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Assignment of the *acyl-CoA synthetase long-chain family member 4 (ACSL4)* gene to porcine chromosome X

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Source/description: Acyl-CoA synthetase long-chain family member 4 (ACSL4) is an essential enzyme in fatty acid metabolism. It converts free long-chain fatty acids into fatty acyl-CoA esters, which are key intermediates in the synthesis of complex lipids.[1] ACSL4 catalyses the formation of these fatty acyl-CoAs by a two-step process that starts with the addition of an AMP at the carboxyl group of the fatty acid. Subsequently, this AMP is released by the incorporation of the CoA group.[2] In humans, an alternative splicing of this gene generates two transcript variants. One of them encodes for a protein that contains an additional 41 amino acid-long N-terminal peptide that introduces a hydrophobic domain in the molecule. This may change the intracellular localization of ACSL4 or its fatty acid specificity.[3]

Primer sequences:
FACL4F11:5′-AAC TCT GTT CAA GAT AGG GTA TGA TTA CAA-3′
FACL4R1:5′-AAT TGG GCA GCA GAA GCA GAC-3′
FACL4RHF:5′-AAT CAT TTA TTT CCC CCC CCT T-3′

Nucleotide sequence: Pig genomic DNA was isolated from blood samples and purified by phenol–chloroform extraction. One set of primers corresponding to exons 10 (FACL4F11) and 11 (FACL4R1) were designed by aligning the human (GenBank accession no. NM_004458), mouse (accession no. NM_207625) and rat (accession no. NM_053623) *ACSL4* nucleotide sequences. The polymerase chain reaction (PCR) was performed in a 25 μl final volume containing 1.5 mM $MgCl_2$, 200 μM dNTPs, 0.3 μM of each primer, 50 ng of genomic DNA and 1.3 U Expand High Fidelity PCR (Roche, Barcelona, Spain). Thermocycling was carried out under the following conditions: initial denaturation (95 °C for 3 min) was followed by 10 cycles (95 °C for 30 s, 58 °C for 1 min, and 72 °C for 2.5 min) and by 25 cycles (95 °C for 30 s, 58 °C for 1 min and 72 °C for 2.5 min) increasing the extension step by 20 s in each cycle and a final extension (72 °C for 10 min). The amplified product was completely sequenced in both directions using the BigDye™ Terminator v3.1 Ready Reaction Cycle Sequencing Kit in an ABI PRISM 3100 Avant sequencer (Applied Biosystems, Foster City, CA, USA). We obtained an 815-bp sequence (GenBank accession no. AY787774) encompassing 17 bp of the 3′ end of exon 10, intron 10, and 53 bp of the 5′ end of exon 11 of the porcine *ACSL4* gene.

Radiation hybrid mapping: Radiation hybrid mapping was performed with the INRA-University of Minnesota porcine radiation hybrid panel (ImpRH).[4] A pig-specific primer (FACL4RHF) was designed from the previously described nucleotide sequence. FACL4R1 and FACL4RHF primers were used to amplify a fragment of 151 bp. The PCR mixture included 25 ng of genomic DNA, 1.5 mM $MgCl_2$, 0.5 μM of each primer, 0.2 mM dNTPs, and 0.6 U Taq DNA polymerase (Invitrogen SA, Barcelona, Spain) in a final 25 μl reaction. The cycling profile was 95 °C for 3 min, 35 cycles of 95 °C for 1 min, 60 °C for 1 min, 72 °C for 2.5 min, and a final extension time of 7 min at 72 °C. Analysis of the data with the ImpRH mapping tool[5] demonstrated that the *ACSL4* gene is linked to the *Sw1426* microsatellite (53 cR, LOD 8.19) on porcine chromosome X. Comparative mapping between pig and human revealed that the assignment of pig *ACSL4* gene is consistent with the position of *ACSL4* to human chromosome Xq22.3.[6] The *ACSL4* gene is located at approximately 5 cM of a QTL for intramuscular fat detected in an Iberian × Landrace F2 intercross[7] between *Sw2476* and *Sw1608* markers. This result, jointly with the involvement of the ACSL4 in lipid metabolism, suggests that *ACSL4* is a positional candidate gene for this QTL.

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References

1 Cao Y. *et al.* (1998) *Genomics* **49**, 327–30.
2 Weimar J. D. *et al.* (2002) *J Biol Chem* **277**, 29369–76.
3 Piccini M. *et al.* (1998) *Genomics* **47**, 350–58.
4 Yerle M. *et al.* (1998) *Cytogenet Cell Genet* **82**, 182–8.
5 Milan D. *et al.* (2000) *Bioinformatics* **16**, 558–9.
6 Vitelli F. *et al.* (2000) *Cytogenet Cell Genet* **88**, 259–63.
7 Pérez-Enciso M. *et al.* (2002) *Genetics* **161**, 1625–32.

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Map assignments of 373 previously unreported porcine microsatellites

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Source/description: A phage library was constructed by insertion of size-selected (220–1000 bp) pig genomic DNA, restricted with *Mbo*I, into dephosphorylated *Bam*HI digested M13mp18. The library was screened with ^{32}P-labelled $(CA)_{16}$ and $(GT)_{16}$ probes. Positive clones were sequenced with an

Table 1 Porcine microsatellite information. The GenBank accession number, primer sequences, PCR annealing temperature, map information (chromosomal assignment, closest marker, distance from closest marker and two-point LOD score) and fragment size are included for each locus.

Marker	GenBank accession	Forward primer (5′ → 3′)	Reverse primer (5′ → 3′)	Temp	Chr.	*Linked marker*	Dist (Ray)	LOD	Fragment size (bp)
UMNp595	AY285436	GGAACTTTCATATGCTGCAGC	CGTTTTTTTTTCCTCCTCAGG	60	13	*SWR2189*	0.21	11.86	136
UMNp629	AY285437	TTTCTCCCCAAACTGTCCC	TTGAGACAGAGTTTGTGTGCG	54	12	*S0090*	0.17	13.83	131
UMNp638	AY285438	TGGTTTAAGGCCATACTGTGC	AATGCAGGCAAGTTATCATGG	54	4	*SWR2179*	0.15	16.30	168
UMNp641	AY285439	GTGGTTAACAGAGCAACCAGTG	ACACCTGTTTACCTCTTCAGGC	56	13	*SW1979*	0.07	16.06	195
UMNp643	AY285440	CATGTCTTTTCAGAGCTTTTGC	CACATGCCATGGTTAAGCC	54	9	*SW174*	0.44	7.30	109
UMNp648	AY285442	GTTTATTCCACTCCTTTGCTGC	CTTCGTGGCTGTCTCCTTTC	54	16	*SW977*	0.18	13.71	163
UMNp682	AY285444	GAGAGCCACACATGCGTG	TGGTGGATATTTAATTCCCAGC	56	6	*SW446*	0.12	16.17	157
UMNp684	AY285445	GTCTTGGAAGGCTAATTTGGG	AGAACCAGAGAGGCAAAATATG	54	16	*SW742*	0.46	7.24	197
UMNp686	AY285446	GGAGGTTCTAGCCAGGGAAA	ATAGGTCCGATTAGACCCTAA	54	X	*SW1943*	0.25	11.63	175
UMNp691	AY285448	GATCTGCTAAACCATTACCAAA	ATTGCATAAAATTGTTCAGCTG	60	2	*SWR1342*	0.17	15.01	206
UMNp693	AY285450	TTGGAGTCTTCTTCATTATGGC	TTTAGTGGGCTTTTCCCATG	54	8	*SW916*	0.07	20.34	191
UMNp696	AY285453	AAGATAGGACATTCCATGTGGC	GAGCCCTTAAGCTGCAAATG	60	1	*SW1430*	0.23	12.60	188
UMNp705	AY285455	TTGCCACTCTATCTCTTTCTGG	ATGGGCCCAAATATATGAAGC	54	10	*SW1829*	0.34	9.67	222
UMNp707	AY285456	TGGGGATTTTTATTTCATTGTC	GTTGCTGCCTTGGTTTTTTG	54	2	*ADM*	0.27	11.22	283
UMNp709	AY285457	TGACACAAGTGGACTATGAAGG	TAACTCACTGAGCCACAAGGC	54	7	*TNFB*	0.37	8.94	186
UMNp714	AY285458	GATACTGTGCCAGATGCGC	TAGAAAGGATTGCCTCTCAAGG	54	5	*AC02*	0.36	8.83	197
UMNp715	AY285459	TTTCTGTGGAAGTCTGGAATTG	AATTTCCCAAGGAAACCAGG	54	1	*SSC10D08*	0.22	11.77	178
UMNp716	AY285460	TCTCCTTCTCTCTCCACCCC	ATAAGCTTTGCTCCCTTCCC	58	2	*S0091*	0.26	11.39	200
UMNp717	AY285461	TTCCTAGTCGGATTCGTTAACC	GCTCCCTCTTGTTCTTGGC	58	11	*SW1377*	0.25	11.45	175
UMNp720	AY285462	GTTTGCATGGACGTTTATTGG	GAGCAGATGTCGCTACTGACC	54	6	*SW1059*	0.42	7.99	200
UMNp724	AY285464	ATGATGGGTCTGCAGGACTC	TTTACGTGAAGGAGATGGGG	56	4	*S0097*	0.15	15.47	212
UMNp729	AY285466	GCCTCCACTGAGCAAAAAAG	TGAAGTTGCAGATGCCACTC	54	9	*SW1651*	0.32	10.12	191
UMNp730	AY285467	TCTCTGCCTGGGTCTTGC	AGTACTTCTTCCCTGGGAAAGG	54	9	*SWR1939*	0.12	17.24	159
UMNp735	AY285470	TCTGTGTGTAAGGACAGGTTGG	CTCCAAGCTACCCGTCACTC	54	3	*SW72*	0.39	8.46	196
UMNp738	AY285471	TTATGAGCCAGAGAAATTCCTC	CTTCCCATTGAATTCTACTGCC	54	4	*SW1336*	0.04	21.35	156
UMNp741	AY285472	TACAATTCAATGCTGTTCCTGG	CAGCTTCCATAATCATGTGAGC	56	1	*SW1332*	0.14	14.07	191
UMNp742	AY285473	AGGAGTTTACAGCCTGCTTCC	TTTTGGTCCTTGAGGAATGC	56	2	*SW2167*	0.16	14.73	182
UMNp746	AY285474	AGCTGGCATCTGTCTGGG	CATGGAAAACCTGATGATTCTG	56	3	*SW72*	0.15	14.99	200
UMNp747	AY285475	ATTAGGGGCCTTGCCAAG	AGGCAGAATGTTGGCAGAAC	54	6	*S0220*	0.14	12.60	163
UMNp748	AY285476	TCATATCCTGCTATGCACGC	AAAACATGCCCAAAATGAGG	58	3	*SW2532*	0.5	6.39	195
UMNp749	AY285477	GTCATCTCTAACTCCCTGGCC	GACACTGGGGTGTGGAGC	60	14	*SW2515*	0.47	6.36	195
UMNp750	AY285478	ATGACCAAGACCAAAACAGATG	GAGTGATGTCTCTTCTGGGACC	62	X	*SW2470*	0.16	15.23	195
UMNp752	AY285480	AGTTGACACACACACTTCTGGG	CCGCTAGTTTGTTCTCTGTCTG	62	6	*S0087*	0.24	12.43	194
UMNp754	AY285481	CATGGATGTGTTTCCCAGG	ATAGTTCGTTTGGTCCAAATGG	56	7	*SWR1210*	0.25	11.32	206
UMNp755	AY285482	CCAGACCTCCTGAAACATTAGC	AGCTCTGATTCAACCCCTAGC	62	16	*S0105*	0.18	14.56	193
UMNp759	AY285483	CAAAGCACATATTCTGATTTCG	AAGCTCATCCTGTGTGTGTATG	54	15	*Sw315*	0.12	16.27	159
UMNp760	AY285484	TGTTGCTGCAGATTCAGGTC	GTCCTTTAATGTCAAAGGCACC	60	3	*SW1443*	0.11	17.27	174
UMNp761	AY285485	TGGGAATCTCCATAAGCCAG	TGTGGAGCTATCCTGAAATGC	54	5	*SW332*	0.11	17.31	156

