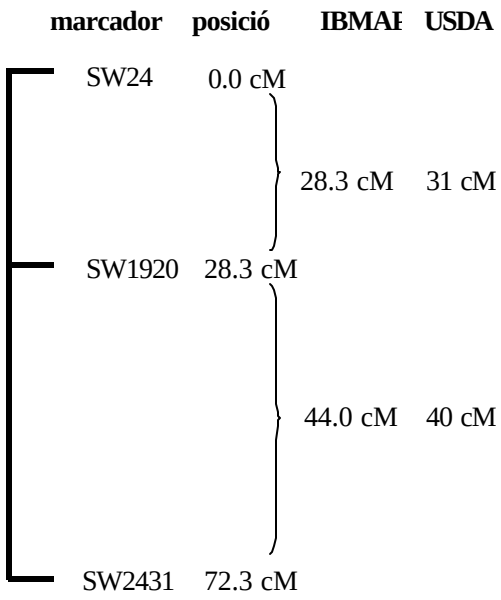
LOD *score* = -342.24

CROMOSOMA 13



LOD score = -319.51

CROMOSOMA 16



LOD score = -264.644

CROMOSOMA 17

ANNEX 6

Gens mapejats als cromosomes porcins 2, 4, 7 i 8.

Gens mapejats al cromosoma 2 porcí (Sscr2).

gen, símbol	*gen, nom*	*mapa físic*	*mapa genètic*
ACP5	*Uteroferrin*	q1.2-q2.1	no determinat
AMH	*Anti-Müllerian hormone*	q1.4-q2.1	no determinat
C3	*Complement Component*	p1.7-p1.4	no determinat
CANX	*Calnexin Precursor*	p1.7-p1.4	no determinat
CAPN1	*Calpain I*	p1.7-p1.4	no determinat
CAST	*Calpastatin*	q2.1-q2.4	no determinat
CAT	*Catalase*	p1.6-p1.5	no determinat
CD59	*CD59*	p1.7-p1.4	no determinat
CLTC	*Clathrin, Heavy Polypeptide*	p1.7-p1.6	no determinat
CNTF	*Ciliary Neurotrophic Factor*	p1.6	no determinat
COX8	*Cytochrome C Oxidase, subunit C IX*	p1.7	no determinat
CPLX2	*complexin 2*	p1.7-p1.4	no determinat
EPOR	*Erythropoietin Receptor*	q1.2-q2.1	no determinat
FGFR4	*Fibroblast Growth Factor*	no determinat	no determinat
FSHB	*Follicle Stimulant Hormone, Beta subunit*	p1.6-p1.2	(3)
GM2A	*GM2 Activator Protein*	q2.6	no determinat
HARS	*Histidyl-tRNA Syntethase*	q2.8-q2.9	no determinat
HMGCR	*3 Hidroxy-3-methylglutaryl CoA*	q2.2	no determinat
IGF2	*Insuline Growth Factor 2*	p1.7	no determinat
IL4	*Interleukine 4*	no determinat	no determinat
INSL3	*Insuline Like 3*	q1.2-q3	no determinat
INSR	*Insuline Receptor*	q1.1-q2.1	(3-4)
LDHA	*Lactate Dehydrogenase A*	p1.7-p1.4	no determinat
MANA2	*Mannoside Alpha Type II*	no determinat	no determinat
MGAM	*Maltase-Glucoamylase*	q2.1	no determinat
MUC5AC	*Pig Gastric Mucin*	no determinat	no determinat
MYOD1	*Myogenin Myogenic Factor 3 (MYF3)*	p1.7-p1.4	no determinat
NFIC	*Nuclear Factor I/CTF*	q1.2-q1.3	no determinat
NPY6R	*Neuropeptide Y Receptor Y6*	q2.4-q2.9	no determinat
P4HA1	*Proly4-Hydroxylase Alpha II subunit*	q2.1-q2.2	no determinat
PAX6	*Paired Box Homeotic Gene 6*	p1.4	no determinat
PC1/3	*Protein Convenase 1/3*	q2.1	(4)
PDGFRB	*Platelet-derived Growth Factor Receptor, Beta*	no determinat	no determinat
PGA	*Pepsinogen A*	p1.7	no determinat
PST1	*Tripsinogen Complex*	q2.4-q2.9	no determinat
PTH	*Parathyroid Hormone*	no determinat	no determinat
PYGM	*Glucogen Phosphorylase, Muscle*	p1.7-p1.4	no determinat
RASA1	*RAS p21 Activator (GTPase activating protein)*	q2.3	no determinat
RLNCE	*Pro-relaxin Converting Enzyme*	q2.1	no determinat

gen, símbol	*gen, nom*	*mapa físic*	*mapa genètic*
SCAMP1	*Secretory Carrier Membrane Protein 1*	q2.1-q2.2	no determinat
TDPX1	*Thiol Specific Antioxide Protein 1*	p1.7-p1.4	no determinat
TPM4	*Tropomyosin 4*	q2.4-q2.9	no determinat
WT1	*Wilms'Tumor gene1*	p1.4-q1.1	no determinat

