The Human Obesity Gene Map: The 2005 Update

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Abstract

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This paper presents the 12th update of the human obesity gene map, which incorporates published results up to the end of October 2005. Evidence from single-gene mutation obesity cases, Mendelian disorders exhibiting obesity as a clinical feature, transgenic and knockout murine models relevant to obesity, quantitative trait loci (QTL) from animal cross-breeding experiments, association studies with candidate genes, and linkages from genome scans is reviewed. As of October 2005, 176 human obesity cases due to single-gene mutations in 11 different genes have been reported, 50 loci related to Mendelian syndromes relevant to human obesity have been mapped to a genomic region, and causal genes or strong candidates have been identified for most of these syndromes. There are 244 genes that, when mutated or expressed as transgenes in the mouse, result in phenotypes that affect body weight and adiposity. The number of QTLs reported from animal models currently reaches 408. The number of human obesity QTLs derived from genome scans continues to grow, and we now have 253 QTLs for obesity-related phenotypes from 61 genome-wide scans. A total of 52 genomic regions harbor QTLs supported by two or more studies. The number of studies reporting associations between DNA sequence variation in specific genes and obesity phenotypes has also increased considerably, with 426 findings of positive associations with 127 candidate genes. A promising

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observation is that 22 genes are each supported by at least five positive studies. The obesity gene map shows putative loci on all chromosomes except Y. The electronic version of the map with links to useful publications and relevant sites can be found at http://obesitygene.pbrc.edu.

Key words: human obesity gene map, association, linkages, Mendelian disorders, quantitative trait loci, candidate genes

Introduction

This paper represents the 12th in a series (1-11) on the status of the human obesity gene map, the 11th report published in Obesity. As in previous reports, we reviewed the literature published up to the end of October 2005 searching for the relevant publications through a variety of sources: PubMed using a combination of key words, authors, and journals; continuous reviews of obesity and genetics journals; personal collection of reprints; and papers made available to us by colleagues from around the world. Publications dealing with a wide variety of phenotypes pertaining to obesity, such as BMI, body fat mass, percentage of body fat, abdominal fat, fat-free mass, skinfolds, resting metabolic rates, plasma leptin levels, and other components of fat distribution and energy balance, were retained. As in previous reports, negative findings are not systematically reviewed but are briefly introduced when such data were available to us.

Each collaborating author was assigned one section of the report for an in-depth review. In addition to an introduction and a brief discussion (C.B), the report includes sections dealing with monogenic obesity cases (G.A.), Mendelian disorders exhibiting obesity as clinical feature (J.W.), murine gene-deficient [knockout (KO)¹/floxed], transgenic models in which altered expression of a gene (or genes) results in phenotypes relevant to obesity and quantitative

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¹ Nonstandard abbreviations: KO, knockout; QTL, quantitative trait locus; *MC4R*, melanocortin receptor 4; BDNF, brain-derived neurotrophic factor; *NTRK2*, neurotrophic tyrosine receptor kinase 2; AHO, Albright Hereditary Osteodystrophy; BW, body weight; MGI, Mouse Genome Informatics; LOD, logarithm of the odds ratio; WHR, waist-to-hip ratio; cM, centimorgan(s); WC, waist circumference.

trait loci (QTL) from murine models (A.Z.), QTLs from other animal model studies and gene-drug interactions (Y.C.), association studies in humans with specific candidate genes (T.R.), and human linkage studies including genome scans performed to identify QTLs of obesity or obesity-related phenotypes (L.P.). The other collaborating author (B.W.) is involved in the management of the database, the generation of the tables and the map from the database, and the electronic version of the human obesity gene map (http://obesitygene.pbrc.edu). Readers are referred to previous publications (9,11) for detailed information on the electronic version of the map and on browsing and querying capabilities of the online Obesity Gene Map Database.

As in the past, the published references for each entry in the current human obesity gene map are provided for convenience. We are using gene symbols and chromosomal locations given in the Entrez Gene database (http://www. ncbi.nlm.nih.gov/) available from the National Center for Biotechnology Information. The appendix provides a complete list of genes and map locations cited in this paper.

Although the authors have taken every possible effort to provide correct information, in the rapidly changing world of genetics and bioinformatics and the ever-present world of human fallibility, it is almost inevitable that inaccuracies will emerge. The full responsibility for errors is ours. Furthermore, we seek your indulgence in errors of omission and hope you will notify us of any oversights. All correspondence to maximize the precision and quality of the map is welcomed and, indeed, solicited.

Sadly, we have to inform the readership that this is likely to be the last time that we are able to publish the review of the human obesity gene map. We have tried unsuccessfully to obtain the funding to support the enormous amount of work that is necessary every year to prepare this popular review. The printed version of the map in *Obesity* is highly cited, and the e-version is accessed $\sim 200,000$ times a year by $\sim 40,000$ unique users based mainly in academic institutions and pharmacological or biotechnology companies. Although we recognize that the yearly review in its printed and electronic versions is a valuable tool for those involved in this field, the project has become too large to be handled solely by us without support staff.

Monogenic Effects and Mendelian Disorders

Monogenics Section

The majority of disorders previously summarized in Table 2 have now been associated with a candidate gene or a genetic defect. Therefore, this year they are being merged with the monogenic obesity cases into a new table, Table 1.

This year, there has been relatively nominal reporting of monogenic cases of obesity. The majority of the monogenic obesity cases remain those with a genetic defect (mutation, deletion, or insertion) in the melanocortin receptor 4 (MC4R) gene. Table 1 summarizes all of the cases that were reported in previous years. A publication by Farooqi and O'Rahilly (12) elegantly summarizes cases of monogenic obesity that received treatment for the mutated gene that resulted in improvement of the health status of the patients. These cases were covered in the 2004 Obesity Gene Map report. The same group recently described a new rare mutation in the receptor of the neurotrophin brain-derived neurotrophic factor (*BDNF*) gene, *TrkB* (13).

Neurotrophic Tyrosine Receptor Kinase 2 (NTRK2)

In humans, the receptor of the murine BDNF gene, TrkB, is encoded by the NTRK2 gene. A study was reported by Yeo and colleagues (13) whereby a de novo heterozygous mutation arose in a child with severe early-onset obesity and hyperphagia. The A-to-G transition resulted in amino acid substitution of the tyrosine residue at position 722 by a cysteine (Y722C) (Table 1). An additional cohort of 192 alleles and the proband's parents were screened for the presence of this rare mutation, but nobody was found to carry it. In vitro functional studies showed that the mutation impaired activation of MAPK when cells were treated with BDNF (13). This new rare mutation provides another example of single-gene mutations in genes involved in energy balance regulation that result in severe and early onset obesity. In another preliminary study of 288 individuals with a history of early onset obesity, five missense mutations were identified in NTRK2 (A74T, I98V, M354V, P660L, T821L) that have yet to be functionally characterized and described in greater detail (13).

Mendelian Disorders

Since last year's review, there has been limited development in the area of Mendelian disorders related to obesity, although many novel mutations in known genes have been reported. Updated references on new mutations for the Albright hereditary osteodystrophy (AHO), Bardet-Biedl, Berardinelli-Seip congenital lipodystrophy, Borjeson-Forssman-Lehmann, familial partial lipodystrophy, multiple endocrine neoplasia (type 1), and WAGR syndromes are provided (see Table 1).

In the present review, we now properly report AHO in the context of all disorders related to parathyroid hormone resistance, as described by DeSanctis et al. (131). To date, the AHO phenotype is always associated with mutations in *GNAS1*. In the AHO-like syndrome linked to 2q37, a French group narrowed down the critical region to a 4-megabase-pair interval delimited by D2S2338 (present) and D2S2253 (deleted) (149).

A new mutation was discovered for familial partial lipodystrophy, Dunnigan type (167). The affected 21-year-old woman had a great excess of subcutaneous fat on the face, neck, trunk, and abdomen, with relative lack on the gluteal region, arms, and legs. She was insulin resistant and had the

OMIM no.	Syndrome	Locus	Candidate gene	Reference
Single-gene m	utations with an obesity phenotype			
122561	Corticotropin-releasing hormone receptor 1	17q12-q22	CRHR1	(14)
602034	Corticotropin-releasing hormone receptor 2	7p14.3	CRHR2	(14)
601751	G-protein-coupled receptor 24	22q13.2	GPR24	(15)
164160	Leptin (obesity homolog, mouse)	7q31.3	LEP	(16–20)
601007	Leptin receptor	1p31	LEPR	(21)
601665	Melanocortin 3 receptor	20q13.2-q13.3	MC3R	(22–24)
155541	Melanocortin 4 receptor	18a22	MC4R	(25-47)
600456	Neurotrophic tyrosine kinase receptor type 2	9a22 1	NTRK?	(12 13)
176830	Proopiomelanocortin (adrenocorticotropin/ β_{-} ipotropin/ α_{-}	2p23.3	POMC	(12,13) (18,19)
170050	melanocyte stimulating hormone/ β -melanocyte stimulating hormone/ β -endorphin)	2023.5	Tome	(+0,+7)
162150	Proprotein convertase subtilisin/kexin type 1	5a15-a21	PCSK1	(50,51)
603128	Single-minded homolog 1 (Drosonhila)	6a16 3-a21	SIM1	(52,53)
Autosomal rec	essive	0410.5 421	01011	(52,55)
203800	Alstrom syndrome	2n13 1	AT MS1	(54, 59)
203800	Ristom syndrome 1	2p13.1	ALMSI DDC1	(54-59)
209901	Bardet-Biedi syndrome 1	11013.1	BBSI	(00-00)
606151	Bardet-Biedl syndrome 2	16q13	BBS2	(61,63,67-70)
600151	Bardet-Biedl syndrome 3	3p13-p12	BBS3 (ARL6)	(63,71–75)
600374	Bardet-Biedl syndrome 4	15q22.3-q23	BBS4	(61,76–81)
603650	Bardet-Biedl syndrome 5	2q31	BBS5	(63,82–84)
604896	Bardet-Biedl syndrome 6	20p12.2	MKKS	(63,68,71,85-88)
607590	Bardet-Biedl syndrome 7	4q27	BBS7	(67,89)
608132	Bardet-Biedl syndrome 8	14q32.1	BBS8	(89,90)
269700	Berardinelli-Seip congenital lipodystrophy 1	9a34.3	AGPAT2	(91–95)
606158	Berardinelli-Sein congenital lipodystrophy 2	11013	BSCL2	(92,94,96–98)
212065	Carbohydrate-deficient glyconrotein syndrome type 1a	16n13 2	PMM2	(92,) 1,) 0 (90)
212005	Coben syndrome	8022.2	COH1	(100, 105)
210550	Combined nitriteres hormone definiteres	6422.2 5-25-2		(100-103)
001538	Combined pluttary normone deliciency	5435.5	PROPI	(100-108)
227810	Fanconi-Bickel syndrome	3q26.31	SLC2A2	(109–117)
139191	Isolated growth hormone (GH) deficiency	7p14	GHRHR	(118–120)
Triallelic diger	nic			
138090	Cortisone reductase deficiency	1pter-p36.13	H6PD	(121)
604931	Cortisone reductase deficiency	1q32-q41	HSD11B1	(121,122)
Digenic				
600917	Severe insulin resistance with obesity	3p25	PPARG	(123)
Autosomal dor	minant	/q31.1	PPPIRSA	
100800	Achondronlasia	4n163	FGFR3	(124 - 127)
103580	AHO (Pseudonseudohypoparathyroidism)	20a13 2-a13 3	GNAS	(124 127) (128 - 147)
102591		20q13.2-q13.3	4102	(120 - 1 + 7)
103381	Ano 2 Deschadastala mentel estadation conducada	2-27.2	AIIO2 STEV25	(140)
600430	Brachydactyly mental retardation syndrome	2q37.3	STK25 GPC1 GPR35	(149–155)
105820	Angelman syndrome with obecity	15011 012	ANCP	(156)
105850	Angelman syndrome with obesity	15q11-q12	ANCK	(156)
005740 160980	Anisomastia Carney complex with primary pigmented podular	16q13-q21 17a24 3	ANMA PRKARIA	(157) (158-164)
(05244	adrenocortical disease and Cushing's syndrome (CNC1)	2-16	ΤΑΚΑΛΙΑ	(155-104)
003244	adrenocortical disease and Cushing's syndrome (CNC2)	2010		(103)
604367	Familial partial lipodystrophy, Dunnigan, type 3	3p25	PPARG	(166–169)
151660	Familial partial lipodystrophy, type 2 (Dunnigan type)	1q23.1	LMNA	(170–180)
147670	Insulin resistance syndromes	19p13.3-p13.2	INSR	(181–188)
139250	Isolated GH deficiency (139250)	17q22-q24	GH1	(189)
131100	Multiple endocrine neoplasia, type 1 with Cushing's disease	11q13	MEN1 (Menin)	(190–196)
122000	Posterior polymorphous corneal dystrophy (chromosome 1)	1p34.3-p32.3	COL8A2	(197)
605020	Posterior polymorphous corneal dystrophy (chromosome 20)	20n11.21	VSX1	(198,199)
176270	Prader-Willi syndrome	15a11 2	IPW	(200_212 216_218 220)
1/02/0	rader wini syndrome	15911.2	MKRN3	(200 212,210-210,220)
		15q11.2	PWCR1	

Table 1. Single-gene and obesity-related Mendelian disorders

OMIM no.	Syndrome	Locus	Candidate gene	Reference
		15q12	SNRPN	
		15q11.2	MAGEL2	
		15q11.2	NDN	
		15q11-q12	GABRG3	
603128	Prader-Willi-like syndrome (chromosome 6q)	6q16.3-q21	SIM1	(202,213–215, 219,220)
190160	Thyroid hormone resistance syndrome	3p24.1	THRB	(221)
181450	Ulnar-Mammary (Schinzel) syndrome	12q24.21	TBX3	(222-225)
194072	WAGR syndrome with obesity	11p13	WT1	(226-232)
		11p13	PAX6	
X linked				
301900	Borjeson-Forssman-Lehmann syndrome	Xq26.3	PHF6	(233-240)
303110	Choroideremia with deafness and obesity	Xq21.2	СНМ	(241,242)
		Xq21.1	DFN3	
309550	Fragile X syndrome with Prader-Willi-like phenotype	Xq28	FMR1	(243-246)
300148	MEHMO syndrome	Xp22.13- p21.1	МЕНМО	(247–249)
300218	Mental retardation X-linked, syndromic 7	Xp11.3-q22.1	MRXS7	(250)
300458	Mental retardation X-linked, syndromic 16	Xq28	MECP2	(251,252)
300238	Mental retardation, X-linked, syndromic 11	Xq26-q27	MRXS11	(253,254)
176270	Prader-Willi-like syndrome, X-linked	Xq23-q25	PWLSX	(255)
312870	Simpson-Golabi-Behmel 1	Xq26.2	GPC3	(82,256–264)
		Xq26.1	GPC4	
300209	Simpson-Golabi-Behmel 2	Xp22	SGBS2	(265)
309585	Wilson-Turner syndrome	Xq21.2-q22	WTS	(266,267)

Table 1.	(continued))
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metabolic syndrome and type 2 diabetes. She was heterozygous for a novel A>G mutation at position -14 of intron B, upstream of PPARG exon 1 within the promoter of the PPAR γ 4 isoform, implicating this isoform as being potentially important in adipocyte biology.