Table 1 Continued.

Marker	GenBank accession	Forward primer (5′ → 3′)	Reverse primer (5′ → 3′)	Temp	Chr.	*Linked marker*	Dist (Ray)	LOD	Fragment size (bp)
UMNp763	AY285486	ACACTCTGACTCCACCCCAC	AATGAAGATTAGTGTGGGGGG	60	16	*SW2411*	0.2	13.55	221
UMNp764	AY285487	CAGACTAGAAAAAGCATGTGCG	CAGTGGCTCCTCTGTGTCTATG	60	9	*SW2401*	0.05	20.76	133
UMNp765	AY285488	ATTTTGTTATCCATCACCCCC	TCGGTAGCACCTGAATCTCC	60	11	*SW1486*	0.33	9.90	217
UMNp766	AY285489	ATGAGAAACGGCCATACCTG	ACCATTACTGACTACTTGAAAAATGG	60	6	*S0087*	0.32	10.22	234
UMNp767	AY285490	TGAACTCCAAAGCCAGGC	CATGTTCTGTAGTTTTGCAGGC	54	10	*SW1626*	0.38	8.26	174
UMNp769	AY285491	TAAGGCTACAGCTGCACTCG	TGCAAAGTACACGCATGTTG	54	6	*SW133*	0.17	12.40	163
UMNp778	AY285493	ATATACTGTGGGTGCAGCCC	CCTTGTTCACAGTTTTCAGGC	60	9	*SW174*	0.46	7.14	194
UMNp779	AY285494	TTTTGTTTTCATTCATTGTTGG	ATGCAGACGACTGCCTTTG	54	5	*SW1904*	0.2	13.34	249
UMNp780	AY285495	GCTATAGTCTGGCTGCTGGG	AGTGACCATCTGGCTATGCC	60	10	*SW497*	0.28	10.96	172
UMNp781	AY285496	TGTGGCTGCTTGAAATTCAG	CAATCCAACTTTGAGCATTTC	54	9	*SW2571*	0.16	15.49	177
UMNp782	AY285497	CTCCAAGCTGTAGGAGACCG	GCTTGTTATTACGGAGAGGGG	54	2	*SW766*	0.22	11.46	148
UMNp784	AY285498	TTAATAGGCAGGAAACTCAGGC	TCGAATATGACGGAGGATAATG	54	1	*SW1621*	0.36	9.25	236
UMNp785	AY285499	GGGAAAGGAGTAGGACCGAC	CTGGTCCAGTCTCGTGTGTG	54	X	*SW1411*	0.06	19.79	199
UMNp786	AY285500	CTAGAAATGGCAAAAAGACACG	CTGTGAATGCTGCCTTATTTG	54	16	*SW1897*	0.46	7.33	244
UMNp787	AY285501	CTGCTTTTATCCAGAGCTCATC	AAAGAGGAATGATTTCTGCAAC	54	12	*SW957*	0.4	8.11	130
UMNp789	AY285502	GGTGTGAGGTGGACAGCC	AGAAACCATTGGGAGTCAAGG	54	17	*CST3*	0.16	12.99	148
UMNp790	AY285503	CCCTTCAGATGAGACCACTACC	TTCATCTTCCTTGGTCCCAG	54	1	*SW64*	0.2	12.46	141
UMNp793	AY285504	ATGGACCACGCTTTGAGAAC	AAAGAACAAAAAGATGGCTTGC	54	4	*S0214*	0.15	13.92	197
UMNp795	AY285505	GGGTGGGGATTAGAGGAGAG	AGCCCTTCCTGATTGCTTG	54	12	*SW943*	0.51	6.31	177
UMNp796	AY285506	AATGCAGCGTGAACAGTGTC	CATCCCTTGGCTTGTTGC	56	13	*S0289*	0.27	10.47	156
UMNp799	AY285507	ATAACAAAGTACACACGTGCGC	CATTAGGAGAAAAAGCCCCC	62	3	*S0002*	0.14	14.52	116
UMNp801	AY285508	AGCCTACTGAGCCACAATGG	TCAACCTCAGTAAAACCACCG	54	X	*SWR17*	0.13	16.31	205
UMNp802	AY285509	TTGGAAGAGAATGACCTGGG	GAGTAGCCCAGCTGTGCAG	60	10	*SW1894*	0.25	10.51	235
UMNp803	AY285510	AGTATTGTCCCTGCAGTGGC	CTCACTTAGAACCACCCAAAGC	62	3	*IGKC*	0.07	20.14	169
UMNp804	AY285511	GGAGAAAAGGACCCTCCAAG	TTAGAAGGCATGCTTAGAAGCC	54	17	*Sw1031*	0.51	6.29	144
UMNp807	AY285513	ACTCATGTGTCTGAGCGTGC	GCAACCCCATTTGCATTC	54	13	*SW882*	0.17	13.70	242
UMNp808	AY285514	AGAGTCTCGTGGCACTTCTACC	GCACTGTGCTCGGTGTTG	54	9	*SW1651*	0.09	18.47	156
UMNp809	AY285515	GATTCATCTCTCAGGGGCAG	CTTGCCACAGGTGCAGTG	54	5	*SW1383*	0.18	14.73	241
UMNp812	AY285516	CAAATCAAGCCCACTTAAGTCC	AGTCCCTGAAAATGTGTGTGC	54	15	*SW1339*	0.15	12.20	167
UMNp813	AY285517	AAAGGGGGTCAGGATACCAC	AAAGCCAGAATCAGTCGGC	62	1	*SW1061*	0.23	12.74	174
UMNp816	AY285519	TGCCTCCATTTTCCTTATCG	ACATGTCTGTTCACGCATCTG	54	6	*SW133*	0.08	14.12	151
UMNp817	AY285520	AACCTCCATATGCCATGAGTG	TAGCACATGTGTTTTGTGTTGG	60	14	*SW857*	0.09	18.86	153
UMNp818	AY285521	GTGGGTACAGCCCTCAAAAG	CAGTTCATGTCACAGCCCC	54	X	*SW949*	0.52	6.17	129
UMNp819	AY285522	TAACATGCCTCGAAATGCAG	GGGCTAGAAAATGAACATGTCC	54	6	*SW1473*	0.26	11.02	182
UMNp820	AY285523	CAGAGAGCTGCACGAATTACC	GAAGTTGGTCAATTATAGCCCG	62	12	*SW957*	0.43	7.88	151
UMNp823	AY285524	AGTGCCAGAAAATAGGTTTTGC	GGCATTTATTTAATGCCTTGAG	54	11	*SW1460*	0.26	10.10	235
UMNp825	AY285525	CATGCTGCAGGTGTAACTGG	TCTCTCGTTTTGGTGTGTGC	54	8	*S0086*	0.14	16.42	101
UMNp826	AY285526	TACGCAGGATACTGGAGTTGC	GAGGACTGTCTTTCGTGTTGTG	60	5	*DK*	0.17	15.35	184
UMNp827	AY285527	ACATCTGGGGTAAGGGGAAG	ACTGAACCAGGATGCAAACC	60	2	*S0141*	0.17	14.77	196