*La posició dels gens en els diferents mapes de lligament es descriu en relació a les regions flanquejades per els microsatèl.lits posicionats en el mapa genètic IBMAP. IGF2-S0141 (1), S0141-SW240 (2), SW240-SW395 (3), SW395-S0226 (4), S0226-S0378 (5), S0378-SWr308 (6).

Gens mapejats al cromosoma 4 porcí (Sscr4).

gen, símbol	*gen, nom*	*mapa físic*	*mapa genètic**
AMPD1	*Adenosine Monophosphate deaminase, M isoform*	no determinat	no determinat
AMY1B	*Amylase Alpha 1 B*	q2.4	no determinat
AT3	*Antithrombin III*	q1.5-q1.6	no determinat
ATP1A1	*ATPase, Na^+ K^+ Transporting, Alpha 1 Polypeptide*	q1.6-q2.3	(5)
ATP1A2	*ATPase, Na^+ K^+ Transporting, Alpha 2 Polypeptide*	no determinat	no determinat
ATP1B1	*ATPase, Na^+ K^+ Transporting, Beta 1 Polypeptide*	q1.3-q2.1	(4)
CD1	*Cluster Differentiation locus 1*	q1.5-q1.6	no determinat
CRH	*Corticotropin Releasing Hormone*	q1.3	no determinat
CRP	*C-ReactiveProtein Pentraxin Related*	q2.1	no determinat
DDB1	*Damage-specific DNA Binding Protein*	q1.5-q1.6	no determinat
EAL	*Erytrocyte Antigen L*	no determinat	(4-5)
ETV3	*ETS Variant Gene 3*	q2.1	no determinat
F13B	*Coagulation Factor XIII, Beta Polypeptide*	no determinat	(3)
FABP4	*Adipcyte Fatty Acid Binding Protein*	no determinat	(3)
GBA	*Glicosidase Beta Acid*	no determinat	(4-5)
HSD3B	*hidroxi delta 5 esteroid dehydrogenase 3 beta*	q2.1-q2.3	no determinat
HSP	*Heat Shock Protein*	no determinat	(4-5)
IVL	*Involucrina*	q2.2-q2.3	no determinat
c-MYC	*c- Myc proto-oncogene*	no determinat	no determinat
NGFB	*Nerve Growth Factor*	q1.5-q2.3	(1)
N-RAS	*V-RAS Neuroblastoma RAS Viral Oncogene Homologue*	q2.1-q2.2	no determinat
ODF1	*Outer Dense Fiber of Sperm Tails*	p1.4-p1.1	no determinat
PKLR	*Pyruvate Kinase, Liver and Red Blood Cells*	q2.1-q2.3	no determinat
POU2F1	*Pou Domain, Class 2, Transcription Factor 1*	no determinat	no determinat
S100A6	*S100 Calcium-Binding Protein A6 (Calcyclin)*	q2.1	no determinat
SGC10	*Neuronal Growth Factor-Associated Protein*	q1.5-q1.6	no determinat
SSC9C8	*A10 Murine Transcription Factor*	q1.1-q1.4	no determinat
TG	*Thyroglobulin*	pter	no determinat

gen, símbol	*gen, nom*	*mapa físic*	*mapa genètic**
THH	*Trichohyalin*	q2.1	no determinat
TSHB	*Thiroyd stimulant hormone beta*	q2.1	(5)
V-ATPase	*Vacuolar H(+) ATPase Subunit Gene*	q1.5-q1.6	no determinat
VCAM1	*Vascular Cellular Adhesion Molecule*	no determinat	(6)

*La posició en el mapa de lligament dels diferents gens es descriu en relació amb els segments flanquejats per els microsatèl.lits posicionats en el mapa de lligament IBMAP. SW2404-S0301 (1), S0301-S0001 (2), S0001-SW839 (3), SW839-S0214 (4), S0214-SW445 (5), SW445-S0097 (6).