Finally, in recent clinical reviews of large groups of Alstrom (58) and WAGR (229) syndrome patients, the central role of childhood obesity and hyperinsulinism in Alstrom syndrome was confirmed, as well as a significant prevalence of obesity (of 18%) in WAGR subjects. In this last syndrome, the new acronym WAGRO (obesity) has even been suggested (227).

Transgenics and KOs

The murine obesity gene map identifies 248 genes (Table 2) that, when mutated or expressed as transgenes in the mouse, result in phenotypes affecting body weight (BW) and adiposity. We include genes that promote obesity and genes that promote leanness, with the exception of genes that seem to promote failure-to-thrive phenotypes or mutant genes impacting developmental issues affecting multiple organs systems during embryogenesis or early growth. The list was compiled from the primary literature, accessible through PubMed and corroborated with information captured by the Mouse Genome Informatics (MGI) group (www.informatics.org). Official gene no-

menclature rules have been followed, even where the use of this nomenclature differs from the gene name used in the primary publication. We have attempted to capture common synonyms, but the list is not exhaustive. Readers are directed to MGI for a more complete list of synonyms and nomenclature history.

Of the new genes added to the list this year, three are imprinted. Maternal inheritance of the Gnas KO allele (400), a KO of the paternally expressed Peg3 gene (493), and transgenic overexpression of the paternally expressed Mest (Peg1) in adipose tissue all promote obesity. Imprinted loci are well documented in the mouse genome, but the degree of imprinting can also be tissue dependent. Clearly, the role of imprinted genes in the development of obesityrelated phenotypes must be considered in cases where simple Mendelian inheritance relationships seem uninformative. Three new genes listed for the first time this year are relevant to the molecular characterization of three wellknown human obesity syndromes: Alstroms, Bardel-Biedl, and McKusick-Kaufman. The respective murine homologs, Alms1, Bbs2, and Mkks, all present obesity phenotypes when mutated in mice. Interestingly, Bbs2-deficient mice weigh less than controls at birth, suggesting an additional effect on early development. These three mutants will provide valuable model systems to study the roles of these genes in the development of these polygenic syndromes.

Table 2.	Murine	models	of	obesity
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Mouse chromosome (cM/band)	Mouse gene	Human chromosome	Human homolog	Gene description	Details	Reference
2(89)	A^{k}	20q11.2-q12	ASIP	Agouti. Expression limited to adipose cells	Transgene: aP2 promoter regulating expression of murine wild-type agouti cDNA Increased BW and fat mass	(268,269)
2(89)	A^{k}	20q11.2-q12	ASIP	Agouti, also known as BAP20 mouse. Ubiquitous expression. Unexpectedly high in skeletal muscle	Transgene: human β actin promoter regulating expression of murine wild- type agouti cDNA Obesity	(270)
2(89)	A^{k}	20q11.2-q12	ASIP	Agouti. Ubiquitous expression	Transgene: murine <i>Pgk1</i> promoter regulating expression of murine wild- type agouti cDNA Obesity	(270)
10(44)	Abca7 ^g	19p13.3	ABCA7	ATP-binding cassette, subfamily A (ABC1), member 7	Reduced fat and circulating high-density lipoprotein and total cholesterol in females	(271)
5	Acacb ^g	12q24.1	ACACB	Acetyl CoA carboxylase β , also known as Acc2	Reduced adiposity; resistant to diet- induced obesity	(272,273)
11(38)	Acadvl ^g	17p13-p11	ACADVL	Acyl-CoA dehydrogenase, very long chain	Lipid accumulation in myocytes; impaired temperature regulation Adult-onset fat mass gain	(274,275)
7(F4)	Adam12 ^g	10q26.3	ADAM12	A disintegrin and metallopeptidase domain 12 (meltrin α)	Moderate resistance to diet-induced obesity due to an impairment in the increase of the number of adipocytes in high-fat-fed mice	(276)
16(53.4)	Adamts1 ^g	21q21.2	ADAMTS1	A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1	Reduced BW and adiposity	(277)
17	Adcyap1 ^g	18p11	ADCYAP1	Adenylate cyclase activating polypeptide 1	Wasting; reduced adiposity	(278)
11(19) 19(50)	Adra1b ^g Adra2a ^k	5q23-q32 10q24-q26	ADRA1B ADRA2A	Adrenergic receptor, α 1b Transgene expresses adrenergic receptor α 2 in adipose cells	Accelerated weight gain on high-fat diet Transgene: aP2-driven human <i>ADRA2A</i> cDNA When expressed in Adra3b- deficient mice, leads to obesity. When expressed in mice heterozygous for Adra3b, there is no adipose phenotype	(279) (280)
19(51)	Adrb1 ^g	10q24-q26	ADRB1	Adrenergic receptor, $\beta 1$	Obesity in conjunction with mutations in <i>Adrab2</i> and <i>Adrab3</i>	(281)
19(51)	Adrb1 ^k	10q24-q26	ADRB1	Transgene insertion 1, Susan R. Ross, expresses adrenergic receptor β 1 in adipose cells	Transgene: aP2-driven expression of human <i>ADRB1</i> cDNA Reduced adiposity and partially resistant to diet-induced obesity	(282)
18(34)	Adrb2 ^g	5q31-q32	ADRB2	Adrenergic receptor, $\beta 2$	Reduced adiposity Obesity in conjunction with targeted mutations in <i>Adrab1</i> and <i>Adrab3</i>	(281)
8(10)	Adrb3 ^g	8p12-p11.2	ADRB3	Adrenergic receptor, β 3	Increased body fat. Mildly obese on chow. High obesity on high-fat diet. Obesity in conjunction with mutations in <i>Adrab2</i> and <i>Adrab3</i>	(283)
8(10)	Adrb3 ^g	8p12-p11.2	ADRB3	Adrenergic receptor, $\beta 3$	Increased adiposity on chow or high-fat diets	(284)
11	Aebp1 ^k	7p13	AEBP1	AE-binding protein 1	Transgene; expressed in adipose tissue; obesity in females	(285)
8(D1-D2)	$Agrp^{g}$	16q22	AGRP	Agouti-related protein	Age-related lean phenotype	(286)
ð(D1-D2)	Agrp~	16q22	ΑĠΚΡ	Agouti-related protein; expressed ubiquitously	expression of human <i>AGRP</i> cDNA; elevated weight gain and obesity	(287)

Mouse chromosome (cM/band)	Mouse gene	Human chromosome	Human homolog	Gene description	Details	Reference
8(D1-D2)	Agrp ^k	16q22	AGRP	Agouti-related protein	Transgene. Post-embryonic deletion of AGRP-expressing neurons	(288)
13(16)	A atr la ^g			Angiotensin II recentor, type 1a	Lean Resistant to diet-induced obesity	(289)
X(12.5)	Agtr14 Aotr2g	Xa22-23	AGTR?	Angiotensin II receptor, type 7a	Resistant to diet-induced obesity	(20)
16(15)	Ahse ^g	3027	AHSG	α -2-HS-glucoprotein	Resistant to diet-induced obesity	(291)
1(51.7)	Akp3 ^g	2q37.1	ALPI	Alkaline phosphatase 3, intestine, not Mn requiring; also known as IAP	Accelerated weight gain on high-fat diet	(292)
12(57)	Akt1 ^k	14q32.3	AKT1	Thymoma viral proto-oncogene 1	Transgene, cDNA of constitutively active Akt expressed in skeletal muscle from the human skeletal actin promoter Reduced in adiposity	(293)
7(6.5)	Akt2 ^g	19q13.1-13.2	AKT2	Thymoma viral proto-oncogene 2	Reduction in adiposity, especially in young females. Age-related adipocyte loss in both sexes	(294)
6	Alms1 ^g	2p13	ALMS1	Alstrom syndrome 1 homolog (human)	Gene trapped Obesity	(295)
15(B1)	Amacr ^g	5p13.2-q11.1	AMACR	α -methylacyl-CoA racemase	Reduction in BW and adiposity on phytol-supplemented diet	(296)
17	Angptl4 ^g	19p13.3	ANGPTL4	Angiopoietin like 4, also known as fasting-induced adipocyte factor (FIAF)	Reduction in body fat gain upon transfer from germ-free to conventional housing	(297)
9	Angptl6 ^g	19p13.2	ANGPTL6	Angiopoietin like 6, also known as adipopoietin-related growth factor (AGF)	The 20% of mice that survive development manifest obesity and insulin resistance	(298)
9	Angptl6 ^k	19p13.2	ANGPTL6	Angiopoietin like 6, also known as adipopoietin-related growth factor (AGF)	Transgenic: ubiquitous expression using the chicken β-actin promoter and cytomegalovirus (CMV)-enhancer Reduced adiposity on chow and resistance to diet-induced obesity on high-fat diets	(298)
7(4)	Apoc1 ^k	19q13.2	APOC1	Apolipoprotein C1. transgene insertion 1, Louis M. Havekes- overexpressing human <i>APOC1</i> gene	Transgenic (Tg) mice expressing the human APOC1 gene from its own promoterModerate reduction in adiposity relative to non-Tg mice. When crossed with the Lep background, however, Tg mice were protected against obesity and insulin resistance	(299)
9(27)	Арос3 ^g	11q23.1- q23.2	APOC3	Apolipoprotein C-III	Obesity on high-fat diet	(300,301)
4(B1)	$Aqp7^{g}$	9p13	AQP7	Aquaporin 7	Increased gonadal fat pad mass	(302)
4(B1)	$Aqp7^{g}$	9p13	AQP7	Aquaporin 7	Adult-onset obesity	(303)
X(36)	<i>Ar^c</i>	Xq11.2-q12	AR	Androgen receptor	Floxed gene + Cre transgene expressed from the cytomegalovirus promoter Obesity. Decreased energy expenditure	(304,305)
10(B5)	Arid5b ^g	10q21.2	ARID5B	AT-rich interactive domain 5B (Mrf1 like), also known as Mrf2	Reduced adiposity on chow. Resistant to diet-induced obesity	(306)
11(B4)	Aspa ^e	17pter-p13	ASPA	Aspartoacylase (aminoacylase) 2	Reduced adiposity	(307)
14(C3)	Atp12a ^g	13q12.12	ATP12A	ATPase, H ⁺ /K ⁺ -transporting, non- gastric, α polypeptide	Increased weight loss on potassium-free diet	(308)
18	Atp8b1 ^f	18q21-q22	ATP8B1	ATPase, class I, type 8B, member 1	Targeted knock-in Increased weight loss on bile salt- supplemented diet	(309)
12	Batf ^k	14q24.3	BATF	Regulator of transcription factor B-ZIP	Loss of all adipose tissue	(310)
19	Bbs1 ^g	11q13.1	BBS1	Bardet-Biedl syndrome 1 homolog (human)	KO due to gene trap insertion in exon 11 Reduced BW at birth. Obesity at 10 weeks in 10% of the mutants	(311)