UMNp829	AY285528	TCATCTGGGAACCTCCATATG	TTCTCCCATTTAGGGGGTTC	60	2	*SW1602*	0.45	7.22	139
UMNp832	AY285531	GTCAGTCTGGAAGCCTCCC	AGTCAAGCCAGGTTTGGATG	60	8	*SW1679*	0.16	15.24	233
UMNp833	AY285532	CAAAGTCGTGGTGGTCACAG	GTACTCTTCTCCCAGCATCCC	65	16	*S0111*	0.42	7.49	241
UMNp838	AY285534	ACCCTGACTGTCCAGCTCC	TGAGTGTGAGGGAAGACCG	60	1	*SW64*	0.3	9.76	137
UMNp839	AY285535	ACAGGAAGACACTCTTATCGCC	AAGCAGAGACTTCTGGCTATGG	56	16	*SW419*	0.18	14.40	245
UMNp840	AY285536	GGTACGGCCTTCAAACTGTG	CCGAGCGTCTAGGACCTTC	60	9	*SW21*	0.38	8.87	209
UMNp843	AY285538	CTTGTGGTTCGTCTAAGTGGC	TGTGCCATTGCTGACTTCTC	60	7	*S0115*	0.1	17.71	179
UMNp847	AY285541	GGGGTGTTTTGTAATGGCAC	AGTTCTGAGACCACCATGTGG	56	15	*SW2072*	0.09	19.05	168
UMNp848	AY285542	GATAGATGTCCGTTCTCCTTGG	TTTGAATTCACCCGAGTTCC	56	X	*SW2588*	0.39	7.97	246
UMNp849	AY285543	TAGCACACAGCATGTTTCATTG	GCATGGCTACACCATGGAG	56	7	*S0334*	0.54	6.03	193
UMNp850	AY285544	TGGAGTCTGCTTTCTCTCTGC	AGATAAATCACCTGCGGGG	56	4	*MOS*	0.25	11.57	240
UMNp852	AY285545	AGATGCAACAGGAACTCCTAGG	ACAGTGTTCAGTTTATGCTGGG	56	7	*SW352*	0.44	7.50	250
UMNp853	AY285546	AGTGTGCTGAGTGTTGTGGG	AGGCTCTTAGAACTATTGGGGG	56	4	*SW512*	0.39	8.12	137
UMNp855	AY285547	TGGGAGAACAGGCAGGAG	CTCTTGTCTTTGCCCAAAGG	60	13	*S0287*	0.19	13.64	236
UMNp858	AY285549	TCTGCCCCTCAAATAAGGC	TCCAGCTGTGCGACCTTAG	56	7	*SW2537*	0.25	10.97	249
UMNp859	AY285550	GTGCTCTAGCAGAGCGGC	ATCCCCAAATACTATCGGGG	56	7	*TNFB*	0.06	20.51	188
UMNp860	AY285551	ATCCCACATCAGAGACCACC	ATTGTGTCTACCAGTGTGTGCC	62	2	*SSC2F05*	0.38	8.72	159
UMNp861	AY285552	GCCACCTAAAGATTCCAATCC	AGCCAAATGGGTAACAGTGC	54	X	*S0218*	0.19	12.67	248
UMNp865	AY285554	GTCAGGCTGTTAAAGCAAATCC	ACAGGATTCCTCCCACCAG	64	2	*SW1686*	0.2	11.43	191
UMNp866	AY285555	TCCCTCCAGTCCTATCATGTG	TACATACCACATCCCTGGAGTG	54	11	*SSC6E09*	0.15	16.23	133
UMNp867	AY285556	GACCTCTCCTAGGGATGATGG	CCTACTCCTGACCAATGAGACC	54	13	*SW344*	0.13	15.10	135
UMNp868	AY285557	GCAAGGGACTGAGTTCAGATG	TCCTACATGCCCTCAGTATGG	54	13	*S0282*	0.2	12.79	280
UMNp870	AY285559	TTCCTTGGGGGAAAAAAAAC	GTTGCTCTTTATCCTGAGGGG	54	X	*SW1943*	0.53	5.97	186
UMNp873	AY285560	AGAAGCAACCCAGGTGTCC	TCATCTAAATTGCTCCAAATGG	54	13	*CP*	0.16	13.26	142
UMNp874	AY285561	TCACAGATGCAGCTTGGTTC	CTGAAGCCTTTTATTGTTTGGG	54	15	*SW2608*	0.33	9.90	189
UMNp875	AY285562	AGAGGAAACAGCTGGAGAAGG	TTCCCAAGCATTCTCATTCC	54	10	*SWC19*	0.23	12.37	207
UMNp876	AY285563	TTCATTTAACCAAAATCCCTGG	CAGAAACCATTTCTTTCAAGGG	54	10	*SSC10G07*	0.48	6.76	249
UMNp879	AY285566	ATTCACATACCTCATCGCAGG	TCCCCACCTCTTAACCACAG	54	10	*S0038*	0.08	18.30	244
UMNp880	AY285567	GAGGGAGAAAGCAGGCAAG	TTCCTCCCTGCGATGGAG	60	1	*SW65*	0.44	7.44	109
UMNp881	AY285568	ACATCCATATGCTGGAAGTGTG	GCAGCTCTGGGCTGAGAG	54	1	*SW1430*	0.37	8.60	111
UMNp883	AY285569	AATTCCATATGCCGCAGTG	AGGTCAACTCCATGAGAAAAGC	54	5	*SW967*	0.13	17.29	149
UMNp884	AY285570	AAAGGGGCAGGGTAAGAGTG	AACAGGCAGTTTCCTCAGTAGC	62	13	*S0075*	0.31	10.16	138
UMNp885	AY285571	GAATGCAGAATATTGGAAAAGC	TTTGGTTTGTGCTTTACCAGG	54	10	*SWC19*	0.48	6.62	144
UMNp886	AY285572	TCAAGCTTCTTTCAATCATATGTG	CCTTCTAATTGCACTTTGTAATAAGC	54	11	*SW1494*	0.47	7.06	129
UMNp889	AY285573	GATCTTTTTCACTGGGGTGTG	CCAAGGAAACAAGAGAATCCC	60	14	*SW245*	0.07	19.55	172
UMNp890	AY285574	TTGTAATCCCACTACCCAGAGG	CGAACAGCCCAACCAAAC	60	16	*SW2411*	0.09	18.47	176
UMNp893	AY285576	ACTCCACGCTTCCAGGTG	TAGGTCCATCCATGTTTCTGC	54	3	*SW1432*	0.34	9.42	218
UMNp894	AY285577	AAAAGGAAAGCTAGGAATTGGG	TTTTTAGGTAGGGTGGTTGGG	54	13	*S0075*	0.32	9.87	208
UMNp896	AY285578	TGGAGAAATTTCATTGGAAAGG	ACACATCCAGCAATTCCTCC	60	6	*SW709*	0.27	10.58	169
UMNp897	AY285579	AGAGGGCTCAAAACTTGAAGG	AGTTTACCACCTGCTGGGG	54	2	*SW834*	0.26	11.78	125
UMNp898	AY285580	ATTCCAGAGCATTCCAGGG	AAGCTAAAGGGCAGACAGAGG	54	1	*SWR817*	0.11	18.20	163
UMNp900	AY285581	GGAAGCAAGATGCTGGACTC	ACCCATATCCACTCAGGCAC	54	9	*SWR1939*	0.02	24.11	215
UMNp901	AY285582	ACCTCTATATGTCGCGGGTG	AAACCACCAACGTTCACCTC	54	14	*SW1631*	0.2	13.38	222

Table 1 Continued.