Gens mapejats al cromosoma 7 porcí (Sscr7).

gen, símbol	*gen, nom*	*mapa físic*	*mapa genètic**
AACT	*Alpha-1-antichymotrypsin*	q2.3-q2.6	(5)
ADPRF	*Porcine EST ADP ribosilation factor*	q1.2-q2.6	no determinat
ANPEP	*Alanyl aminopeptidase*	cen-q2.1	S0066
ARF	*ADP-ribosylation factor*	q2.3-q2.6	no determinat
BF	*B-factor, properdin*	cen	no determinat
CALM1	*Calmodulin 1*	q1.2-q2.3	no determinat
CD79A	*CD79A antigen*	q2.6	no determinat
C-FOS	*C-fos proto-oncogene*	q2.3	no determinat
CHGA	*Chromogranin A*	q2.4-q2.6	no determinat
CHRNA3	*Neuronal nicotinic acetylcholine receptor alpha 3*	no determinat	S0066
CKB	*Creatine kinase B chain*	q1.2-q2.6	no determinat
CLPS	*Colipase*	no determinat	(2)
CPS	*Campus syndrome*	no determinat	(4)
CYP1A1	*Cytochrome P450, subfamily I, polypeptide 1*	q1.2-q2.6	TNFB
CYP21A2	*Cytochrome P450, steroid 21-hydroxylase*	no determinat	no determinat
DDR1	*Discoidin domain receptor family member 1*	p1.1	no determinat
DNCH1	*Dynein, cytoplasmatic, heavy polypeptide 1*	q2.4-q2.5	no determinat
EAC	*Erythrocyte antigen C*	no determinat	S0066
EAJ	*Erythrocyte antigen J*	no determinat	S0066
EDN1	*Endothelin-1*	p1.3-pter	(2)
F13A1	*Blood coagulation factor XIII A subunit*	p1.3	no determinat
F14943	*Porcine EST SSC2B02*	p1.1-q1.1	no determinat
GLO1	*Glyoxyilase*	no determinat	no determinat
GPX5	*Glutathione peroxidase-5*	p1.2-p1.1	no determinat
HEXA	*Hexosaminidase alpha*	q1.5	no determinat
HSPAs	*Heat shock 70 kDa proteins*	p1.1-cen	no determinat
HSPCA	*Heat shock 90 kDa alpha*	q1.2-q2.6	no determinat
IGHs	*Immunoglobulin heavy chains*	q2.5-q2.6	no determinat
MEP1A	*Meprin A*	q1.2-q2.6	no determinat

gen, símbol	*gen, nom*	*mapa físic*	*mapa genètic**
MHCTA-1	*Porcine EST MHC class I major transpl. Ag*	p1.2-p1.1	no determinat
MPI	*Mannose phospate isomerase*	pter-q2.1	no determinat
MYH6	*Myosin heavy chain 6, cardiac muscle, alpha*	q2.1	no determinat
MYH7	*Myosin heavy chain 7, cardiac muscle, beta*	q1.2-q2.3	no determinat
NFKBIA	*Nuclear factor of kappa light polypeptide*	q1.5-q2.1	no determinat
NP	*Nucleoside phosphorilase*	q2.1-q2.2	no determinat
PBX2	*Pre-B-cell leukemia transcription factor*	no determinat	no determinat
PI	*Protease inhibitor*	q	(5)
PKM2	*Pyruvate kinase, muscle*	no determinat	S0066
PO1	*Postalbumin*	no determinat	(5)
PRL	*Prolactin*	p1.2-p1.1	no determinat
PSMA4	*Proteasome subunit A4*	q1.3-q1.4	no determinat
RXRB	*Retinoid X receptor, beta*	cen	no determinat
RYR3	*Ryanodine receptor 3*	q2.2-q2.3	no determinat
SCA1	*Ataxin 1*	p1.2-p1.1	no determinat
SERF13	*ERF-1 protein*	q1.2-q2.6	no determinat
SLA-I	*Swine Leucocyte Antigen I*	p1.2-q1.2	(3)
SLA-II	*Swine Leucocyte Antigen II*	q1.1	(3)
SPTB	*Beta spectrin*	q2.3	no determinat
SSTR1	*Somatostatin receptor*	q1.2-q2.6	TNFB
TAP1	*Transporter associated with antigen processing 1*	no determinat	(2)
TAP2	*Transporter associated with antigen processing 2*	no determinat	(1)
TCRA	*T-cell receptor alpha cluster*	no determinat	no determinat
TGFB3	*Transporting growth factor beta-3*	no determinat	no determinat
TGM1	*Transglutaminase*	q2.3	no determinat
TNFA	*Tumor necrosis factor, alpha*	p1.1-q1.1	no determinat
TNFB	*Tumor necrosis factor, beta*	p1.1-q1.1	TNFB
TSHR	*Thyroid stimulan hormone receptor*	q	no determinat
TTF1	*Transcription termination factor 1*	q1.2-q2.6	TNFB
UBS27	*Ubiquitin-S27a fusion protein*	no determinat	no determinat
WARS	*Tryptophanyl-tRNA synthetase*	q1.2-q1.6	no determinat
ZMOK2	*Zinc finger MOK 2*	no determinat	no determinat