Mouse chromosome (cM/band)	Mouse gene	Human chromosome	Human homolog	Gene description	Details	Reference
8	Bbs2 ^g	16q21	BBS2	Bardet-Biedl syndrome 2 homolog (human)	Reduced BW at birth. Increased abdominal fat mass at 4 months	(312)
9(33)	Bbs4 ^c	15q22.3-23	BBS4	Bardet-Biedl syndrome 4 homolog (human)	Low BW at weaning, adult-onset obesity after weaning	(311)
9(33)	Bbs4 ^g	15q22.3-23	BBS4	Bardet-Biedl syndrome 4 homolog (human)	Low BW at weaning, adult-onset obesity after weaning	(81)
2(62)	Bdnf ^g	11p13	BDNF	BDNF. The mutation is homozygous lethal	Mature-onset obesity in heterozygotes. Can be treated by food restriction	(313,314)
X(A7.1) 2	Brs3 ^g Bub1b ^g	Xq26-q28 15q15	BRS3 BUB1B	Bombesin-like receptor 3 Budding uninhibited by benzimidazoles 1 homolog, β (<i>S. cerevisiae</i>)	Obesity Age-dependent loss of body fat; reduced lifespan	(315) (316)
17(34.3)	C3 ^g	19p13.3	С3	Complement component 3; acylation- stimulating protein	Females possess a lean phenotype and are resistant to diet-induced obesity	(317,318)
13(D1)	Cart ^g	5q13.2	CART	Cocaine- and amphetamine-regulated transcript	Increased susceptibility to diet-induced obesity	(319,320)
6(A2)	Cav1 ^g	7q31.1	CAVI	Caveolin 1	Decreased adiposity; resistant to diet- induced obesity	(321)
6(48.3) 9(26)	Cav3 ^g Cbl ^g	3p25 11q23.3	CAV3 CBL	Caveolin 3 Casitas B-lineage lymphoma, also known as c-cbl	Increased adiposity Reduced adiposity	(322) (323)
5(34)	Cckar ^g	4p15.1-15.2	CCKAR	Cholecystokinin (CCK) A receptor	Resistant to CCK-mediated inhibition of food intake but normal long-term weight regulation; increased cholesterol absorption on lithogenic diet; altered thermogenic regulation	(324–326)
17(28.8) 5(2)	Ccnd3 ^g Cd36 ^g	6p21 7q11.2	CCND3 CD36	Cyclin D3 CD36 antigen/fatty acid translocase	Resistant to diet-induced obesity Altered metabolic adaptation to dietary modulation	(327) (328)
18(6)	Cdh2 ^k	18q11.2	CDH2	Cadherin 2, also known as N-cadherin or Ncad. Truncated gene used in this construct acts as a dominant negative allele	Transgene: expressing truncated <i>Cdh2</i> using an osteoblast-specific promoter, Og2 Increased adiposity	(329)
17(15.2)	Cdkn1a ^g	6p21.2	CDKN1A	Cyclin-dependent kinase inhibitor 1A (P21)	Increased adiposity	(330)
6(62)	Cdkn1b ^g	12p13.1-p12	CDKN1B	Cyclin-dependent kinase inhibitor 1B (P27)	Increased adiposity	(330)
7(12)	Cebpa ^g	19q13.1	CEBPA	CCAAT/enhancer-binding protein (C/ EBP), α	Reduced adiposity	(331)
7(12)	Cebpa ^d	19q13.1	CEBPA	CCAAT/enhancer-binding protein (C/ EBP), α	KO + gene replacement. A <i>Cebpb</i> knock- in was generated by replacing the entire coding region of the <i>Cebpa</i> locus with the <i>Cebpb</i> coding region Lean and resistant to diet-induced obesity	(332)
2(95.5)	Cebpb ^g	20q13.13	CEBPB	CCAAT/enhancer-binding protein (C/ EBP), β	Reduced adiposity	(333)
16(9)	Cebpd ^g	8p11.2-11.1	CEBPD	CCAAT/enhancer-binding protein (C/ EBP), Δ	Reduced adiposity	(334)
13(7)	Chrm3 ^g	1q41-q44	CHRM3	Muscarinic receptor M3	Reduced adiposity	(335)
18	Cidea ^g	18p11.21	CIDEA	Cell death-inducing DNA fragmentation factor, α subunit-like effector A	Reduced adiposity and resistant to diet- induced obesity	(336)
5(43)	Clock ^b	4q12	CLOCK	Clock	ENU-generated mutant Obesity	(337)
4(13.9)	Cnr1 ^c	6q14-q15	CNR1	Cannabinoid receptor 1 (brain), also known as CB1 receptor	Floxed gene + ubiquitously expressed Cre Reduced adiposity	(338)

Mouse chromosome (cM/band)	Mouse gene	Human chromosome	Human homolog	Gene description	Details	Reference
4(13.9)	Cnr1 ^g	6q14-q15	CNR1	Cannabinoid receptor 1 (brain), also known as CB1 receptor	On standard chow at 20 weeks, the BWs and adiposity are 24% and 60% lower, respectively, than control mice Resistant to diet-induced obesity	(339)
5	<i>Corin</i> ^g	4p13-12	CORIN	Corin	Increased BW	(340)
8(32.6)	Cpe ^g	4q32.3	CPE	Carboxypeptidase E	KO: floxed and deleted	(341)
10(2)	C-+1-8	11-121 122	CDT14	Constitue aslasitestana formas 1. lista	Obesity	(242)
19(2)	Cpt1a®	11q13.1-13.2	CPIIA	Carnitine paimitoyirransferase Ta, fiver	Fasting hypoglycemia in heterozygotes Increased fasting serum free fatty acids	(342)
3(8)	Crh ^k	8q13	CRH	Corticotropin-releasing factor hormone, also known as CRF Expression of the transgene, however, is restricted to endogenous Crh- expressing cells due to a tissue- specific enhancer present within the Crh cDNA sequence	Murine corticotropin-releasing hormone cDNA expressed from the mouse metallothionein promoter Transgenic mice exhibit elevated ACTH release, high circulating levels of CRH and adrenal corticosterone. They display excess fat accumulation and	(343)
				en el a sequence	muscle atrophy	
6(28)	Crhr2 ^g	7p14.3	CRHR2	Corticotropin-releasing hormone receptor 2	Normal adiposity on low-fat diet. Lower feed efficiency on high-fat diet (higher food intake but same weight gain as wild-type mice)	(344)
9	Cyb5r4 ^g	6pter-q22.33	CYB5R4	Cytochrome b5 reductase 4	Reduced adiposity, increased food intake, hyperglycemia and hypoinsulinemia at 7 weeks	(345)
9(31)	Cyp19a1 ^g	15q21.1	CYP19A1	Cytochrome P450, family 19, subfamily a, polypeptide 1, also known as aromatase	Elevated gonadal fat pad weight; obesity prevented by cholesterol feeding	(346,347)
2(15.5)	Dbh ^d	9q34	DBH	Dopamine β hydroxylase. Dopamine- deficient (DD) mice are homozygous for this mutation and also for a KO of the endogenous tyrosine hydroxylase (Th) locus. The Th knock-in in the <i>Dbh</i> gene restores tyrosine hydroxylase activity	 KO + gene replacement. A <i>Th</i> knock-in was generated by inserting the <i>Th</i> gene into the mutated <i>Dbh</i> locus These <i>DD</i> mice do not possess altered adiposity on chow diet. However, when the Th−/− and Dbh<tm2(th)rpa also="" are="" for="" homozygous="" in="" lep<sup="" mice="" mutations="" that="" the="">ob mutation, there is a significant reduction in BW and adiposity gain</tm2(th)rpa> 	(348,349)
11	del(17)	17p11.2	del(17)	Smith-Magenis syndrome	Transgenic: chromosomal rearrangement	(350)
15(46.9)	(p11.2) ^k Dgat1 ^g	8q24.3	(p11.2) DGAT1	Acyl CoA: diacylglycerol O-	Obesity Lean and resistant to diet-induced obesity	(351)
15(46.9)	$Dgatl^k$	8q24.3	DGAT1	acyltransferase 1 Acyl CoA: diacylglycerol <i>O</i> -	Transgenic; expressed in adipose cells	(352)
15(46.9)	Dgat1 ⁱ	8q24.3	DGAT1	Acyl CoA: diacylglycerol <i>O</i> - acyltransferase 1	Adenovirus-mediated overexpression in liver Increased gonadal but not subcutaneous	(353)
4(C7)	Dhcr24 ^g	1p33–31.1	DHCR24	24-dehydrocholesterol reductase	fat mass Reduction in subcutaneous and mesenteric	(354)
12(54)	Dlk1 ^k	14q32.3	DLK1	Δ -like 1 homolog (<i>Drosophila</i>), also known as Pref-1. Expressed as fusion to human immunoglobulin- γ constant region in liver	Transgene. Murine cDNA expressed from albumin promoter Reduced adiposity	(355)

Mouse chromosome (cM/band)	Mouse gene	Human chromosome	Human homolog	Gene description	Details	Reference
12(54)	Dlk1 ^k	14q32.3	DLK1	 Δ-like 1 homolog (<i>Drosophila</i>), also known as Pref-1. Expressed as fusion to human immunoglobulin-γ 	Transgene. Murine cDNA expressed from aP2 promoter Reduced adiposity	(355)
14	Dnajc3 ^g	13q32	DNAJC3	constant region in adipocytes DnaJ (Hsp40) homolog, subfamily C, member 3	Increased food intake; decreased adiposity	(356)
1(H2)	Dpt^{g}	1q12-23	DPT	Dermatopontin	Increased subcutaneous adipose number and volume	(357)
16(23.3)	Drd3 ^g	3q13.3	DRD3	Dopamine receptor 3	Increased adiposity and diet-induced	(358)
11	dup(17) (p11.2) (p11.2) ^k	17p11.2	dup(17) (p11.2) (p11.2)	Smith-Magenis syndrome	Transgenic: chromosomal rearrangement Obesity	(350)
8(8)	Eif4ebp1 ^g	8p12	EIF4EBP1	Eukaryotic translation initiation factor 4E-binding protein 1	Reduced adiposity	(359)
5	Ereg ^g	4q13.3	EREG	Epiregulin	Increased weight loss with dextran sulfate sodium exposure	(360)
19(3)	Esrra ^g	11q13	ESRRA	Estrogen-related receptor α	Reduced BW and adiposity. Resistant to diet-induced obesity	(361,362)
3(13.9)	Fabp4 ^g	8q21	FABP4	Fatty acid-binding protein 4, adipocyte	Like the control strain, homozygous mutants become obese on a high-fat diet but remain insulin sensitive	(363)
3(A1-A3)	Fabp5 ^g	8q21.13	FABP5	Fatty acid-binding protein 5, adipocyte, also known as Mal1	Less adiposity than controls on high-fat diet	(364,365)
7(B2)	Fgf21 ^k	19q31.1-qter	FGF21	Fibroblast growth factor 21	Transgene. Expressed human gene in liver Resistant to diet-induced obesity	(366)
2(H2) 7(5)	Fkhl18 ^g FosB ^k	20q11.1-11.2 19q13.32	FKHL18 FOSB	Forkhead-like 18 (<i>Drosophila</i>) FBJ osteosarcoma oncogene B	Resistant to diet-induced obesity Transgene: expressing ∆FosB, an alternative spliced mRNA variant of FosB under the control of the neuron- specific enolase promoter	(367) (368,369)
2(84)	Foxa2 ^g	20p11	FOXA2	Forkhead box A2, also known as Hnf3b or Tcf3b	KO + reporter Homozygous KO mice are embryonic lethal Heterozygotes rapidly develop obesity on a high-fat diet	(370)
8(65.5)	Foxc2 ^k	16q22-q24	FOXC2	Forkhead Box C2 expressed in adipose cells	Transgene: human <i>FOXC2</i> cDNA expressed from the aP2 promoter Reduced adiposity (lipid content) on chow diet and resistance to diet-induced obesity	(371,372)
17(E5)	Fshr ^g	2p21	FSHR	Follicular-stimulating hormone receptor	Obesity	(373)
6	Fxyd4 ^g	10q11.21	FXYD4	FXYD domain-containing ion transport regulator 4	Increased food intake but reduced BW	(374)
19(2)	Gal^{g}	11q13.2	GAL	Galenin	Exaggerated obesity in NPY-deficient mice	(375)
10(43)	<i>Gamt^g</i>	19p13.3	GAMT	Guanidinoacetate methyltransferase	Decreased adiposity	(376)
8(5)	Gas6 ^g	13q34	GAS6	Growth arrest specific 6	Resistant to diet-induced obesity	(377)
11(60)	Gast ^g	17q21	GAST	Gastrin	Obesity	(378)
11(E2)	Gcgr ^g	17q25	GCGR	Glucagon receptor	Decreased white and brown adipose mass	(379)
11(1)	Gck ^ĸ	7p15.3-p15.1	GCK	Glucokinase. Expressed in skeletal muscle	Transgene. Murine Gck cDNA expressed from the murine myosin light-chain 1 promoter Resistant to diet-induced obesity	(380)
11(1)	Gck ^k	7p15.3-p15.1	GCK	Glucokinase. Expressed in liver	Transgene. Murine Gck cDNA expressed from the murine Pepck promoter Increased weight gain on a high-fat diet	(381)