Marker	GenBank accession	Forward primer (5′ → 3′)	Reverse primer (5′ → 3′)	Temp	Chr.	*Linked marker*	Dist (Ray)	LOD	Fragment size (bp)
UMNp902	AY285583	CAGTGAAATTGGCCTGTAGTTG	GGACAGGACACTCCCAACC	54	3	*SW236*	0.28	10.96	150
UMNp904	AY285585	TACCTCACACCGTCAGTTGG	AGGACATGAACCTATTTGGGG	54	2	*SW2513*	0.03	19.99	154
UMNp905	AY285586	GATCGATGACTTTTTTGGTGTG	TTGGCTCCTGTGACAGAGG	54	13	*SW882*	0.09	16.22	140
UMNp908	AY285587	AACAACTGACATGTGAGGATGC	GCTACCGGATGTGGATGC	54	6	*SW446*	0.05	18.33	169
UMNp909	AY285588	TGAGCTGATTTCGGAGGC	AAAAGTTTCCTTAGGCTGTCCC	56	8	*S0353*	0.29	9.89	210
UMNp910	AY285589	GGGAATTAAGCTGAATCAGGC	ATGCATTTTTTGTGCTGAAGG	56	17	*CST3*	0.48	6.68	211
UMNp911	AY285590	ATCCATTTTGAGCTGATTTGG	AATCGAGGCAGGTGAATGAC	56	16	*SW1897*	0.02	24.16	182
UMNp914	AY285592	GTTGCTGCCTTGACAAAGC	TCCTTCCACTGTACTCATCTGC	56	13	*S0282*	0.38	8.38	127
UMNp916	AY285593	AAAAATTAAGGCCTATTTGGGG	ACTCAGTTGGTACCTCATGCG	56	13	*SWR2054*	0.44	6.36	183
UMNp917	AY285594	AACTCATGTCGCATCCAGTG	ACTTCCAGCCTCCAGAACC	56	14	*SW1081*	0.07	19.38	189
UMNp918	AY285595	ATCAAAGCTGATGTCTTTCTCC	TTTTCCCTGACTCTCTATTGGC	56	6	*S0228*	0.11	16.20	152
UMNp919	AY285596	CATGCACAAGCTCACACATG	GTATACAGGCCTTGTGTGCTTG	56	15	*SW159*	0.38	8.63	115
UMNp920	AY285597	ATCCAGTGCAGGTGAATGTATG	CGTTCTGAATTATCCTTCAGGG	56	6	*S0031*	0.32	10.12	147
UMNp921	AY285598	TTTGTTTGTGGTTTCCTTTGC	ATGTCTTATGTGCAGGTGCG	56	3	*SW271*	0.33	9.90	246
UMNp922	AY285599	GGCATTGTAGTCTCTCTCCACC	ATCTTGGCTCTCAGAGAAGGC	56	14	*SW55*	0.36	8.55	244
UMNp924	AY285600	TGCTGCAGATTGCAAAAAAG	AATTTCAAGATGCACAGCAGG	56	10	*SW1626*	0.31	10.10	181
UMNp925	AY285601	ACGTCAGACAAATTCCTGGG	CATGCGTCTGAATTTTGGTG	56	10	*SWC19*	0.09	17.87	231
UMNp926	AY285602	CTGGAACACACGTGTATAAACA	ACAAAAGGCAGTCTGTGCCT	54	8	*SW1980*	0.24	9.69	149
UMNp928	AY285604	AAACCGTGCATGTGTGTCC	TTGTAAATCCATTCACTTTGCG	56	1	*SW552*	0.43	7.72	210
UMNp929	AY285605	CATGAGAGTTAGCAGTGCGG	ATCATCCCACCAAAAAGTGC	56	8	*S0098*	0.19	14.30	127
UMNp935	AY285609	CTGACGAACGCCTGGTAAAC	GGGCCCTTCTCTGTAGCTG	58	2	*PTH3*	0.13	16.94	245
UMNp940	AY285610	CCAAAGACTGCAAACCATTG	ATGGTTCTGTTTGAATTTTGGG	62	2	*SW1450*	0.11	15.78	222
UMNp942	AY285612	TACACATGCACATGGGTGC	CCCCTCCTTTGAATCCTTTC	54	7	*SWR1210*	0.29	10.43	164
UMNp944	AY285614	ATGCAAGCCATCCAAGGTAG	AGAGTCTCCTGCTGGAAGACC	64	14	*SW328*	0.19	11.25	180
UMNp947	AY285615	TGCTCAATGTCAGCTCAAGC	CTGAAAGGTGGCTTTGCTTC	58	13	*SIAT1*	0.23	11.24	145
UMNp948	AY285616	GGCTGTGGCTGGCAGTTAC	GCTTCCTCTCTCCATTGCAC	60	1	*SW1311*	0.12	16.33	217
UMNp949	AY285617	CATTCATCTTCCACACACCG	ACCACATCCTGCTCTGCAG	54	4	*SW835*	0.36	9.06	193
UMNp953	AY285619	TGAGGTTGGACTTTGGGAAG	GCTCTGCTTTGTCTGTGCTG	62	3	*S0002*	0.51	6.33	213
UMNp954	AY285620	GAAAAAAATAGACAATCCCCCC	GGTCCCCTCTATTCCCACTC	60	12	*SSC8F12*	0.32	10.19	147
UMNp956	AY285622	TTTTTCCTTTGTTGGCCATC	GCACAAGTGTACCTCCCCTC	58	7	*SW581*	0.3	9.89	190
UMNp959	AY285623	AATGTGAGAATCAGCCCCAC	TTGTAACTCCAAATCCATCACG	60	8	*S0144*	0.41	7.85	275
UMNp962	AY285625	GGATTCCACAGTGACCGAAG	TTTGGAGAATGGCAGAAACC	60	2	*SW1686*	0.43	7.56	277
UMNp965	AY285627	CTGCAGTCTTATCACTTCGCC	TGGTCTGAAAACTCAACCCC	60	2	*SWR308*	0.46	7.26	158
UMNp967	AY285628	CAAATGATGTGTGGACATTGC	ATCTGAATGAGATGGGGCAG	62	6	*SW2419*	0.17	14.84	220
UMNp969	AY285629	GCGCTGTTTCTTTCAAGGTC	CGCAAGCACACATATATGGG	60	X	*SW2470*	0.23	12.53	248
UMNp971	AY285630	TCTCCTCCTGACTCCTTCTCC	TGGGCTGCACTAGACAGATG	60	3	*S0216*	0.4	8.16	196
UMNp974	AY285631	CATATGCTGTGGGATTGGC	AGGCAAGTCTGCTAGCCAAC	60	5	*SW1468*	0.25	12.20	192
UMNp977	AY285633	TAGCTGTTCACAGGGGTGTG	AGGCCATTTCCAAGGTCTG	60	6	*SW709*	0.15	14.73	195
UMNp982	AY285635	CTTGACCCAGAAACCATTTACC	AGCAGAAACTTTGTGGGCC	60	6	*S0003*	0.48	6.50	167