*La posició dels gens en els diferents mapes de lligament es descriu en relació amb les regions flanquejades pels microsatèl.lits posicionats al mapa genètic IBMAP. S0025-S0064 (1), S0064-TNFB (2), TNFB-S0066 (3), S0066-SW632 (4), SW632-S0101 (5), S0101-SW764 (6).

Gens mapejats al cromosoma 8 porcí (Sscr8).

gen, símbol	*gen, nom*	*mapa físic*	*mapa genètic**
ADH3	*Alcohol dehydrogenase 3*	no determinat	S0225
ALB	*Albumin*	q1.2	S0017
CCKAR	*Cholecystokinin type A receptor*	no determinat	(4)
CHGA	*Chromogranin A*	no determinat	S0017
CPE	*Carboxypeptidase E*	no determinat	(4)
CSN1 (s1)	*Casein, alpha s1*	no determinat	S0017
CSN1 (s2)	*Casein, alpha s2*	no determinat	S0017
CSN10	*Casein, kappa*	no determinat	(5)
CSN2	*Casein, beta*	no determinat	S0017
EGF	*Epidermal growth factor*	q2.3-q2.4	no determinat
FGA	*Fibrinogen, alpha*	no determinat	S0017
FGB	*Fibrinogen, beta*	no determinat	S0017
FGF2	*Fibrinogen growth factor 2*	q2.2-q2.4	no determinat
FGFR3	*Fibrinogen growth factor R3*	p1.1	(4)
FGG	*Fibrinogen gamma*	no determinat	S0017
GNRHR	*Gonadotropin-releasing hormone receptor*	q1.1-q1.2	no determinat
GRIA2	*Glutamate receptor, ionotropic,AMPA 2*	p2.1-p1.1	no determinat
IL2	*Interleukin 2*	no determinat	(4)
IL8	*Interleukin 8*	no determinat	no determinat
KIT	*c-KIT*	p2.1-p1.2	no determinat
MAN2B2	*Mannosidase alpha*	p2.3-pter	no determinat
NPY1R	*Neuropeptide Y receptor Y1*	p1.1	no determinat
NPY2R	*Neuropeptide Y receptor Y2*	q2.1	no determinat
NPY5R	*Neuropeptide Y receptro Y5*	p1.1	no determinat
NR3CR	*Nuclear receptor subfamily 3, group C*	no determinat	no determinat
PDE6B	*Phosphodiesterase 6 B*	p2.3-pter	no determinat
PDGFRA	*Platelet-derived growth factor receptor,alpha*	p1.2	(3)
PEPS	*Aminopeptidase S*	p1.1	no determinat
RFC1	*Replication factor C, large subunit*	p2.1-p2.3	no determinat
RNR1	*Ribosomal RNA (NOR)*	p1.2	no determinat
SPP1	*Secreted phosphoprotein 1*	q2.5-q2.7	no determinat
SSC20B10	*Cell division CDC25 protein homolog*	q2.3-q2.7	no determinat
UCP1	*Uncoupling protein*	q2.1	no determinat
UGT2B	*UDP-glucuronosyltransferase 2 family*	q2.1	no determinat
	Neuromedin-K-receptor	q2.3-q2.7	no determinat
TXK	*Tyrosine kinase*	q2.1	no determinat
UGT8	*UDP-glucuronosyltransferase 8*	q2.5	no determinat

*La posició dels gens en els diferents mapes de lligament es descriu en relació amb les regions flanquejades per els microsatèl.lits posicionats al mapa genètic IBMAP. SW2410-SW905 (1), SW905-SWr1101 (2), SWr1101-S0017 (3), S0017-S0225 (4),S0225-SW61 (5).