Mouse chromosome (cM/band)	Mouse gene	Human chromosome	Human homolog	Gene description	Details	Reference
6(60.6)	Gdf3 ⁱ	12p13.1	GDF3	Growth differentiation factor 3	Adenovirus-mediated overexpression Increase in BW and adiposity on high-fat	(382)
1(27.8)	Gdf8 ^g	2q232.2	GDF8	Growth differentiation factor 8, also known as myostatin	Reduced adiposity and increased muscle mass Loss of <i>Gdf8</i> expression also results in a significant reduction in adipose mass accumulation in agouti lethal yellow (Δ^{3}) and Lep ^{ob} mutants	(383,384)
1(27.8)	Gdf8 ^k	2q232.2	GDF8	Growth differentiation factor 8, also known as myostatin	Transgene Overexpressed in muscle Resistant to diet_induced obesity	(385)
6(35.5)	<i>Gfpt1</i> ^k	2p13	GFPT1	Glutamine fructose-6-phosphate transaminase 1	Transgene Overexpressed in adipose cells Increased adiposity	(386)
14(D3-E1)	Gfra2 ^g	8p21	GFRA2	Glial cell line-derived neurotrophic factor family receptor $\alpha 2$	Growth retardation accompanied by reduced fat mass and elevated basal metabolic rate	(387)
11(65)	Gh^{k}	17q24.2	GH	Growth hormone (GH)	Transgene. Bovine GH overexpressed from metallothionein promoter Resistant to diet-induced obesity	(388)
11(65)	Gh^k	17q24.2	GH	Growth hormone (GH)	Transgene. Bovine GH expressed in central nervous system Obese	(389)
15(4.6)	Ghr ^f	5p13-12	GHR	Growth hormone (GH) receptor	Knock-in. Independent deletion of two domains designated m569 and m391 Increased adiposity in males	(390)
2(89)	<i>Ghrh</i> ^k	20q11.2	GHRH	Growth hormone (GH)-releasing hormone	Transgenic mouse expressing human <i>GHRH</i> cDNA from the mouse metallothionein I promoter Increased adiposity	(391)
6(E3)	Ghrl ^g	3p26-p25	GHRL	Ghrelin	KO (lacZ fusion) On a high-fat diet, homozygous mutants tend to have a decrease in percentage body fat and an increase in percentage lean body mass without any significant difference in BW compared with wild-type mice	(392)
3	Ghsr ^g	3q26.31	GHSR	Growth hormone (GH) secretagogue	Decreased BW	(393)
3	Ghsr ^k	3q26.31	GHSR	Growth hormone (GH) secretagogue receptor Expression limited to GHRH (GH- releasing hormone-expressing neurons)	Transgene. Rat <i>GHRH</i> 5' and 3' genomic sequences driving expression of human <i>GHSR</i> cDNADecreased BW and adiposity	(394)
7	<i>Gipr^g</i>	19q13.3	GIPR	Gastric inhibitory polypeptide receptor	Resistant to diet-induced obesity; reduced adiposity in aged mice; lower respiratory exchange ratio and higher fat oxidation in the light phase	(395–397)
2(104)	Gnas ^g	20q13.2- q13.3	GNAS	Imprinted locus GNAS (guanine nucleotide-binding protein, α- stimulating) complex locus	KO (exon 2) Loss of maternal expression leads to obesity, with increased lipid per cell in white and brown adipose tissue, whereas loss of paternal expression leads to a lean phenotype, with decreased lipid in adipose tissue	(398,399)
2(104)	Gnas ^g	20q13.2- q13.3	GNAS	Imprinted locus GNAS (guanine nucleotide-binding protein, α- stimulating) complex locus	KO (exon 1) Maternal inheritance of the mutant allele gives larger BW in heterozygous mice	(400)

Mouse chromosome (cM/band)	Mouse gene	Human chromosome	Human homolog	Gene description	Details	Reference
19(4)	Gng3 ^g	11p11	GNG3	Guanine nucleotide-binding protein (G-protein), γ3 subunit	KO. Floxed and deleted Female homozygotes have reduced	(401)
19(52)	Gpam ^g	10q25.2	GPAM	Glycerol-3-phosphate acyltransferase,	Reduced BW and adiposity	(402)
2(33)	Gpd2 ^g	2q24.1	GPD2	Glycerol phosphate dehydrogenase 2, mitochondrial	Reduced BW and adiposity	(403)
2(33)	Gpd2 ^g	2q24.1	GPD2	Glycerol phosphate dehydrogenase 2, mitochondrial	Enhanced adipose and BW gain of females on a high-fat diet. This effect was not observed in males	(404)
12	Gphb5 ^k	14q23.2	GPHB5	Glycoprotein hormone β 5, also known as GPB5 and OGH	Transgene. Ubiquitous Resistant to diet-induced obesity	(405)
19 5(F)	Gpr10 ^g Gpr109a ^g	10q26.13 12q24.31	GPR10 GPR109A	G-protein-coupled receptor 10 G-protein-coupled receptor 109a	Adult-onset obesity Absence of nicotinic acid-induced inhibition of free fatty acid release from adipocytes	(406) (407)
15	Gpr24 ^g	22q13.3	GPR24	G-protein-coupled receptor 24, also known as Mch1r	Lean and resistant to diet-induced obesity	(408)
7	Gpr40 ^g	19q13.1	GPR40	G-protein-coupled receptor 40	Resistant to diet-induced obesity-mediated changes	(409)
1(A1) 9(57)	Gpr7 ^g Gpx1 ^k	8p22-q21.13 3p21.3	GPR7 GPX1	G-protein-coupled receptor 7 Glutathione peroxidase 1	Adult-onset obesity Transgene consisting of complete genomic <i>Gpx1</i> gene Increased BW and adiposity	(410) (411,412)
7	Grm5 ^g	11q14.3	GRM5	Glutamate receptor, metabotropic 5	Lower BW and reduced adipose gain on high-fat diet	(413)
6(A3)	Grm8 ^g	7q31.3-q32.1	GRM8	Glutamate receptor, metabotropic 8	Increased fat mass	(414)
16(B4)	Gsk3b*	3q13.3	GSK3B	Glycogen synthase kinase 3β	Transgene expressing human cDNA in skeletal muscle Increased BW and adiposity in male transgenic mice	(415)
6(48.7)	Gt(ROSA)26	Sor ^k	Unknown	Gene trap ROSA 26, Philippe Soriano	Transgene. Conditional activation of Akt in skeletal muscle Decreased adipose mass and increased muscle mass after treatment with tamaxiphen	(293)
10(43)	Gtrgeo22 ^e	19p13.3	C19orf20	Gene trap 22, Philippe Soriano	Reduced BW and adiposity	(416)
11(61.2)	Hcrt*	1/q21	HCKI	Hypocretin (orexin). Loss of orexin- containing neurons	 Iransgene. Expression of MJd (Ataxin 3) with expanded repeats in orexinergic neurons Late-onset obesity (C57BL/6J and DBA/2 	(417)
11(61.2)	<i>Hcrt</i> ^k	17q21	HCRT	Hypocretin (orexin). Loss of orexin- containing neurons	 mixed genetic background) Transgene. Expression of Mjd (Ataxin 3) with expanded repeats in orexinergic neurons No weight difference between mutant and wild type when both on a C57BL/6J genetic background 	(418)
2(71) 5(20)	Hdc ^g Hdh ^k	15q21-q22 4p16.3	HDC HD	Histidine decarboxylase Huntington disease (HD) gene homolog, also known as Huntington, R6/2	Increased BW and adiposity Transgenic. Human exon 1 of the <i>HD</i> gene carrying ~141 to 157 CAG repeats expressed from the endogenous <i>HD</i> gene promoter Despite an overall growth retardation, the transgenic mice have increased adiposity Adult-onset wasting	(419) (420)
13(46)	Hexb ^g	5q13	HEXB	Hexosaminidase B	syndrome Lean	(421)

Mouse chromosome (cM/band)	Mouse gene	Human chromosome	Human homolog	Gene description	Details	Reference
10(67.5)	Hmga2 ^g	12q15	HMGA2	High mobility group AT-hook 2	Resistant to diet-induced obesity	(422)
6(49)	Hrh1 ^g	3p25	HRH1	Histamine receptor H1	Late-onset obesity	(423)
2	Hrh3 ^g	20q13.3	HRH3	Histamine receptor H3	Increased adiposity and BW	(424)
1	Hsd11b1 ^g	1q32-q41	HSD11B1	Hydroxysteroid 11- β dehydrogenase 1	Resistant to diet-induced obesity	(425)
1	Hsd11b1 ^k	1q32-q41	HSD11B1	Hydroxysteroid 11- β dehydrogenase 1	Transgenic. Promoter aP2-specific expression	(426)
8(50.8)	Hsd11b2 ^k	16q22	HSD11B2	Hydroxysteroid 11- β dehydrogenase 2	Transgenic. Human gene expressed in adipose cells	(427)
X(66)	Htr2c ^g	Xq24	HTR2C	5-Hydroxytryptamine (serotonin) receptor 2C	Resistant to diet-induced obesity Late-onset obesity	(428)
9(7)	Icam1 ^g	19p13.2	ICAM1	Intercellular adhesion molecule-1	Late-onset obesity Accelerated adiposity on a high-fat diet (N4 mice)	(429)
9(7)	Icam1 ^g	19p13.2	ICAM1	Intercellular adhesion molecule-1	Transient increased adiposity after 11 days of high-fat diet but reduced BW and adiposity relative to controls after 50 days of high-fat diet (N8 mice)	(430)
9(7)	Icam1 ^k	19p13.2	ICAM1	Intercellular adhesion molecule-1 (ICAM-1)	Transgene. Expressing soluble <i>ICAM-1</i> in liver Increased weight gain on a Western-type diet	(431)
1(29.8)	Idh1 ^k	2q33.3	IDH1	Isocitrate dehydrogenase 1 (NADP ⁺), soluble, also known as IDPc	Transgene, <i>Idh1</i> cDNA expressed from the rat cytosolic <i>Pepck</i> promoter	(432)
				tissue	Obesity	
12(21.5)	Ifrd1 ^k	7q22-q31	IFRD1	Also known as Tis7, interferon-related developmental regulator 1	Transgene. Expressed in gut small intestine Increased adiposity	(433)
15	Igfbp6 ^k	12q13	IGFBP6	Insulin-like growth factor-binding protein 6	Transgene (human). Expressed in glial cells	(434)
2(10)	Il1rn ^g	2q14.2	IL1RN	Interleukin 1 receptor antagonist	Reduced BW	(435)
2(10)	Il1rn ^g	2q14.2	ILIRN	Interleukin 1 receptor antagonist	Reduced adiposity, resistant to diet- induced obesity and resistant to obesity due to monosodium glutamate treatment	(436)
5(17)	Il6 ^g	7p21	IL6	Interleukin 6	Increased adiposity and BW	(437)
5(17)	Il6 ^g	7p21	IL6	Interleukin 6	No effect on adiposity. Reduced BW in 3-month-old mice	(438)
7(F1)	Inppl1 ^g	11q23	INPPL1	Polyphosphate phosphatase-like 1 (SHIP-2)	Resistant to diet-induced obesity	(439)
8(1)	Insr ^c	19p13.3- p13.2	INSR	Insulin receptor not expressed in muscle cells	Floxed gene and muscle-specific Cre expression Increased adipose depots and obesity	(440)
8(5)	Irs2 ^c	13q34	IRS2	Insulin receptor substrate 2. Conditional KO in pancreatic β cells	Floxed gene + Cre transgene expressed from the rat insulin promoter	(441)
8(5)	Irs2 ^c	13q34	IRS2	Insulin receptor substrate 2. Conditional KO in pancreatic β cells	Figure 1 and C_{re} transgene expressed from the rat insulin promoter	(442)
3(52)	Kcna3 ^g	1p13.3	KCNA3	and hypothalamus Potassium voltage-gated channel, shaker-related subfamily, member 3,	Reduced BW and resistant to diet-induced obesity	(443)
7(41)	Kcnj11 ^g	11p15.1	KCNJ11	Potassium inwardly rectifying channel, subfamily J, member 11, also known as Kir6.2	Increased BW (10%) and epididymal fat pad (70%) weight	(444)

Mouse chromosome (cM/band)	Mouse gene	Human chromosome	Human homolog	Gene description	Details	Reference
14(E2.1)	Klf5 ^g	13q22.1	KLF5	Kruppel-like factor 5	Deficiency in white adipose tissue	(445)
6(10.5)	Lep ^k	7q31.3	LEP	Mouse Lep cDNA was cloned 3' of the liver-specific Apoe promoter and 5' of liver-specific enhancer sequence. Serum leptin expression is 200- to 300-fold higher than in wild-type mice Transgene: Apoe promoter expressing murine leptin cDNA Absence of fat pads		(446)
6(10.5)	Lep ^k	7q31.3	LEP	This transgene consists of a mouse Lep cDNA fused to the human APCS promoter with hormone expression targeted to the liver. In mutants carrying 30 copies of the transgene serum, leptin expression is about 12-fold higher than in wild-type mice	Transgene: human APCS promoter expressing murine leptin cDNA Decreased BW. Absence of adipose tissue	(447)
4(46.7)	Lepr ^f	1p31	LEPR	Selective loss of long form of leptin receptor	Obesity	(448)
4(46.7)	Lepr ^k	1p31	LEPR	Transgene insertion 1, Gerard Karsenty. An isoform of Lepr cDNA lacking the transmembrane domain found in all other isoforms was cloned 3' of the liver-specific Apoe promoter and 5' of liver- specific enhancer sequence	Transgene: Apoe promoter expressing murine-soluble leptin receptor cDNA Mice carrying this transgene possess normal body fat. However, in mice heterozygous for the lep ^{ob} mutation, the transgenic mice show significantly increased adiposity	(446)
4(46.7)	Lepr ^c	1p31	LEPR	Neuronal-specific deletion of leptin receptor	Floxed gene + <i>Cre</i> transgene expressed from the Syndecan 1 promoter Obesity	(449,450)
4(46.7)	Lepr ^k	1p31	LEPR	Leptin receptor. Mutation due to insertion of rabbit smooth muscle myosin heavy chain promoter region	Mutation due to transgene insertion Obesity	(451)
4(46.7)	Lepr ^k	1p31	LEPR	Leptin receptor	Transgenic: neuron-specific expression Rescue of obesity of Lepr ^{db} mutant mice	(452)
4(46.7)	Lepr ^k	1p31	LEPR	Leptin receptor	Transgenic: neuron-specific expression (50% and 75%)Adiposity and obesity are proportional to hypothalamic LEPR deficiency, but fertility and cold tolerance remain intact	(449)
7(23) 19	Lhb ^k Lip1 ^g	19q13.32 10q23.2- q23.3	LHB LIPA	Luteinizing hormone β polypeptide Lysosomal acid lipase 1	Obesity in females Decreased BW, fatty liver, loss of brown and white fat depots; ectopic fat deposition into liver, spleen, and bowel	(453) (454,455)
9(39)	Lipc ^g	15q21-23	LIPC	Lipase, hepatic	KO with background strain effects Increased adiposity mediated by background susceptibility	(456)
7(5.5)	Lipe ^g	19q13.2	LIPE	Lipase, hormone sensitive	Reduced fat pad size, heterogenous adipocyte size, increased brown fat. Resistant to diet-induced obesity	(457,458)
7(5.5)	Lipe ^k	19q13.2	LIPE	Lipase, hormone sensitive	Transgene; human <i>LIPE</i> expressed in adipose tissue Corrects adipose defects of <i>Lipe</i> -deficient mice	(459)
12(9)	Lpin1 ^h	2p25.1	LPIN1	<i>Lipin 1</i> , gene responsible for phenotype of fatty liver dystrophic mouse	Spontaneous null allele Reduced adiposity on chow. Resistant to diet-induced obesity	(460)