UMNp984	AY285637	TTCCCTTAGACCCCTGCC	GTGGTCACCATGTCGTGTTC	60	3	*SW314*	0.05	20.59	143
UMNp987	AY285638	TCATGGTGGTACACTACCTGTG	TCACAGCCTCTGGTCATCC	64	8	*S0144*	0.34	9.50	221
UMNp993	AY285642	CAATGGTCAATGTCCTTCCC	CATTCCTCCTCAGAAGCAGC	62	17	*ENDO3*	0.29	10.23	182
UMNp1000	AY285165	GGACTCAAACTGCAATTCTTCC	GGTTTTCCACAGAAACAGAACC	60	2	*S0226*	0.14	15.02	210
UMNp1003	AY285167	GCTTTACAGCTGTGTTCTGGG	GAGGACTCCGAGGTGAAGC	58	1	*SW1824*	0.38	8.38	298
UMNp1005	AY285169	TTTACCTTTGAGTGGGTGGC	CAGCGTGAGAAGAACAGCTG	60	14	*SW245*	0.14	16.61	207
UMNp1007	AY285170	TCCAGTGTCCCTACCTGGTC	CCATGTCTGCCCATACCAG	60	7	*SW859*	0.28	10.20	285
UMNp1008	AY285171	AGAACTTCCCCATGCCAAG	CTGTAGCCTCCAGCCTATGC	62	X	*SW1943*	0.42	7.71	310
UMNp1013	AY285175	AGATGATGTGTACTGCTGGGG	CAATGAGGGTCTCCACGG	54	8	*SW2410*	0.23	11.83	400
UMNp1016	AY285177	GCATCAACCCTTTTCTGGTC	GAAACAATAGGGTGCGCG	60	16	*SW1035*	0.37	8.91	270
UMNp1017	AY285178	ACTCCAGGAGTGAGGGGG	GGGGGTGAAACATGACAATC	60	15	*SW1989*	0.11	15.66	248
UMNp1018	AY285179	CCTTTAGTTACCGATGCTTTGC	GACATACAAATGGCCAACAGG	60	2	*SW2167*	0.19	13.64	203
UMNp1019	AY285180	CTGCTCATCAAGAGCACTGC	TCAATCAACCATTGAGGAAGC	60	2	*PTH3*	0.23	12.53	245
UMNp1021	AY285182	GGCCCACTAGAAGCCAGAG	GCAGCTGCAGCTCTGATTC	64	4	*SW489*	0.44	7.45	190
UMNp1022	AY285183	AATGAAAATCAGCATGAAAGCC	CACATTTCTTTGCTTTCTGGG	60	2	*SWR1445*	0.28	9.61	246
UMNp1023	AY285184	GGGCGAAAGGTAAGAGCAG	TGTCTAGCAACCGAGTGCC	60	2	*SW2623*	0.21	12.67	161
UMNp1026	AY285187	GAGCCACTGTGAGTTACACAGC	GAACTGAAAAGCGGCAAAAG	60	13	*SWR1008*	0.17	12.40	206
UMNp1028	AY285188	TACTTGCTCCCAGCAGGTG	CAAACTCTTTCTCTCCCCCC	60	18	*SW787*	0.14	16.18	193
UMNp1029	AY285189	TTCCCCCAAAATTTCTGTTG	TTGAGATTCTGGGAAACATGG	60	6	*S0031*	0.55	5.90	204
UMNp1030	AY285190	CCTGACTCCTGTGTTTTGACC	TCCCCTTCATTTTCATAGCG	60	2	*S0141*	0.26	11.78	224
UMNp1031	AY285191	CCAGTACAAGTGTGTGCATGC	CATTGATTGAGTGCATTGCC	60	6	*SW709*	0.25	11.46	164
UMNp1032	AY285192	AATACAACTGCATTGCTTGGG	AAAATGTTTTCCATCATCACCC	60	6	*SW1473*	0.43	7.43	183
UMNp1033	AY285193	CAAAGAAAAATACAGGGAAAATTAC	TATTTGGCTTGGCTGAAAGG	60	2	*SW1686*	0.25	10.81	217
UMNp1034	AY285194	GATGAAAAAGTTCTGGAGGTGG	ATATCGGTGAAAGCACCGAG	60	13	*SWR2189*	0.17	13.94	214
UMNp1037	AY285195	TAGAGCTACCTGCATGTGAAGG	TTGAAGCAACACTGGGGG	56	7	*SSC12B09*	0.46	7.31	253
UMNp1038	AY285196	CCATAAAGGTCATTTTCAGCC	CCCCACACCACATACTTTTG	56	13	*SWR2054*	0.21	10.09	250
UMNp1039	AY285197	TGCCACAACTCAAGAAGTCTG	GAATGTTGTGGGGGAGAGG	60	15	*S0149*	0.2	13.99	182
UMNp1041	AY285199	GGCCACCTCCTGAACATG	TGTTTGCTTTCAGTGCCAAG	60	8	*S0353*	0.31	10.16	220
UMNp1042	AY285200	CATACAACCACGCCGTTTC	TCTTACACTGGGAGAACACACG	60	4	*SW480*	0.21	12.96	231
UMNp1043	AY285201	CGGATTAGACCCCTAGTCTGG	TAGGGTTACTCTGCCCCATG	60	5	*IFNG*	0.5	6.80	168
UMNp1044	AY285202	TTGTATCCCTGGAGAGAGAATG	AACAAATGGGAGACACGGTC	60	8	*SWR1101*	0.28	10.96	231
UMNp1045	AY285203	TGAGAATTCAAGGACTGGGC	TGTGTCTCCAATTTTTTTTCCC	60	4	*SW1513*	0.33	9.24	242
UMNp1049	AY285206	CCTGGTTCCTGCTTTCTCAG	GTTAGACAACAAGCAGCACAGG	60	10	*SWC19*	0.35	9.27	203
UMNp1053	AY285209	GGTACGGTACGGAAGGGG	GGGTACGGATGTTTGGTCC	58	13	*S0291*	0.16	9.62	255
UMNp1054	AY285210	TCCAGGGCAGAGAGTAGTTAGC	CGCCCACAATGACTTTCC	60	12	*SW943*	0.3	10.42	200
UMNp1056	AY285212	CTGTCCATGATGTTGAAGATGG	GGATCTTGGGAAAGGGTGTC	60	2	*SW1320*	0.07	19.30	151
UMNp1057	AY285213	TCTAAAGCATCCAAGGGCAC	GCGGAGAGTTAAGTGGATGC	60	3	*SW2618*	0.25	12.03	183
UMNp1058	AY285214	TCACTTTTCTGGGCTGTGG	ATTGGTTAGCCAGACATGCC	60	8	*S0098*	0.36	9.25	250
UMNp1059	AY285215	TCCCAGAGTCCTTTGAATGG	AAGAGACACCTTGAGAGAATGG	60	1	*SW1332*	0.36	8.77	273
UMNp1062	AY285217	GTCCCCAGGTATTTTCCTCC	ACTTGCTCCTATTTCCTTTCCC	58	13	*SW482*	0.37	7.39	270
UMNp1063	AY285218	GAAGCCAAAAAAAAAGAGCCC	GACCAAAGAGGCAGCTGTTC	60	12	*SW2494*	0.07	18.15	176
UMNp1064	AY285219	CTCAAGCTGGCATTTTATACCC	AATGGATAAGTGGTTTGCAGTG	60	4	*S0107*	0.52	6.36	242
UMNp1065	AY285220	CTCCCTCTCTCCTTCCACG	CAGAAGCTAAGACATGCTGGG	60	8	*SW1337*	0.26	10.89	175

Table 1 Continued.

Marker	GenBank accession	Forward primer (5′ → 3′)	Reverse primer (5′ → 3′)	Temp	Chr.	*Linked marker*	Dist (Ray)	LOD	Fragment size (bp)
UMNp1067	AY285221	GGGTTGTTGTAATGGCCAAG	AGCCACTAGGGAACTTCAAATG	60	13	*SW1407*	0.19	12.17	237
UMNp1068	AY285222	GCTGAGTGATTTGCCTTTTACC	CTGCTGCAGTGAGGTAGCTG	60	16	*SWR2080*	0.15	15.32	152
UMNp1069	AY285223	TCTTTGGGTGCCTATGATATCC	GGTGCTGAATGCAGCATG	60	6	*UOX*	0.2	13.88	133
UMNp1070	AY285224	AGACTGATGCTGCTGGGG	CTTGAGCTGCTGCCTCTTG	60	2	*SWR1338*	0.22	12.91	255
UMNp1074	AY285228	ATGTTTCTGATGGTTTCCGC	CTTCCAAATGCCACAGGC	60	3	*SW1443*	0.22	12.90	200
UMNp1075	AY285229	AGGGTTCTCCAGAGAAAACAG	CAGTTGCTGACTGGAACTTACG	60	7	*SW1369*	0.44	7.59	236
UMNp1076	AY285230	AGAGCCTGCTCATCACGG	CTTCCAGAAAGGTAACTGCTCC	60	7	*S0115*	0.24	12.15	226
UMNp1080	AY285232	GAAGGCTACTGTTTTGGTCACC	TTGGAAATGACCTCATTCTCG	60	7	*SW2537*	0.08	17.31	297
UMNp1082	AY285233	GAAGCTGGAAACAGCAGGAG	GAAACTAACCGAAACCCTTGC	60	9	*SW511*	0.24	12.60	153
UMNp1084	AY285235	TTTCCCCACCAAGAACTACG	TGTACAGATGAGCGGAGGG	60	14	*SW6*	0.36	9.06	176
UMNp1085	AY285236	AGAGGCAGAGAGAAGGGTCC	GCTGTGCACACACAAATGC	60	5	*SW70*	0.29	10.80	210
UMNp1086	AY285237	GCACCAAAAAGGTGTTAGAAGG	TGTTGATGCTGGACTCTTCG	60	11	*SW903*	0.22	12.87	195
UMNp1090	AY285239	TTTTTAAAGAAAAAAGACAGCTTCC	TAAAACTCTCTGTGCCTCAGTAGC	60	3	*SW833*	0.22	12.90	230
UMNp1091	AY285240	GAGAGAAGAAGGGGTGGGAG	TGCTTGAACTCTTGCCTGG	60	4	*SW1364*	0.41	8.13	106
UMNp1092	AY285241	AGGAAACATTAAGGAGAGATGTAATG	AGTTCTCCTGCAAAAGCTGC	60	8	*SW1679*	0.21	13.90	166
UMNp1093	AY285242	AGGGGTCTAGGACTAGAGGGG	CCCCTACATGGGTGAAAATG	60	6	*RYR1*	0.09	15.39	201
UMNp1095	AY285243	AGAAAAATGGTGATGCCAATG	GCTGACATTCTTCTCAGGTCG	60	10	*SWR67*	0.53	6.05	254
UMNp1097	AY285245	GAACCTCCATATGTCGTGGG	GGGCAAAACAGGTGATGTG	60	9	*SWR1848*	0.48	6.76	241
UMNp1099	AY285247	GTTCTTTCAGGAGCAGGAAGG	GGGTTTCTTGTTGCAAAAGC	58	6	*S0220*	0.16	13.37	244
UMNp1101	AY285248	CTTTCTGTGCCAGGAGAAGG	GAGTCCTCCCACCTACCTCC	60	9	*SW2074*	0.13	15.73	276
UMNp1103	AY285250	ACCTCTATATGCCGCAGGTG	ATGAAGGGAGGAGGTCGG	60	7	*SWR1210*	0.22	12.53	182
UMNp1105	AY285252	CTGGGTATAAGTCCAGTCCTCG	GGAGGTAGGAGAAAAATAGGGC	60	1	*SW301*	0.17	15.05	275
UMNp1106	AY285253	CTAGGACTTTTCATGGCAAACC	TGGACATAAACATTTGGGAGC	60	6	*SWR726*	0.28	10.59	291
UMNp1107	AY285254	GTGTGTGAGCCAAACAATCTG	TGCTGTCTAGGGGAGACCC	60	2	*SWR308*	0.36	9.40	183
UMNp1108	AY285255	TTCTGTTTTTCATGGACAGCC	TTGTACATCAACAGTGTGGGG	60	17	*SWR1133*	0.3	9.64	255
UMNp1109	AY285256	AACCCACATGGTGAAAATAAGG	CATGGTGGGAACTCCACTG	60	3	*IL1B*	0.23	12.38	210
UMNp1111	AY285257	GGAAGGTCTGAACATAACAGCC	CTGTGGTCAGCAGCTGTAGC	60	1	*SW1431*	0.25	11.46	303
UMNp1113	AY285258	TTGCTGAGCCTGTGGTGTAG	TTTATCCCTCCCTGTTTCCC	60	11	*SW1486*	0.51	6.52	205
UMNp1114	AY285259	CTTTCACTGCGTAATGCACTG	ATCAACCAGGGACTGCTCC	60	7	*SW1369*	0.35	9.20	173
UMNp1115	AY285260	CGTTAGGCTATCTCTTCGATGG	TTGCAGGCACTAGTATGTCAGG	60	10	*SW1829*	0.31	10.78	238
UMNp1116	AY285261	GTAGGGGCAAGAGCCAAAG	TTTGGACTTGCAGTCCTGTG	60	2	*IL4*	0.41	7.91	169
UMNp1118	AY285262	GAGTGTCGGTTTGTGGCC	TCTTCCACTTTCCGACCG	60	3	*SW717*	0.43	7.52	254
UMNp1120	AY285264	GAGGCCTATGAATTCTGGACC	AGCTCTGATTTGACCCCTAGC	60	11	*SW878*	0.12	17.12	154
UMNp1122	AY285265	TTGGAATAAAGAGCCATGGC	TGGAAGGGACCTTGTACCAG	54	7	*SW1369*	0.38	8.58	316
UMNp1127	AY285268	TCAATTTTGTGGGTATGACCTG	TCTCCCCTCGGGTTTAGTG	60	X	*S0218*	0.31	8.83	218
UMNp1130	AY285270	AGAAACCTCTGAACCATTCTAAGC	CCATCTTTTGCCATTGGG	58	13	*SSC24F05*	0.49	6.32	344
UMNp1131	AY285271	GTTTTCCAAATAGCAGAGACCC	TTGCATTTGGAATGGATAAGC	60	6	*SW1129*	0.1	16.49	203
UMNp1133	AY285273	ACCATGATAGAAAATAAGAAAGCG	CAACAACAACAACAAAAGACAC	60	14	*S0007*	0.16	13.26	180
UMNp1134	AY285274	TGCCCACTCTCAGCTTCC	AAGAATCAGGCTCTGGTCTCC	60	3	*SW1327*	0.1	17.55	188