Mouse chromosome (cM/band)	Mouse gene	Human chromosome	Human homolog	Gene description	Details	Reference
12(9)	Lpin1 ^k	2p25.1	LPIN1	Lipin 1	Transgene. Expressed in adipose tissue	(461)
12(9)	Lpin1 ^k	2p25.1	LPIN1	Lipin 1	Transgene. Expressed in skeletal muscle Obesity due to changes in energy expenditure	(461)
7(61)	Mapk3 ^g	6р12-р11.2	MAPK3	Mitogen-activated protein kinase 3, also known as ERK1, Prkm3, p44	N6 mice. Reduced adiposity, resistant to diet-induced obesity	(462)
2(E1)	Mapk8ip1 ^g	11p11.2	MAPK8IP1	Mitogen-activated protein kinase 8 interacting protein 1. Acts as an inhibitor of c-Jun N-terminal kinase	Reduced adiposity	(463,464)
2(100)	Mc3r ^g	20q13.2- q13.3	MC3R	Melanocortin receptor 3	Obesity	(465)
2(100)	Mc3r ^g	20q13.2- q13.3	MC3R	Melanocortin receptor 3	Obesity	(466)
18(E1)	Mc4r ^g	18q22	MC4R	Melanocortin receptor 4	Obesity	(467)
18(E1)	Mc4r ^k	18q22	MC4R	Melanocortin receptor 4 Obesity Melanocortin receptor 4 Transgene. Expressed in paraventricular hypothalamic nucleus and subpopulation of amygdala Prevents 60% of obesity, rescues hyperphagia but not reduced energy expenditure of <i>Mc4r</i> -deficient mutant mice		(468)
6(7.5)	Mest ^k	7q32	MEST	Mesoderm-specific transcript Transgene. Expressed in adipose tissue Increased adiposity		(469)
2	Mkks ^g	20p12	MKKS	McKusick-Kaufman syndrome protein	Obesity	(470)
5	<i>Mlxipl</i> ^g	7q11.23	MLXIPL	MLX interacting protein-like Lean; rapid death on high-sucrose and high-fructose diets		(471)
10(40.9)	Mmp11 ^g	22q11.23	MMP11	Matrix metalloproteinase 11	Obesity	(472)
10(70)	Mmp19 ^g	12q14	MMP19	Matrix metalloproteinase 19	Accelerated BW and adipose mass gain on a high-fat diet	(473)
8(45)	Mt1, Mt2 ^g	16q13	MTIA	Metallothionein I and II	KO; both mutations generated with the same targeting construct Increased BW. Adult-onset obesity	(474,475)
15(32)	Myc ^k	8q24.12- q24.13	МҮС	Myelocytomatosis oncogene. Expression limited to liver	Transgene. Murine c-myc expressed under the control of the <i>Pepck</i> promoter Resistant to diet-induced obesity	(476)
9	Ncb5or ^g	6pter-q22.33	NCB5OR	NADPH cytochrome B5 oxidoreductase	Reduced adipose mass	(345)
3	Nhlh2 ^g	1p12-p11	NHLH2	Nescient helix loop helix 2, also known as neural transcription factor 2 or NSCL2	Adult-onset obesity	(477)
5	Nmu ^g	4q12	NMU	Neuromedin U	Elevated BW and obesity	(478)
5	Nmu ^k	4q12	NMU	Neuromedin U	Transgene. Expressed ubiquitously Lean and hypophagic	(479)
11(45.6)	Nos2 ^g	17q11.2-12	NOS2A	Nitric oxide synthase 2, inducible, macrophage, also known as iNOS	Reduced adiposity	(480)
11	Npb ^g	17q25.3	NPB	Neuropeptide B; ligand for GPR7	Mild obesity	(481)
6(26)	Npy ^g	7p15.1	NPY	Neuropeptide Y	No obesity phenotype except with Galenin (Gal) KO	(375)
	Npy-/- + Gal-/ _ ^g			Double homozygote for neuropeptide Y and galenin deficiency	KO: compound double homozygous mutant strain Obesity	(375)
8(33)	Npy1r ^g	4q31.3-q32	NPY1R	Neuropeptide Y receptor Y1	Obesity	(482)
8(32.5)	Npy5r ^g	4q31-q32	NPY5R	Neuropeptide Y receptor Y5	Increased adiposity leading to mild adult- onset obesity	(483)
7	Nr1h2 ^g	19q13.3-13.2	NR1H2	Nuclear receptor subfamily 1, group H, member 2, also known as LXR β	Reduced adiposity	(484)

Mouse chromosome (cM/band)	Mouse gene	Human chromosome	Human homolog	Gene description	Details	Reference
1(92.6)	Nr1i3 ^g	1q23.3	NR113	Nuclear receptor subfamily 1, group I, member 3	Accelerated adipose loss on calorie- restricted diet	(485)
18(20)	Nr3c1°	5q31	NR3C1	Nuclear receptor subfamily 3, group C, member 1; also known as glucocorticoid receptor Heating to reduced adiposity preweaning, leading to reduced adiposity in older mice due to altered food intake and metabolic efficiency		(486)
2(107) 10(8)	Ntsr1 ^g Oprm1 ^g	20q13-20q13 6q24-q25	NTSR1 OPRM1	Neurotensin receptor 1 Adult-onset increase in BW and adiposity Opioid receptor, μ1, also known as Resistant to diet-induced obesity MOR. MOR-1 Adult-onset increase in BW and adiposity		(487) (488)
1(98.6)	Parp1 ^g	1q41-q42	PARP1	ADP-ribosyltransferase [NAD+, poly(ADP-rose)polymerase] 1, also known as Admt1 or Admm		(489,490)
13(44)	Pcsk1 ^g	5q15-q21	PCSK1	Proprotein convertase subtilisin/kexin	Increased adipose mass in heterozygous mice	(491)
Х	Pcsk1n ^k	Xp11.23	PCSK1N	Proprotein convertase subtilisin/kexin type 1 inhibitor	Transgene: expressing Pcsk1n cDNA using the β -actin promoter Adult-onset obesity	(492)
7(6.5)	Peg3 ^g	19q31.4	PEG3	Paternally expressed 3, also known as Zfp102 End4 Pw1	Obesity	(493)
11(31)	Pemt ^g	17p11.2	PEMT	Phosphatidylethanolamine <i>N</i> - methyltransferase	Liver abnormalities on high-fat diet	(494,495)
13(50)	Pik3r1 ^g	5q13.1	PIK3R1	Phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1 (n85α)	Smaller adipocytes and reduced adiposity	(496)
11(58.2)	Pip5k2b ^e	17q12	PIP5K2B	Phosphatidylinositol-4-phosphate 5- kinase, type IL B	Reduced BW and adiposity; resistant to diet-induced obesity	(497)
5(F1/G1)	Pla2g1b ^g	12q23-q24.1	PLA2G1B	Phospholipase A2, group IB, pancreas	Normal BW and fat pad weight on chow diet; resistant to diet-induced obesity when fed a western diet. KO mice also displayed increased lipid content in the stool, thus displaying decreased fat absorption	(498)
7	Plin ^g	15q26	PLIN	Perilipin	Reduced adiposity. Resistance to diet- induced obesity	(499)
9	Plscr1 ^g	3q23	PLSCR1	Phospholipid scramblase 1	Elevated adiposity	(500)
11(43)	Plscr3 ^e	17p13.1	PLSCR3	Phospholipid scramblase 3	Elevated BW and adipose mass	(501)
10(47)	Pmch ^g	12q23-q24.1	РМСН	Promelanin-concentrating hormone, also known as MCH	Reduced BW and adiposity; resistant to diet-induced obesity	(502,503)
12(4)	Pomc1 ^g	2p23.3	POMC	Pro-opiomelanocortin- α	Obesity on chow and high-fat diets	(504,505)
5(75)	Por ^g	7q11.2	POR	P450 (cytochrome) oxidoreductase	Conditional KO (liver specific) Increased liver weight and fatty liver	(506,507)
15(48.8)	Ppara ^g	22q13.31	PPARA	Peroxisome proliferator-activated receptor α	Moderate elevation in gonadal fat in chow-fed females; significant increase in adiposity relative to wild-type mice in both males and females in high-fat diet-fed mice	(508)
15(48.8)	Ppara ^k	22q13.31	PPARA	Peroxisome proliferator-activated receptor α	Transgene. Expressed in muscle Resistant to diet-induced obesity	(509)
17(13.5)	Ppard ^e	6p21.2-p21.1	PPARD	Peroxisome proliferator activator receptor Δ , also known as peroxisome proliferator-activated receptor β . Specific loss of Ppard from adipose cells	Floxed gene and aP2-driven <i>Cre</i> Resistant to diet-induced obesity and reduced adiposity in Lepr ^{db} homozygous mutants	(510)

Mouse chromosome (cM/band)	Mouse gene	Human chromosome	Human homolog	Gene description	Details	Reference
17(13.5)	Ppard ^e	6p21.2-p21.1	PPARD	Peroxisome proliferator activator receptor Δ, also known as peroxisome proliferator-activated receptor β , overexpressed in skeletal muscleFloxed transgene. Cre-Lox strategy overexpress Ppard in skeletal mu using HAS-CreReduction in fat mass and adipocyt musclesize		(511)
17(13.5)	Ppard ^g	6p21.2-p21.1	PPARD	Peroxisome proliferator activator receptor Δ , also known as peroxisome proliferator-activated receptor β On a high-fat diet, KO mice develop greater adiposity than controls despite a lower overall total BW		(512)
6(52.7)	<i>Pparg</i> ^c	3p25	PPARG	Loss of peroxisome proliferator- activated receptor γ from adipose cells Floxed gene and aP2-driven Cre Reduced adiposity and resistant to diet- induced obesity		(513,514)
6(52.7)	<i>Pparg</i> ^c	3p25	PPARG	Loss of peroxisome proliferator- activated receptor γ from muscle	Floxed gene and muscle creatine kinase (MCK)-driven Cre	
6(52.7)	<i>Pparg</i> ^c	3p25	PPARG	Loss of peroxisome proliferator- activated receptor γ from β cells	Floxed gene and rat insulin promoter- driven Cre Attenuated <i>β</i> cell hyperplasia in response	
6(52.7)	<i>Pparg</i> ^c	3p25	PPARG	Peroxisome proliferator-activated receptor γ	KO + reporter Selective loss of PPARg2 isoform leads to reduced BW, smaller adipocytes, and resistance to diet-induced obesity	(517)
6(52.7)	<i>Pparg</i> ^f	3p25	PPARG	Peroxisome proliferator-activated receptor γ	Knock-in expressing dominant negative allele Lethal in homozygotes. Heterozygotes are lean and resistant to diet-induced obesity	(518)
5(C1)	Ppargc1a ^g	4p15.1-15.2	PPARGCIA	Peroxisome proliferative-activated receptor, γ , coactivator 1 α	Resistant to diet-induced obesity; cold sensitive	(519)
5(C1)	Ppargc1a ^g	4p15.1-15.2	PPARGC1A	Peroxisome proliferative-activated receptor, γ , coactivator 1α	Increased adiposity in young females and old males	(520)
18	Ppargc1b ^k	5q32	PPARGC1B	Peroxisome proliferative-activated receptor, γ , coactivator 1 β	Transgene. Murine cDNA expressed from the chicken β -actin promoter Resistant to diet-induced obesity	(521)
6(A2)	Ppp1r3a ^g	7q31.1	PPP1R3A	Protein phosphatase 1, regulatory (inhibitor) subunit 3A	Increased BW and obesity	(522)
19(C3)	Ppp1r3c ^g	10q23-q24	PPP1R3C	Protein phosphatase 1, regulatory (inhibitor) subunit 3C, also known as PTG	Homozygous mutants are embryonic lethal. Heterozygotes show increased intramyocellular lipid stores and elevated circulating leptin, triglycerides and free fatty acids	(523)
11	<i>Ppy</i> ^k	17q21	РРҮ	Pancreatic polypeptide	Transgenic. Mouse Ppy cDNA expressed from the chicken β -actin hybrid promoter	(524,525)
4	Prkaa2 ^g	1p31	PRKAA2	Protein kinase, adenosine monophosphate-activated, $\alpha 2$ catalytic subunit. No expression in adipocytes	KO. Floxed gene + aP2 expressed Cre Increased adiposity	(526)

Mouse chromosome (cM/band)	Mouse gene	Human chromosome	Human homolog	Gene description	Details	Reference
1	Prkag3 ^k	2q35	PRKAG3	Transgene insertion 1, Leif Andersson.An Myl1 promoter and enhancerExpression of the mutated protein was seen in the skeletal muscle. Levels of the endogenous PRKAG3 protein were reduced, resulting in no significant change in overall PRKAG3 protein expressionAn Myl1 promoter and enhancer expressing a full-length mouse Prkag3 cDNA (encodes protein kinase, AMP- activated, $\gamma 3$, noncatalytic subunit) with a single missense mutation (R225Q)PRKAG3 protein expressionTransgenic mice have lowered adiposity and are protected against high-fat diet- induced triglyceride accumulation and insetance		(527)
12(B1)	Prkar2b ^g	7q22	PRKAR2B	Protein kinase, cAMP-dependent regulatory, type IIβ, also known as RIIβ	Decreased adiposity; resistant to diet- induced obesity	(528,529)
2(2)	<i>Prkca</i> ^k	10p15	PRKCO	Protein kinase C. θ	Obesity	(530)
19	Prkhr ^g	10q26.13	PRLHR	Prolactin-releasing hormone receptor	Obesity	(406)
1(106.3)	Prox1 ^g	1q32.2-q32.3	PROX1	Prospero-related homeobox 1	Obesity in heterozygotes	(531)
2(H3)	Ptpn1 ^g	20q13.1- q13.2	PTPN1	Protein tyrosine phosphatase, non- receptor type 1	Reduced adiposity	(532,533)
5(F1/G1)	Ptpn11 ^g	12q24	PTPN11	Protein tyrosine phosphatase, non- receptor type 11	Forebrain-specific KO Obesity	(534)
2(73.1)	Ptpns1 ^g	20p13	PTPNS1	Protein tyrosine phosphatase, non- receptor-type substrate 1, also known as SHPS-1	Decreased BW and fatty livers	(535)
11	Pttg1 ^g	5q35.1	PTTG1	Pituitary tumor-transforming 1	Reduced BW and cessation of weight gain after 6 months in males accompanied by loss of epididymal fat mass	(536)
11(B2)	Rai1 ^g	17p11.2	RAII	Retinoic acid induced 1	Homozygote lethal. Heterozygotes are obese	(537)
9(50)	<i>Rasgrf1</i> ^g	15q24	RASGRF1	RAS protein-specific guanine nucleotide-releasing factor 1	Reduced BW and adiposity	(538)
1(69.9)	Ren1 ^k	1q32	REN	Renin 1	Transgene: human REN gene expressed from endogenous promoter Late-onset obesity	(539)
8(0.4)	<i>Retn^k</i>	19p13.2	RETN	Resistin/ADSF/Fizz3. Adipocyte- specific overexpression of dominant negative Retn	Transgene: aP2 promoter expressing Retn fused to the human $IgG\gamma$ constant region Increased adiposity but enhanced glucose	(540)
16(33)	<i>Retnlb</i> ^k	3q13.1	RETNLB	Resistin-like β ; expressed in liver	Hyperlipidemia and fatty liver on high-fat	(541)
X(65.7)	Rps6ka3 ^g	X p22.2-	RPS6KA3	Ribosomal protein S6 kinase	Reduced BW and adiposity; resistant to diet-induced obesity	(542)
11	Rps6kb1 ^g	17q23.2	RPS6KB1	Ribosomal protein S6 kinase, polypeptide 1, S6K1	Resistant to diet-induced obesity	(543)
4	Rsc1a1 ^g	1p36.1	RSC1A1	Regulatory solute carrier protein, family 1, member 1	Obesity	(544)
1(88.1)	Rxrg ^g	1q22-q23	RXRG	Retinoid X receptor γ	Resistant to diet-induced obesity	(545)
19(43)	Scd1 ^g	10	SCD1	Stearyl-CoA desaturase 1	Reduced BW and adiposity; resistant to diet-induced obesity	(508,546)
12(1)	Sdc1 ^k	2p24.1	SDC1	Syndecan 1	Transgenic. Mouse Sdc1 cDNA expressed from the cytomegalovirus promoter/ enhancer	(547)
4(60.8)	Sdc3 ^g	1pter-p22.3	SDC3	Syndecan 3	Reduced adiposity on chow. Resistant to diet-induced obesity	(548)

Mouse chromosome (cM/band)	Mouse gene	Human chromosome	Human homolog	Gene description	Details	Reference
5	Serpine1 ^g	7q21.3-q22	SERPINE1	Serine (or cysteine) proteinase inhibitor, clade E, member 1, also known as plasminogen activator inhibitor, type I	Resistant to diet-induced obesity	(549)
5	Serpine1 ^g	7q21.3-q22	SERPINE1	Serine (or cysteine) proteinase inhibitor, clade E, member 1, also known as plasminogen activator inhibitor, type I	Same BW gain as control mice on high- fat diet. No difference in subcutaneous fat mass but elevated gonadal adipose mass. Mutant and litter mates are 80% B6 and 20% 129 composite	(550)
5	Serpine I ^k	7q21.3-q22	SERPINE1	Serine (or cysteine) proteinase inhibitor, clade E, member 1, also known as plasminogen activator inhibitor, type I. Expressed in adipose cells	Transgene. Murine cDNA expressed from the aP2 promoter Resistant to diet-induced obesity	(551,552)
8(9.5)	Sfrp1 ^g	8p12-p11.1	SFRP1	Secreted frizzled-related sequence	KO + reporter	(553)
7(61)	Sh2bpsm1 ^g	16p11.2	SH2B	protein 1 SH2-B PH domain-containing signaling mediator 1 also known as SH2-B	Reduced adiposity in males Obesity	(554)
10(26.5)	Sim1°	6q16.3-q21	SIM1	Single-minded 1	Floxed gene and EIIa-expressed Cre Obesity in heterozygous mice	(555)
10(26.5)	Sim1 ^g	6q16.3-q21	SIM1	Single-minded 1	Obesity in heterozygous mice	(556)
11(40)	Slc2a4 ^g	17p13	SLC2A4	Solute carrier family 2 (facilitated glucose transporter), member 4 (encodes GLUT4)	Reduced adiposity	(557)
11(40)	Slc2a4 ^k	17p13	SLC2A4	Solute carrier family 2 (facilitated glucose transporter), member 4 (encodes GLUT4)	Transgene. Expressed in adipose tissue Increased fat mass	(558)
6	Slc6a1 ^k	3p25-p24	SLC6A1	γ-aminobutyric acid transporter I	Transgenic. Mouse Slc6a1 brain-derived cDNA expressed from the cytomegalovirus promoter/enhancer Obesity	(559)
15(31.7)	Soat2 ^g	12q13.13	SOAT2	Sterol O-acyltransferase 2	Resistant to fatty liver but elevated circulating triglycerides and high- density lipoprotein cholesterol	(560)
11(E2)	Socs3°	17q25.3	SOCS3	Suppressor of cytokine signaling 3. Cerebrum- and hypothalamus- specific loss of Socs3	Floxed gene + transgenic Cre expressed from rat nestin promoter Decreased BW and resistant to diet- induced obesity	(561)
11(E2)	Socs3°	17q25.3	SOCS3	Suppressor of cytokine signaling 3. Cerebrum and hypothalamus- specific loss of Socs3	Floxed gene + transgenic Cre expressed from Syndecan I promoter Decreased BW and resistant to diet- induced obesity	(561)
17(8) 11(29.9)	Sox8 ^g Sparc ^g	16p13.3 5q31.3-q32	SOX8 SPARC	SRY box-containing gene 8 Secreted acidic cysteine-rich	Decreased fat mass Increased adiposity with no effect on BW	(562) (563)
11	Srebf1 ^k	17p11.2	SREBF1	Transgene expresses sterol regulatory element-binding factor 1 in adipose	Transgene: aP2-driven human SREBF1c cDNA	(564)
11	Srebf1 ^k	17p11.2	SREBF1	cell Sterol regulatory element-binding factor 1, transcript 1a, also known as Srebp1. Expressed in adipose	Reduced BW and adiposity Transgene expressing the human SREBF1–1a cDNA using the murine aP2 promoter Adiposite hypothesister human fatty liver	(565)
11	Srebf1 ^k	17p11.2	SREBF1	Sterol regulatory element-binding factor 1, transcript 1c, also known as Srebp1. Expressed in adipose cells	Transgene expressing the human SREBF- Ic cDNA using the murine aP2 promoter Loss of all adipose tissue	(564)

Mouse chromosome (cM/band)	Mouse gene	Human chromosome	Human homolog	Gene description	Details	Reference
11(60.5)	Stat3 ^c	17q21.31	STAT3	Pancreatic- and hypothalamic-specific deletion of Stat3; signal transducer and activator of transcription 3 Bellevia dense + Cre transgene expressed from the rat insulin II promoter Obesity. Transplantation of wild-type pancreatic islets into the mutants did not alleviate obesity, suggesting that lack of hypothalamic Stat3 expression is responsible for the obesity		(566)
11(60.5)	Stat3 ^c	17q21.31	STAT3	Neuronal-specific deletion of Stat3; signal transducer and activator of transcription 3	Floxed gene + Cre transgene expressed from the rat Nestin promoter	(567)
11(60.5)	Stat5b ^g	17q11.2	STAT5B	Signal transducer and activator of transcription 5B	Increased adiposity	(568)
7(6.5)	Tgfb1 ^k	19q13.31	TGFB1	Transforming growth factor, β 1 Transgenic. Human TGFB1 cDNA expressed from the rat PEPCK promoter Reduced adiposity: lipodystrophy		(569)
11(57)	<i>Thra^g</i>	17q11.2	THRA	Thyroid hormone receptor α	KO; gene replacement with dominant negative mutant allele	(570)
14(B1)	Tkt ^g	3p14.3	TKT	Transketolase Homozygous mutants are embryonic lethal. Heterozygotes display reduced BW and adiposity		(571)
17(19.1)	Tnf ^g	6p21.3	TNF	TNF	Reduction in BW and adiposity	(572)
17(19.1)	Tnf ^k	6p21.3	TNF	TNF. Non-cleavable mutant protein expressed in TNF-deficient mice		(573)
7(51.5)	Tub ^g	11p15.5	TUB	Tubby candidate gene	Late-onset obesity	(574)
3(47.1)	<i>Txnip</i> ^g	1q21.1	TXNIP	Thioredoxin-interacting protein	Increased fat-to-muscle ratio	(575)
2(67.4)	Ubr1 ^g	15q13	UBR1	Ubiquitin protein ligase E3 component Lean n-recognin 1		(576)
8(38)	Ucp1 ^g	4q28-q31	UCP1	Uncoupling protein 1, mitochondrial	Jncoupling protein 1, mitochondrial Temperature-dependent resistance to diet- induced obesity on C57BL/6J genetic background	
8(38)	Ucp1 ^k	4q28-q31	UCP1	Transgene insertion 1, Frederic Bouillaud. The transgene consists of a rat uncoupling protein 1 (UCP1) cDNA sequence under the control of a mouse Ckmm promoter. Expression limited to skeletal and cardiac muscle	Transgene: murine muscle creatine kinase promoter expressing rat UCP1 cDNA Lower BW and reduced adiposity	(578)
8(38)	Ucp1 ^k	4q28-q31	UCP1	Uncoupling protein 1 (UCP1), mitochondrial	Transgene. UCP1 promoter expressing the diphtheria toxin gene Ablation of UCP1 expressing tissues leads to obesity	(579,580)
7(50)	Ucp2/Ucp3 ^k	11q13	UCP2/UCP3	 ³ Uncoupling protein 2 (UCP2), mitochondrial; uncoupling protein 3 (UCP3), mitochondrial ⁴ Transgene. Murine bacterial artificial chromosome containing the genomic UCP2 and UCP3 genes 		(581)
7(50)	Ucp3 ^k	11q13	UCP3	Uncoupling protein 3 (UCP3), mitochondrial. Expression limited to skeletal muscle	Transgene. Murine UCP3 cDNA expressed from the mouse Mck promoter No difference on chow, but a 4-week exposure to a high-fat diet revealed transgenic mice have less weight gain and reduced adipose gain	(582)

Table 2.	(continued)
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Mouse chromosome (cM/band)	Mouse gene	Human chromosome	Human homolog	Gene description	Details	Reference
3(68.5)	Unc5c ^k	4q21-q23	UNC5C	unc-5 homolog C (C. elegans)	 KO/transgene: a cDNA encoding telomerase reverse transcriptase under the control of the chicken β-actin promoter randomly inserted into intron 1 of Unc5c Reduction in BW and adiposity 	(583)
5(79)	Vgf ^g	7q22	VGF	VGF nerve growth factor inducible	Reduction in BW and adiposity	(584)
19(20)	<i>Vldlr</i> ^g	9p24	VLDLR	Very-low-density lipoprotein receptor	Reduction in BW and adiposity	(585)
5	Wbscr14 ^g	7q11.23	WBSCR14	Williams-Beuren syndrome chromosome region 14 homolog (human)	Lower adiposity on standard diet. Rapid death on feeding a high-fructose or high-sucrose diet	(471)
15(56.8)	Wnt10b ^k	12q13	WNT10B	Wingless-related MMTV integration site 10b	Transgene, cDNA expressed from the aP2 (Fabp4) promoter Reduced adiposity and resistant to diet- induced obesity. Loss of brown adipose tissue	(586,587)
15(56.8)	Wnt10b ^g	12q13	WNT10B	Wingless-related MMTV integration site 10b	Increased muscular adiposity	(588)
7(10.2)	Zfp36 ^g	19q13.1	ZFP36	Zinc finger protein 36	Reduction in BW and adiposity	(589)

^a Antisense; ^b ethylnitrosourea (ENU); ^c floxed; ^d gene replacement; ^e gene trap; ^f knock-in; ^g knock-out; ^h spontaneous; ⁱ overexpression; ^j RNA interference; ^k transgenic.

One particularly interesting addition to the gene list is the murine *Clock* gene. The CLOCK transcription factor is a key component of the molecular circadian clock within pacemaker neurons of the hypothalamic suprachiasmatic nucleus. Characterization of murine *Clock* mutants reveals an obesity phenotype that is accelerated during feeding with high-fat diet. Causative factors include an attenuated diurnal feeding rhythm, hyperphagia, and perturbation of the expression of hypothalamic peptides associated with the regulation of feeding behavior and energy balance. The effects of the CLOCK transcription factor seem to be associated with growth and development only after weaning because no differences in BW are observed in newborn pups or 3- or 4-week weaned mice.