UMNp1135	AY285275	AGACTGGCATTATGGAACCG	TCCCTAAAGGCCTGTCCC	60	4	*SW839*	0.41	7.53	341
UMNp1136	AY285276	TCATTTAGCTCCCCCATCAC	GAGACACAATGGCAGGTGG	60	5	*SW152*	0.29	10.80	280
UMNp1137	AY285277	AGGCTCCATTATTTCATTGGG	GCCCAATAATTGGGACAGC	60	9	*SWR1848*	0.19	14.10	218
UMNp1138	AY285278	CTCTCTGTAATATAACCCCGGC	TTTGTTGAATTTTCTTCTGGGC	60	7	*S0064*	0.39	8.07	235
UMNp1140	AY285279	TTGTAGTAGGCCATGTGGACC	CTAGGAAGGGGTACAGGAACTG	60	6	*SW855*	0.31	10.27	225
UMNp1141	AY285280	CTGCTATTGCCTTGCCTTTC	GAGGACCTGCGATATTAACAGG	56	4	*SW835*	0.3	10.42	282
UMNp1142	AY285281	TCCTTCATCAGACCCTGGAC	CGGCTTGTTTAGAATAAGTGGG	60	3	*S0216*	0.37	8.64	325
UMNp1144	AY285282	GCCGCTCTGAATGATAGCTC	GGCTCTCAATTTTGGCATATG	60	16	*SW1897*	0.34	9.73	166
UMNp1145	AY285283	CAAATAGATAAAATGCCCCCC	CTTGTCATCATGCTTGGGG	60	6	*SW193*	0.11	13.77	218
UMNp1146	AY285284	GGAAGACACCCATGTCTCTAGG	GGTAAAGGATGCTCAGAATTGG	60	4	*SW512*	0.46	7.14	222
UMNp1147	AY285285	AAGTGTTTAAAATCTTAGTGTGTGC	CAAACAGCATCCATCAGGG	60	2	*SW1602*	0.36	8.83	142
UMNp1148	AY285286	GATCACCATAATATCACATACACAC	ATATCTCTTGTCCATTTATTCCTCC	60	1	*GGTA1*	0.33	9.57	220
UMNp1149	AY285287	GCATGTGCACACACGTGC	TCCAACAGCAATACCTATGGC	60	17	*SWR1004*	0.3	10.00	213
UMNp1152	AY285289	ACGCGTGTGTATATAATGCATG	TCCATATGCTGCAAGAGCAG	60	14	*SW55*	0.25	10.14	171
UMNp1153	AY285290	TTTTGAAGAAACCCGGAGG	GCAACTAGGGCACAACTTTAGG	60	6	*SWR1384*	0.32	8.70	365
UMNp1154	AY285291	GGCAACAAAAGGACTCATTAGG	CTTTGGCTCCACTGAGCTG	60	1	*SSC10D08*	0.18	12.80	161
UMNp1155	AY285292	TGCTATACAGCACAGGGAACC	TACAATGTTGTGTGCCAATTCC	60	15	*SW1111*	0.45	7.41	150
UMNp1156	AY285293	CCTGTTGAGTTGGAGATGATTC	TGCATATTGGTTTTGTCTTTCG	60	1	*SWR702*	0.41	8.17	201
UMNp1157	AY285294	GCTCAGAGCTATCCCTGGG	TCCCACATTAGAGCCCCTC	60	1	*SW2551*	0	22.25	315
UMNp1158	AY285295	TTTTTAAAATTGAGCCCCCC	ATTTAGGATGCATTTGTAGGGC	62	3	*SW271*	0.22	13.26	361
UMNp1161	AY285296	ATCCTCTTTGCAAACATGGC	TGCTATATAGATAGCAGACATTGTG	60	12	*SWC23*	0.27	9.97	235
UMNp1162	AY285297	AGCGCACACGTTTTGAAAG	GGAAACTTGTAAATGCCTTTGG	60	2	*SW1686*	0.34	9.37	237
UMNp1165	AY285300	AACAAAGCAAGGTGGGAGAG	TATAGGGCCTCCCTGAGTAATC	60	3	*SW1045*	0.33	9.45	160
UMNp1166	AY285301	GAGCAGAAGTGATGGGAAGC	AGTTGTGCAACTTGGTGCTG	60	1	*SW962*	0.34	9.37	269
UMNp1167	AY285302	GGCTGTGGTGTAGGCTGG	TTATATTGCAACACCACATTGC	60	10	*SW305*	0.21	13.90	220
UMNp1169	AY285303	GGCATAGGTTGGCGATTG	ACATGTGATTTTGTTAGGCGG	60	13	*SW2459*	0.16	14.54	171
UMNp1171	AY285304	TAGCCCTTGGCTCACAGTG	GGTTCGTGGTGACTGGATG	56	12	*S0106*	0.26	8.81	182
UMNp1174	AY285305	TGTGGAGTTCCAGCCTTAGC	TCTGATTAGACCCCTAGCTTGG	60	X	*SSC13B11*	0.25	11.91	115
UMNp1179	AY285308	AGCAAGCAAGCAAACATGTG	AGGGCTGTGGATGGCTATC	60	2	*IL4*	0.39	8.12	183
UMNp1180	AY285309	CTCCAGGTTTGTGAACCTTACC	AGTCACTGATGCTGGCCAG	62	13	*CCK*	0.07	19.94	226
UMNp1185	AY285312	AACTCACTGTGCCACAGCAG	GAAAACCACTCTTGGGTATTGC	60	5	*AC02*	0.3	8.89	207
UMNp1186	AY285313	GGAAGGAGCTTAAGGTGATGG	GGGAGTGTTTATTCCTGAGCC	60	14	*SW2515*	0.19	12.13	193
UMNp1188	AY285315	AGTGTTGCCACAAATTGCAG	AGCATTGGCCAATAGTGGAC	60	8	*S0144*	0.36	8.36	241
UMNp1189	AY285316	ACCAAAGGTCTCACAGCCC	CGTTGCAGTGACCTGGTATG	60	16	*SW1897*	0.19	14.27	200
UMNp1190	AY285317	TGATGCATTTTCTCTATGCCC	TATTCATGCACACATGCTTAGC	60	13	*S0084*	0.35	8.43	180
UMNp1196	AY285319	GAGAAATGTATTTTGGCAAGCC	CATCTTACTCAAATCCCAAGCC	62	3	*S0167*	0.44	7.57	237
UMNp1197	AY285320	TGTGTTCCAGCCAGCCTC	GATAATCAACAGGGACTTGCTG	62	13	*SW1876*	0.24	10.60	248
UMNp1198	AY285321	GATCATGAGTCTGTCTGTCTCAC	TTAGACCTGAAGGGCTGAGG	62	1	*SW780*	0.18	13.53	131
UMNp1199	AY285322	TGCTGTACTGGCAGCATAGG	TGCTTAATTTAATCCACCCCC	62	9	*SW866*	0.09	18.64	259
UMNp1200	AY285323	GGTCCACCCTCATTGCTG	ACCCAAAGTCTTGGTCTACAGG	62	15	*SW1316*	0.29	10.43	182
UMNp1203	AY285325	GAACTTGAATAATAAAACTTTGGGG	ACCAGCCTGGAAACATTGAG	60	4	*SW1336*	0.22	13.10	176
UMNp1205	AY285327	TCCCTTTCTCTCTGGCTCTG	TTGCTCTGACAAGAGGAGACTG	62	9	*SWR1848*	0.14	15.81	226
UMNp1206	AY285328	GGGGAGTAGCAGGAGTTAACG	AAAACCCACAAAGTTTGATTGG	60	2	*SW1320*	0.14	15.47	227

Table 1 Continued.