Animal QTLs

The murine QTL information in Table 3 has been completely revised this year. Primarily, the names assigned to quantitative trait loci (QTLs) have been changed to conform to currently utilized nomenclature, and, in an attempt to more specifically define the location of the QTL on the mouse genome, we have included the genetic location of the peak logarithm of the odds ratio (LOD) score (or other statistical measure utilized) and a confidence interval (usually the 1 LOD interval). Information presented has been summarized from the primary literature and also from the MGI group at the Jackson Laboratory (www.informatics.

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jax.org). Clearly, the concept of QTL significance plays a large role in the identification of a QTL. We have attempted to adopt a uniform standard that identifies QTLs if they satisfy a genome-wide significance level below 0.05. QTLs that do not meet this are termed suggestive, and we have listed only suggestive QTLs that have either been corroborated in follow-up studies or replicated in another study using the same mouse strains. In cases of uncertainty, we have erred on the side of caution and listed the OTLs. For some recent studies, evidence for interactions between QTLs has been presented, despite no evidence of significance for the individual loci alone. Nomenclature rules may need to be revisited to describe these interactions. In the majority of the cases, QTL names listed in the table are not identical to those listed in the primary publication. In these cases, the names were changed by the MGI group to maintain conformity with existing nomenclature. Thus, names that have been listed in previous years may have been altered in this year's table.

QTLs may be identified from several different types of genetic crosses. We have listed this information in this year's table. Typically, F_2 intercrosses or backcrosses are utilized. However, there is likely to be an increasing use of recombinant inbred strains, advanced intercross lines, and congenic strains (that contain a specific donor genetic segment on a different background strain). It must be remembered that QTLs identified from phenotyping and genotyp-

Cross	QTL	Scores	Variance (%)	Phenotypes	Animal chromosome	QTL peak	Reference
Cow							
$CGC \times Hereford$	BTA17LW	F = 8		-24 kg live weight	17		(590)
Chicken	51117,277	1 0		2 mg mee wergin	1,		(0)0)
White Leghorn layer × commercial	BFc7 36-41	F = 13.29	5.24	Abdominal fat weight (9 weeks)	7		(591)
broiler	BFc7 36-41	F = 11.50	4.51	Abdominal fatness (9 weeks)	7		
	BFc7 36-41	F = 11.08	4.4	Fat distribution (9 weeks)	7		
Rhode Island Red layer × Rhode Island Red layer	BWc4 200-207	p = 0.01	25.8	BW (40 weeks)	4		(592)
White Leghorn \times	Gwchr4	p = 0.01	17	Weight	4		(593)
Rhode Island Red	Gwchr27	p = 0.01	6	Weight	27		
White Plymouth	Bw5	F = 2.14		Weight (5 weeks)	1		(594)
Rock \times White Plymouth Rock	<i>Bw7</i>	F = 2.28		Weight (7 weeks)	1		
White Plymouth	Gfchr1	LOD = 2.75	18.1	Fat (%), abdominal	1		(595)
Rock \times Rhode Island Red layer	Gwchr13	LOD = 2.77	26.6	Weight	13		
Rhode Island Red layer \times Rhode	GAA01 263- 287			Weight	1		(596)
Island Red layer	GAA02 23-28			Weight	2		
Mouse (multiple							
crosses) (B6.129-Lipc ^{tm1Unc} \times SPRET/Ei)F1 \times C57BL/6- Lipc ^{tm1Unc}	Bsbob			Body fat and adiposity	2	81.7	(456,597)
(B6.129-Lipc ^{tm1Unc} × SPRET/Ei)F1 × C57BL/6J	Bsbob2			BW, fat mass, adiposity; interacts with Bsbob4 to regulate adiposity and BW	7	62 (60 to 63.5)	
(C57BL/6J × SPRET/Ei)F1 × C57BL/6I	Bsbob3			Interacts with Bsbob4 to regulate total cholesterol	6	26.5	
C57BL/6J/Lipc-/- × Mus spretus SPRET/Ei	Bsbob4			Interacts with Bsbob3 to regulate total cholesterol; interacts with Bsbob5 to regulate body fat	12	52	
	Bsbob5			Interacts with Bsbob4 to regulate body fat	15	20.2	
		LOD = 3.6	26	Interaction between Lipc (chromosome 9) and	7		
$(BALB/cJ \times C57BL/6J)F1 \times (C3H/HeJ \times DB A/2UE1$	D3Mit127	<i>p</i> = 0.01		Leptin, 27%	3	70.3	(598)
$(C3H/He \times Mus$ spretus)F1 ×	Bw1	LOD = 3.4	24	BW	Х	18 cM (DXMit57- DXMit48)	(599)
C57BL/6J	Bw2	LOD = 6.6		BW	Х	DXMit109- DXMit16	
	Bw3	LOD = 4.3		BW	х	32 cM	
	Bw1			BW	x	Distal to DXNds1	
	Bw2			BW	x	DXMit60-DXMit16	
	Bw3			BW	X	DXMit3-DXMit12	

Table 3. QTLs reported for animal polygenic models of obesity

		_			Animal		
Cross	QTL	Scores	Variance (%)	Phenotypes	chromosome	QTL peak	Reference
(C57BL/6- Lipc ^{tm1Unc} × SPRET/Ei)F1 × SPRET/Ei	Bsbob	LOD = 3.7	3	Adiposity QTL present in BSBHLKO cross (BSB hepatic lipase- deficient animals) but not in BSB	2	79 (75.6 to 81.1)	(600)
B6.S(D2mit194- D2Mit311)	Bsbob			Confirmed to contain obesity QTL	2	26.7- to 32.1- megabasepair interval	
(C57BL/6J \times	Hlbsb1	LOD = 4.8	10.7	Hepatic lipase activity	7	64 (48 to 66)	(601)
SPRET/Pt)F1 × C57BL/6J	Hlbsb2		7	Hepatic lipase activity; interaction with Hlbsb1	3 to 7		
(C57BL/6J \times	Mob1	LOD = 4.6	6.5	Fat (%)	7	62	(602,603)
STRET/Ei)F1 ×	Mob2	LOD = 4.8	7.1	Femoral fat	6	3.05	
C57BL/6J	Mob3	LOD = 4.8	7	Fat (%)	12	53	
	Mob4	LOD = 3.4	5.9	Mesenteric fat	15	6.7	
[High BW line (H) × low BW line (L)]F1 × high BW line (H)	Bw19	LOD = 137	20	Candidate gene <i>Gpc3</i> identified in 660- kilobasepair interval	Х	DXMit226- DXMit68 (2 cM)	(604–606)
(Mus m. castaneus) \times C57BL/6J)F1 \times M. m. castaneus	Pbwg1	LOD = 3.1 to 10.9	10	Stronger effect in females than males. Epistatic with Pbwg12 in males	2	32.8 (26 to 44)	(607–609)
	Pbwg2	LOD = 3.1	3.9	Male specific	4	62 (39 to 86)	
	Pbwg3	LOD = 2.6 to 3.6	3	Ĩ	7	72 (40 to 104)	
	Pbwg4	LOD = 3.7	7.5	Female specific; BW 5 weeks	9	71 (46 to 96)	
	Pbwg5	LOD = 3.4	3.7	BW at 7 weeks	10	68 (42 to 94)	
	Pbwg6	LOD = 4.9	5.2	Stronger effect in males than females	13	53 (34 to 72)	
	Pbwg7	LOD = 3.1	6.9	Male specific	Х	19 (0 to 48)	
	Pbwg8	LOD = 4	12.1	Male specific	6	32 (14 to 50)	
	Pbwg9	LOD = 3.8	4.5	Stronger effect in females than males	10	14 (0 to 36)	
	Pbwg10	$p = 2.6 \times 10^{-6}$		Interaction with Pbwg8 in males	Х	2.8	
	Pbwg12	$p = 9.1 \times 10^{-6}$		Male specific and epistatic with Pbwg1 in males	12	34	
	Pbwg13	$p = 2.5 \times 10^{-6}$		Interaction with Pbwg9 in females	5	81	
	Pbwg14	LOD = 2.8		BW at 8 weeks. Female specific	5	1 (0 to 74)	
	Pbwg15	LOD = 2.6 to 2.7		BW at 3 to 4 weeks	9	43	
	Pbwg16	LOD = 4.6		BW at 3 weeks	10	45	
	Pbwg17	LOD = 4.2 to 4.9		BW at 6 to 10 weeks	13	46	
	Pbwg18	LOD = 4.3		Female specific. Weight gain from 6 to 10 weeks	14	30	
	Pbwg19	LOD = 3		Male specific. BW at 5 weeks	16	2	
	Pbwg20	LOD = 3.1 to 6.3		BW at 3 to 4 weeks	19	0 (0 to 25)	

Cross	QTL	Scores	Variance (%)	Phenotypes	Animal chromosome	QTL peak	Reference
	Pbwg21	LOD = 2.6 to 3.6		Male specific. BW at 3 weeks and weight gain 3 to 6 weeks	Х	27	
	Pbwg22	LOD = 2.9 to		Female specific. BW 9 to 10 weeks	Х	35	
	$C10bw^2$	I OD = 3.6		Female specific	9	17	
	C10bw3	LOD = 3.0		Male specific	11	57	
	C10bw4	LOD = 3.3		Female specific	13	46	
	C10bw6	LOD = 4.3		Female specific	x	18.9	
(Quackenbush-Swiss × C57BL/6J) ×	Not assigned	p = 0.009	40	BW and body length	10	56 to 65	(610)
C5/BL/6J	D 5		4.0	DW	2	01 7	((11)
$129P3/J \times C5/BL/$	Bwq5	LOD = 4.4	4.8	BW	2	81.7	(611)
6J	Bwq6	LOD = 4	4.3	BW	9	61	
	Αάιρο	LOD = 3.95	4.7	with Adip9	9	26	
	Adip6	LOD = 3.32	4.4	Adiposity, interaction with Adip5	16	63.2	
129T2/SvEmsJ \times	Obq1	LOD = 8	12.3	Adiposity	7	28	(612)
EL/Suz	Obq2	LOD = 4	6.3	Adiposity	1	15	
AKR/J \times C57L/J	Obq3	LOD = 5.1	7	Adiposity	2	53 (34 to 78.7 cM)	(613)
	Obq4	LOD = 4.6	6.1	Adiposity	17	4 (0 to 7)	
AKR/J \times SWR/J	Dob1	LOD = 4.4 2004 = 4.8			4	50 (D4Mit5- D4Mit11)	(614,615)
	Dob2	LOD = 4.8		Adiposity. QTL Not confirmed in (AKR × SWR) × SWR backcross mice	9	60 (D9Mit11- D9Mit18)	
		2004 = 3.9					
	Dob3	LOD = 3.9		Adiposity. QTL confirmed in (AKR × SWR) × SWR backcross	15	22.8 (D15Nds2- D15Mit22)	
B6.V-Lep ^{ob/ob}	Bwob	LOD = 5			5	44	(616)
(leptin treated) \times	Mors1	LOD = 5.6			1	101.5 to 106.3	
BALB/cJ	Mors2	LOD = 3.4			3	52.5 to 71.8	
	Mors3	LOD = 3.8		Testosterone	14	27.5 to 30	
	Mors4	LOD = 3.4		Testosterone	14	15 to 27.5	
B10.UW H3 ^b we Pax1 un a ^t /Sn X		LOD = 4.61		Fat; adiposity adjusted for weight	2	67.8 to 82	(617)
BALB/cA and	Nidd5	LOD = 5.91		BW and insulin	2	34.5	(618)
TSOD \times TSOD and BALC/cA	Nidd6	LOD = 4.65		BW	1	77	
BTBR.V-Lep ^{ob/ob} ×	Mobe1	LOD = 9.48	14.1	10-Week body mass	2	44 (41 to 47.1)	(619)
B6.V-Lep ^{ob/ob}	Mobe2	LOD = 8	12.5	10-Week body mass	13	37	
1	Mobe3	LOD = 3.6		10-Week body mass	5	65	
	Mobe4	LOD = 2.49		10-Week body mass	17	34.4	
C3H/He \times NSY	Waiting for identification	LOD = 6.8		BMI	6	35.5 (32 to 60)	(620)
C57BL/6-insr ^{tm1Dac} / +, irs1 ^{tm1Jos} / + \times	E1pt	LOD = 3.7	33	Leptin. Interacts with hyperinsulinemia QTL, Hypn	7	50	(621)
12950/SVEVTac	Oba16	IOD = 10		Famalas	o	19 (12 to 52)	(622)
CJ/DL/0J × 12981/	Obq10 Obg17	LOD = 10		Females	ð 1	40 (42 10 33)	(022)
SVIIIJ	Obq17 Obq18	LOD = 2.9 $LOD = 2.9$		Interacts with Obq16	9	65 (0 to 75)	
	01-10			(remaies)	17	0 (20 += 72)	
	Mob2	LOD = 2.6		(Females)	6	o (38 to 72) 0 (0 to 10)	