Marker	GenBank accession	Forward primer (5′ → 3′)	Reverse primer (5′ → 3′)	Temp	Chr.	*Linked marker*	Dist (Ray)	LOD	Fragment size (bp)
UMNp1207	AY285329	AGGAGGTGATGCTGGATAGTAG	TCATTCCTCCAGCAGTACTTCC	60	6	*UOX*	0.15	15.47	249
UMNp1208	AY285330	TTTAGACTGGGAATGCAATGC	CCAGATTTGGTCCCATATGG	60	X	*SW2588*	0.08	17.32	216
UMNp1209	AY285331	TGTGCCTCAAGTCATATAAAATATG	GCAAGGACACCTCCTCTCC	60	1	*SW1824*	0.51	6.36	250
UMNp1211	AY285332	TTTGCTTCTCTGCTTCATTCTG	CTGAAATCAAACTCTCAATGGG	60	5	*SW2003*	0.27	11.48	164
UMNp1212	AY285333	GGCTGGAAGTACTGGTGTCTG	AGAGCATCAAATCCCACAGG	60	9	*SW511*	0.48	7.02	126
UMNp1215	AY285335	CAGGAAGACTCTGTGTCCCTG	TGAATCGAGTTTTGCACAGC	60	13	*S0282*	0.5	6.39	174
UMNp1216	AY285336	TTCTCTGTGGAGGACCCTTG	TGGTTTGTTGCAGACTGAGG	60	1	*SW1332*	0.41	7.74	318
UMNp1217	AY285337	TGTTCCATGAGAATACCTGCC	TGCTCAGAACCATTGAATTCC	54	7	*SW1369*	0.47	6.82	351
UMNp1218	AY285338	AACCGGTAAGCAGGTTCATG	CTCTTTGGCAAGAGGGAGC	58	X	*SW154*	0.07	19.73	357
UMNp1221	AY285341	TTGAGCATTCTTGGATTTTGG	TTACTGCCTTTTGGAATTTTCC	60	8	*SW268*	0.2	13.71	175
UMNp1222	AY285342	GTAAGTGCCTGAACTGTTATAGAAGG	AGAAGCAGCTTTTTGATTTACTTG	60	1	*SW1430*	0.17	14.81	215
UMNp1223	AY285343	ACTCACAAGCACTTCAGTCAGC	GGTGGTTAGGCAAAGCTCAG	60	13	*SW2196*	0.15	13.81	316
UMNp1224	AY285344	GTACTGGCATCTTTTTCAAGGC	GAGGTCATGAAATGGAAGAAAC	60	1	*SWR817*	0.21	13.61	214
UMNp1226	AY285345	AGTAAATGGATTGGCTGACACC	GGTTTCACAAAGCGAAAAGC	60	13	*SW482*	0.37	7.76	168
UMNp1227	AY285346	TTGCCTGGAGCAAAAGATG	GTATCTGATTGGTTAGCTGGCC	60	14	*SW510*	0.04	21.55	234
UMNp1228	AY285347	CTGTGTGGGCAGATGCAG	TTTTGCCTCTGTATTGGTTGG	58	6	*SSC8E02*	0.08	13.63	324
UMNp1230	AY285348	TCTCCTGAGATGGCAGCC	GAGCTGTTTCTTGCAAAGGG	60	7	*TGFB3*	0.16	13.99	165
UMNp1231	AY285349	TGGCCCCGTGATTTGTAC	ACTATGATGTGGTGTGTCAGGG	58	2	*SWR308*	0.16	15.76	364
UMNp1232	AY285350	TAGGAGTGGACCACCCTACG	ATTTGGGCTGCAAGAAACC	60	2	*SW942*	0.13	15.73	173
UMNp1235	AY285352	GTAGGCTGATGGCTACGCTC	TTCTGCTGCACAACGATAGG	60	3	*SW1978*	0.17	14.77	210
UMNp1236	AY285353	GGAGGCCAGCAGCTACAG	GATCTTTCATTCATCATTTTG	56	2	*SW2623*	0.1	17.81	136
UMNp1237	AY285354	AGCCACAGGCACAGAGATG	CTCAAAATACCCGAAGAACAGG	60	10	*SW951*	0.08	19.33	220
UMNp1239	AY285356	ACCCCCAGTATTCACAGCAG	GCTGAGTAACATTCCTGTGTGG	60	13	*SW2007*	0.2	12.52	142
UMNp1240	AY285357	CCTTAATTGGACCCTGAAAAC	CATCGTGCACCAAAGCAG	54	6	*SW855*	0.16	15.70	357
UMNp1242	AY285359	AACTCCGCTGTCAGCTGG	TTGCATGGGCTTCATGTG	60	13	*SSC24F05*	0.15	13.36	184
UMNp1243	AY285360	CCTTTGGAGTGGGTGTGG	GCTCACACATATTCACCCCC	60	X	*SW1044*	0.49	6.92	249
UMNp1244	AY285361	GCTTGAGAAGACCTGCAACC	TGAATGGGAAAGGGAGAGG	60	8	*S0353*	0.36	8.94	210
UMNp1246	AY285362	CTGCCAGGCTACCAGAGAAC	CCAAAGGGAAGGAGAGAAGG	60	13	*SW1400*	0.24	9.84	370
UMNp1247	AY285363	GTATGTGCATTTGGGTGTTCC	CTTCCTGAACAGAAGCCCTG	60	2	*SW1450*	0.2	12.84	241
UMNp1248	AY285364	TCTGGCTTTCACATCACAGC	TCCTCAGGGAGTGTGTATTGG	60	5	*AC02*	0.36	8.72	217
UMNp1249	AY285365	GCAGAGCTACAGCTGCCTG	CTCTTAAAACACTTGATGGGCC	60	15	*S0148*	0.26	11.78	315
UMNp1251	AY285366	ACGGTGGAGGAAGAATTCAG	GGCCAATGTGTAAATAAATGGG	60	1	*SW1430*	0.21	13.40	250
UMNp1252	AY285367	TTGTCTCTGTGGCACCTCAG	TTGTTGCAAATGTAGTTTTCCG	60	14	*SW1333*	0.14	13.22	238
UMNp1256	AY285369	GTCCAATCTGTTCAGTCAAAGG	AAGTCTTTTGAGCCTTGATTGC	60	1	*SW1621*	0.25	12.23	156
UMNp1257	AY285370	TAGTCTGGGTGGCATGGAG	GATAAACACTCTTGCTCTCCCC	60	6	*SW1059*	0.38	8.86	151
UMNp1260	AY285372	CAAAAAGGAGGCAGAGAAATAC	TTGTCCCATAGCCCAGCTAC	60	7	*SW352*	0.35	9.11	190
UMNp1262	AY285373	TCTTGACACAACCTTGGCAG	AGAGAGCTTGGGCCTTTCTC	58	14	*SW1536*	0.11	15.92	230
UMNp1263	AY285374	TGTTCTCCCTCCCCTTCC	TGGAGCTAAGTTGGGAGGG	64	9	*SW2401*	0.34	9.55	295
UMNp1264	AY285375	TGGCCAGGCTTTTCTCTG	TCCCAAAGGCAAGGATAGG	60	1	*SKMC1*	0.54	6.00	169

UMNp1268	AY285376	GTATCTAATGGAGCTGTGTGCG	GAGACATCACAAGAGGCAAGC	60	14	*SW1081*	0.1	17.71	152
UMNp1269	AY285377	ATCTGAAGGGGCAGGCAG	GCAGGGTGGAAGGTGTTG	60	1	*SW705*	0.25	11.32	226
UMNp1271	AY285378	TCAACATAGGTAGGTGAGAAGTTC	GAGAACTATCTGAGAGACCAGGC	60	4	*SW286*	0.24	11.87	148
UMNp1273	AY285379	GCTATTTTCCCTCACTGAACTG	TGCCACTTACTCCTTTCCTACC	60	8	*SW1679*	0.22	12.71	163
UMNp1275	AY285380	TATGTGAGAAGGTGAGGGTGG	TGGAGACAACAGATGCAAGG	65	5	*SW152*	0.32	10.23	203
UMNp1276	AY285381	AGCAAACCACAAAAACCCAG	AGTGCCATGTATCCAAGTCATG	60	1	*SSC1F12*	0.05	20.93	249
UMNp1278	AY285382	CAAACCTAGATGAGCAAATTTC	CAGACGGAAAAACACCCAAG	60	X	*SW949*	0.26	11.91	255
UMNp1284	AY285386	CGGCCCTAAAAAGACAACAG	AGAACACAGCTGGTGAAAAGG	60	9	*SW1651*	0.04	21.36	144
UMNp1285	AY285387	GTAGCTGTGCAAGGCAATAGG	TGAGGCTTTGGTCAAGGC	60	1	*SW1668*	0.39	8.56	132
UMNp1286	AY285388	GTCTGTGTCCACACCATTTCC	GCATAACCATTCTCATTTCACC	60	7	*SW859*	0.18	12.80	234
UMNp1287	AY285389	TTTCTTTTGGGTGGTGAAGG	GACCATATTGGGAATTTGTTGG	60	3	*SW1432*	0.1	17.04	161
UMNp1290	AY285391	AATGTGCTTTTTGTCCTGGG	TGAAACACTTCTGCGACCTG	60	3	*SW487*	0.28	10.00	205
UMNp1291	AY285392	AAGGACAACAACGTTCAATGC	TTTGGCATGCTATAAGACACTC	60	8	*SW211*	0.26	11.78	177
UMNp1292	AY285393	CAATTTTATACAGGGAAAAAAAGC	GCAGCTAAGGCATTTTGAGC	56	1	*SW1061*	0.41	8.02	228
UMNp1293	AY285394	GCTTCGTGAGGCCAAATG	AAGGAGAGAGGGAGGCTCAG	60	14	*SW886*	0.18	13.08	260
UMNp1294	AY285395	GAGAATTTTAAAACTCCCTGAGC	CTGAAATGGACTTGTGGGTG	60	5	*SW1319*	0.37	8.50	234
UMNp1295	AY285396	AAGCAACAACCTGCAGCC	CGACTACTTTACTCAGCTGCCC	60	13	*SIAT1*	0.11	13.51	233
UMNp1298	AY285397	ACACTTTGTTGCCTTGTCTTTC	GAAGGTTCACCAGCAAGAGG	60	13	*SW482*	0.33	7.39	257
UMNp1299	AY285398	GCTTTAGCAACAAGGGCTTG	TAACTGTGGCATCTGTACACCC	60	18	*S0120*	0.18	14.40	187
UMNp1302	AY285399	AGAGGCCTTCTGCCCATC	ATTATGATGTCAGGTTGGGAGG	60	6	*SW1680*	0.38	8.32	191
UMNp1303	AY285400	AAAAGGAAAGGAAAGAAAGAGTG	ATATGCTTCCAGAGTTTTCTATGC	60	13	*S0282*	0.33	9.75	133
UMNp1304	AY285401	TCTGGAGCATCACTGTCTGG	TCTGCCAGCAGGTACAGATG	56	6	*SSC8E02*	0.15	10.37	278
UMNp1305	AY285402	CTCGATTCTGCACCTTCCTC	AAGGTCAGTCTCCCTGAAAGC	60	6	*S0031*	0.52	6.12	321
UMNp1307	AY285404	CTGAGCCATGACAGAAACTCC	CTTTGGGGAGAAAGGTAATGG	60	13	*SW2440*	0.34	8.58	194
UMNp1308	AY285405	ATGAGGGCCCAATACAAGTG	GGCCTGGCTAACATATGAGG	60	1	*SW1123*	0.28	10.62	132
UMNp1309	AY285406	AATTCAGTTTGTCGAGCATTTG	GTTTACCAGGCATTCTGCTAGG	60	1	*S0122*	0.24	12.16	150
UMNp1310	AY285407	ACGTCCTTCAACAGATGAACG	ACGGCAAAATTCCATTTTTG	60	16	*SW262*	0.32	9.95	138
UMNp1311	AY285408	AGCTCCATGCCTGGAGTG	AGGATAAGTTTTCATTGAACGG	60	14	*SW1709*	0.18	14.25	183
UMNp1312	AY285409	TCAACATGCTTCTTTTTTGAGC	ATGGGGAAAAAAGAAATGGG	62	3	*SW236*	0.5	6.67	283
UMNp1313	AY285410	CCACTGCAGGGAAAATATTTC	AGCCAAATGATTTTTGAGAATG	58	12	*S0090*	0.22	12.48	148
UMNp1315	AY285412	GACCCGTTTCAAACTCCTACC	TGTGTATTTACCCATGAGCAGG	62	3	*SSC12E07*	0.37	8.64	197
UMNp1317	AY285413	TTATCCTTAGTTGTCCATTGGC	GGGCCCAGGAATTTCTGTAC	64	15	*SW1118*	0.4	8.33	225
UMNp1320	AY285414	TCTTCTTTGCCAGGTAAGGC	CTGCAACTATCTGAACCATTGG	65	13	*SW1550*	0.48	6.68	137
UMNp1321	AY285415	ATAGCCCATCTCACCTGCC	GACTGATGAACTCGCTGAAGC	60	2	*SW1408*	0.31	9.99	177
UMNp1322	AY285416	CATACACGTGCGAGCCTG	AGTGTGGACAGGAATCAGTGG	60	5	*SW1468*	0.23	12.84	140
UMNp1323	AY285417	AGGGAGCTGTCTGGGTCC	AACTGCATATTGGACGTCCC	66	16	*S0105*	0.46	7.28	242
UMNp1324	AY285418	TTCTCAAGCAAAATTGCCG	AAGCTGCTGCTCTTAGTGTGC	60	7	*S0334*	0.51	6.52	224
UMNp1328	AY285421	GTGTTGCCGTGAGCTGTG	AGGAATTAGACACCGGAATTTG	56	8	*S0086*	0.39	8.76	190
UMNp1329	AY285422	ACTGGGCACAACAGAGCTG	GCCTGGGAACTTCTATATGCC	62	14	*SWR1113*	0.14	14.89	127
UMNp1330	AY285423	CCAGCAGGGAGAGTTTTGAG	ACTTCCAGTTGTCCTGGTGG	66	13	*SW1495*	0.42	7.81	329
UMNp1331	AY285424	CTTCCAGAGCCATGGAAGAG	ACAAGAGGCCAGTCCACG	60	2	*SW1602*	0.17	13.70	181
UMNp1332	AY285425	TCCACTCACCAGGAGATTCC	AGGCAATAAAACGCAAGGG	60	7	*SWR1210*	0.26	10.40	202
UMNp1338	AY285427	ATTTTTTTTCCCCTTCGGTG	GTTTCCTGAAAGGCAGCAAG	60	18	*SW787*	0.18	14.52	223

Table 1 Continued.

Marker	GenBank accession	Forward primer (5′ → 3′)	Reverse primer (5′ → 3′)	Temp	Chr.	*Linked marker*	Dist (Ray)	LOD	Fragment size (bp)
UMNp1339	AY285428	CAAAGAGGAAAGGGGAGGAC	GTAGGTTGTTGTTGGACACTGG	60	3	*SW487*	0.38	7.90	157
UMNp1341	AY285430	CTCGAATCCCAGGCAGAG	AAAAGAGCTTGTCCTATGGGG	60	13	*S0075*	0.05	18.75	144
UMNp1342	AY285431	CTTCAGGGTCCATCCATGTC	CAGATGAATGGATAAAGTCATACG	60	7	*SSC12B09*	0.51	6.52	211
UMNp1343	AY285432	TCCACACACTTTCTAGCATTTG	TTCAAAGTTCCATCAAGGAACC	60	6	*SW1353*	0.17	13.70	145
UMNp1344	AY285433	GAATAGGAAAAAATGGCCTGC	ATTCCCAAGCTCTTGTGCC	60	1	*SW2130*	0.38	8.69	180
UMNp1347	AY285434	TCAGTAACTTATTACCCTTTTGGG	ACGTCCTCTAGAGTTTGAGAACC	60	11	*SW1460*	0.43	7.33	150

automated DNA sequencer (ABI 3100, Foster City, CA, USA). All sequences were queried against each other as well as previously mapped clones.[1–6] Polymerase chain reaction (PCR) primers were designed interactively with Primer v.3 (Whitehead Institute for Biomedical Research, http://www.genome.wi.mit.edu/cgi-bin/primer/primer3_www.cgi) and primer pairs were typed on the porcine IMpRH panel.[7,8] Mapping data have been placed in the INRA RH mapping database (http://imprh.toulouse.inra.fr/). Map distances and two-point LOD scores were derived from the INRA RH website. The position of markers for which the two-point LOD score was <6 should be considered preliminary.

PCR conditions: Oligonucleotide primer-pairs for each locus (Table 1) were optimized for PCR amplification by testing over a range of annealing temperatures against porcine and hamster genomic DNA to ensure porcine-specific amplification. PCR reactions (15 μl total volume) included 25 ng RH DNA, 1.5 mM $MgCl_2$, 2.5 pmol of each primer, 100 μM dNTP, and 0.35 U HotStarTaq polymerase (Qiagen, Valencia, CA, USA). Amplifications were performed on a MJ Research thermal cycler under the following reaction conditions: 15 min at 94 °C; 30 cycles of 30 s at 94 °C, 30 s at annealing temperature, 30 s at 72 °C; and a final extension of 5 min at 72 °C.

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References

1 Rohrer G.A. *et al.* (1994) *Genetics* **136**, 231–45.
2 Rohrer G. A. *et al.* (1996) *Genome Res* **6**, 371–91.
3 Alexander L. J. *et al.* (1996) *Mam Genome* **7**, 368–72.
4 Alexander L.J. *et al.* (1996) *Anim Genet* **27**, 137–48.
5 Korwin-Kossakowska A. *et al.* (2002) *Anim Genet* **33**, 224–27.
6 Krause E *et al.* (2002) *Anim Genet* **33**, 477–85.
7 Yerle M. *et al.* (1999) *Cytogenet Cell Genet* **82**, 182–8.
8 Hawken R. J. *et al.* (1999) *Mamm Genome* **10**, 824–30.

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The *leptin* C73T missense mutation is not associated with marbling and fatness traits in a large gene mapping experiment in Australian cattle

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Overview: Several divergent traits are reported to be associated with single nucleotide polymorphisms (SNP) in the *leptin* gene, including marbling,[1,2] fatness including backfat thickness,[1,2]