					Animal		
Cross	QTL	Scores	Variance (%)	Phenotypes	chromosome	QTL peak	Reference
C57BL/6J \times 129S6/	D3Mit127	LOD = 2.7	78		3	70.3	(623)
SvEvTac	D10Mit162	LOD = 2.9	28		10	59	
	D12Mit231	LOD = 3.2	25		12	48	
	D14Mit192	LOD = 3	52		14	40	
C57BL/6J \times A/J	Bw8q1	LOD = 4.4	2	BW, 8 weeks	1	100 (77 to 102)	(624)
	Bw8q2	LOD = 3.3	4	BW, 8 weeks	4	66	
$C57BL/6J \times B6.A^{Chr16}$	Diobq	LOD = 4.3		Chromosome substitution strain	16	53.8 (29 to 55.2)	(625)
$C57BL/6J \times CAST/$	Mob5	LOD = 5.8		Subcutaneous fat	2	95.5 (75 to 109)	(626,627)
Ei	Mob6	LOD = 7.3		Subcutaneous fat. QTL confirmed in B6.CAST (73 to 83 cM) congenic mice	2	49.6 (35 to 85)	
	Mob7	LOD = 5.8		Retroperitoneal and subcutaneous fat	2	Peak at D2Mit9 37 (30 to 46)	
	Mob8	LOD = 4.7		Body fat (%)	9	D9Mit8	
	Not assigned	LOD = 5.2		Leptin level (no obesity)	4	Dynamo	
	Rdln?	LOD = 4.3		Body length	15	15	
C57BL/6L × CAST/	Mnif1	LOD = 8	71	Fat intake	8	22 (10 to 30)	(628)
Fil	Mnif?	LOD = 6	5.4	Fat intake	18	24 (10 to 50)	(020)
LIJ	Mnif3	LOD = 0 LOD = 4	3.4	Fat intake	x	18 (10 to 58)	
	Mnic1	LOD = 4	5.0	Carbohydrate intake	17	10(10 to 30) 10(3 to 24)	
	Minic?	LOD = 0.7 LOD = 2.4	2 1	Carbohydrate intake	6	10(3 to 24) 16(26 to 64)	
	Mnic2	LOD = 3.4	3.1	Carbohydrate intake	v	40(301004)	
	Winics Koall	LOD = 4.1	5.7	Kilosoloria intola	A 19	40(14 to 01) 20(10 to 26)	
	Kcall Kcall	LOD = 7.7	0.8	Kilocalorie intale	10	20(10 to 20)	
	Kcal2	LOD = 4.9	4.4		1/	10(8(0.57))	((20, (20)
$C_{2}/BL/O_{1} \times DBA/$	Not assigned	LOD = 3.3	3	o-week weight	1	76 (46 to 84)	(029,030)
2J	Not assigned	LOD = 3.3	4	6-week weight	4	26 (24 to 30)	
	Not assigned	LOD = 3.2	4	6-Week weight	5	60 (57 to 64)	
	Not assigned	LOD = 4.3	5	6-Week weight	5	35 (22 to 45)	
	Not assigned	LOD = 4	4	6-Week weight	6	22 (15 to 26)	
	Not assigned	LOD = 3.3	4	6-Week weight	4	26 (24 to 30)	
	Not assigned	LOD = 6.9	9	6-Week weight	7	25 (23 to 33)	
	Not assigned	LOD = 4.4	5	6-Week weight	9	32 (12 to 50)	
	Not assigned	LOD = 5.7	6	6-Week weight	11	45 (29 to 49)	
	Not assigned	LOD = 4.1	4	6-Week weight	13	59 (29 telomere)	
	Not assigned	LOD = 3	3	6-Week weight	14	0 (0 to 22)	
	Not assigned	LOD = 4.9	7	6-week weight	17	14 (11 to 18)	
	Pfat1	LOD = 5	20	Predicted fat (%)	4	30	
	Pfat2	LOD = 4.9	20	Predicted fat (%)	6	31.8	
	Pfat3	LOD = 5.3	20	Predicted fat (%)	13	20	
	Pfat4	LOD = 8.6	20	Predicted fat (%)	15	43.3	
$C57BL/6J \times KK-A^{y}$	Bwq1	LOD = 5.5	15	BW at 50 days of age	4	21.9 (6.3 to 32)	(631,632)
	Bwq2	LOD = 8.8	26	BW from 40 to 100 days of age; modifier of A ^y	6	35.2 (29 to 47)	
$C57BL/6J \times KK/$	Obq5	LOD = 7	17	Adiposity (females)	9	19	(633)
H1Lt	Obq6	LOD = 5	15.7	Adiposity (males); except mesenteric	Х	16	
	Unassigned	LOD = 4.4 (6.9)		-	7		
	Unassigned	LOD = 5.9			9		
	Unassigned	LOD = 4.2			7		
C57BL/6J \times NZB/	Bwefm	LOD = 5.11			5	70	(634)
B1NJ	Bwem1	LOD = 3.16			5	54	
	Bwem2	LOD = 4.53			13	35	
C57BL/6J-Socs2hg/hg	Carfhg1	LOD = 2.5	6.2	Fat content	5	38	(635)
\times CAST/Ei	Carfhg2	LOD = 5.8	12.5	Fat content	9		
	wg1			2 to 9 weeks	2	31	

Cross	QTL	Scores	Variance (%)	Phenotypes	Animal chromosome	QTL peak	Reference
	wg2		10.4	2 to 9 weeks	2	61	
	wg3			2 to 9 weeks	8	45	
	wg4			2 to 9 weeks	11	46	
C57BL/6J-Socs2hg/hg	Mohgl	p = 0.004		,	2	46 to 50.3	(636)
× CAST/Ei	Mohg2	p = 0.021			x	3	(000)
	Mohg 3	p = 0.041			X	37	
C57BLKS/J-Cpe ^{fat}	Final	LOD = 6.84	13	Adiposity index	11	40 (30 to 50)	(637)
\times HRS ^{hr/+}	Bwt1	LOD = 14.03	24	Interaction with locus on chromosome 18 (47 cM)	14	22.5 (20 to 35)	()
CAST/Ei × C57BL/	Dob4	LOD = 3.1 to 4.3	14	Fat, mesenteric	4	18.35	(638)
CFLP (P6) \times JU/	Bw19	LOD = 24.4	17 to 20	10-Week weight	Х	24.64	(639)
$Du6 \times DuK$	Imebt2			BW	14	25 (19 to 32)	(640)
DU6i \times DBA/2J	Bw4	F = 9.52	4.9		11	55 (36 to 65)	(641,642)
	Bw5	F = 10.44	5.4	BW	1	36 (11 to 97)	(-)-)
	Bw7	F = 5.34	2.8		4	59 (34 to 72)	
	Bw9	F = 3.87	2.1		12	17 (0 to 50)	
	Bw10	F = 6.39	3.4		13	47 (33 to 61)	
	Bw13	F = 11.7	6	BW	5	81 (73 to 89)	
	Bw13 Bw14	F = 25.9	12.3	BW	7	28 (23 to 33)	
	Bw17 Bw15	F = 7.36	3.8	BW	13	10(3 to 16)	
	Bw15 Bw16	F = 7.52	3.0	BW	11	10(5 to 10) 14(6 to 17)	
	Afnal	F = 6.17	3.2	Dii	3	29(23 to 37)	
	Afna?	F = 5.72	3		4	66 (60 to 72)	
	Afna4	F = 4.25	23		13	13 (0 to 46)	
	Afna5	F = 5.86	3.1		11	9 (0 to 19)	
	Afna6	F = 8.92	4.6	Abdominal fat (%)	17	36(27 to 51)	
	Afna9	F = 18.5	9.1	Abdominal fat (%)	7	22 (13 to 27)	
	Afpa10	F = 7.48	3.9	Abdominal fat (%)	12	18 (10 to 26)	
	Afw1	F = 4.23	2.3	Abdollillar lat (70)	3	30(23 to 36)	
	Afw?	F = 5.72	3		4	66 (60 to 72)	
	Afw3	F = 5.67	3		5	80 (69 to 91)	
	Afw5	F = 6.48	3 /		11	12 (2 to 19)	
	Afw6	F = 6.03	3.7		13	12 (2 to 19) 11 (4 to 18)	
	A6w7	F = 0.05 F = 0	3.2 4 7		17	30(30 to 52)	
	Ajw7 Afw0	F = 9 E = 24.0	12	Abdominal fat (%)	7	33 (30 to 32)	
	Ajw9 Afw10	F = 24.9 F = 8.56	12	Abdominal fat $(\%)$	12	23 (10 to 23) 21 (15 to 27)	
	Afw10 Afw11	F = 0.50 F = 4.78	7.5	Abdollillar fat (70)	V	17 (0 to 30)	
	Lapal	F = 4.78 E = 7.58	2.5	Lentin	14	17 (0 (0 39)) 28 (21 to 41)	
	Abfp1	1 - 7.56	т. т	Interacts with Abfp2 and Abfp3	17	34	
	Abfp2			Interacts with Abfp1	11	58	
	Abfp3			Interacts with Abfp1	8	16	
	Abfn4			Interacts with Abfp5	3	26	
	Abfn5			Interacts with Abfp4	5	20	
	Abfw1			Interacts with Abfw2, Abfw3, Abfw4	11	60	
	Abfw2			Interacts with Abfw1	4	64	
	Abfw3			Interacts with Abfw1	17	32	
	Abfw4			Interacts with Abfw1	19	43	
	Abfw5			Interacts with Afbw6	5	72	
	Abfw6			Interacts with Afbw5	12	6	
	Bodw1			Interacts with Bodw2	2	18	
	Bodw2			Interacts with Bodw1	11	55	
	Bodw3			Interacts with Bodw4	1	5	
	Bodw4			Interacts with Bodw3	9	34	
DuK imes Du6	Afw1	F = 4.52	4	Abdominal fat weight	3	51	(643)

Cross	QTL	Scores	Variance (%)	Phenotypes	Animal chromosome	QTL peak	Reference
	Bw4	F = 4.79	23.1	BW	11	42 (36 to 50)	
	Afw2	F = 4.89	13.4	Abdominal fat	4	51 (34 to 63)	
	Afpq2	F = 4.89	10.2	Abdominal fat	4	55 (31 to 79)	
	Afw5	F = 4.79	8.3	Abdominal fat	11	6 (0 to 29)	
	Åfpq4	F = 4.7	5.3	Abdominal fat	13	0	
	Afpa1	F = 4.52	8.3	Abdominal fat (%)	3	46 (24 to 76)	
	Afpq3	F = 4.13	4.7		5	51	
	Afw3	F = 4.13	3.9		5	61	
	Afw4	F = 5.13	4.1		9	29	
	Afw6	F = 4.7	7.7		13	0 (0 to 10)	
	Afw7	F = 4.21	2.9		17	46	
	Afw8	F = 3.68	18.1		19	26	
	Bw.5	F = 4.61	7.1		1	14	
	Bw6	F = 5.02	5.1		2	56	
	Bw7	F = 4.89	7		4	55	
	Bw8	F = 4.13	3		5	42	
	Bw0 Bw9	F = 3.8	43		12	49	
	Bw^{j} Bw10	F = 4.7	10.1		12	34	
	Bw10 Bw11	F = 4.72	4.2		15	6	
	Bw11 Bw12	F = 3.72 F = 3.73	4.2		15 V	42	
Ε×Ι	Eobl	I = 3.73	4.9	14-week fat (%)	2	42	(644)
$\Gamma \land L$	Fob?	LOD > 3.3 LOD = 3.3	4.9	14-week fat $(\%)$ (in	12	10	(044)
	F002	LOD = 3.3	19.5	females)	12	19	
	Fob3	LOD = 11.3	14.4	14-week fat (%)	15	34	
	Fob4	LOD = 3.3	7.3	14-week fat (%)	Х	37	
$F \times L$	Fob3	LOD = 11.3	14.4		15	(12 to 78)	(645,646)
	Fob3a			Subcongenics of Fob3	15	27 (22 to 32)	
	Fob3b			Subcongenics of Fob3; positional and expression candidate is Sqle (squalene epoxidase)	15	68 (44 to 72)	
F.L. congenic	Fob3a	F = 13.7	1.6	Fat (%); late-onset	15		(645)
6	Fob3b	F = 11.6	0.7	Fat (%): early onset	15		()
$ICR \times M16$	Mfia5	LOD = 3.4	1.8		1	57 (34 to 103)	(647)
ion · · inio	Mfe5a1	LOD = 3.7	2.3		8	54 (1 to 81)	(017)
	Mfia3	LOD = 3.7	2		9	7 (7 to 60)	
	Mfi5a1	LOD = 4.4	23		9	60 (7 to 60)	
	Mfi7a1	LOD = 53	2.5		11	29 (15 to 74)	
	Mfi8a1	LOD = 4.8	2.1		11	32 (22 to 86)	
	Mfial	I OD = 8.1	47		11	32 (22 to 68) 34 (22 to 68)	
	Mfe5a2	LOD = 3.6	2.2		11	40 (18 to 73)	
	Mfeal	LOD = 4.9	3		11	50 (18 to 73)	
	Mfia4	LOD = 3.7	2		12	35 (17 to 63)	
	Mfiq7	LOD = 3.7 LOD = 4.4	$\frac{2}{24}$		12	53 (17 to 03) 54 (26 to 54)	
	Mlenal	LOD = 7.7	5.7		2	93 (83 to 104)	
	Mlepq1	LOD = 7.7	23		17	53 (05 to 104)	
	Not assigned	LOD = 3.4 LOD = 16.8	2.5		2	$\frac{32}{84}$ (82 to 92)	
	Not assigned	LOD = 10.0 LOD = 4	1 2		8	$\frac{04}{22} (1 \text{ to } 82)$	
	Not assigned	LOD = 4	1.2		11	51(36 to 65)	
	Not assigned	LOD = 3.2 LOD = 4.3	1.0		11	51 (30 to 03) 52 (22 to 58)	
	Not assigned	LOD = 4.3 LOD = 12.1	۲ ۸ ۹		17	32 (22 10 30) 83 (80 to 80)	
	Not assigned	LOD = 12.1	4.0		∠ 	41 (2 to 62)	
	Not assigned	LOD = 4.0 LOD = 2.6	1.8		4	41 (2 10 02) 58 (41 to 75)	
	Not assigned	LOD = 5.0	1.5		11	30(4110/3)	
	Not assigned	LOD = 5.1	2		1/	38(18105/)	
	Not assigned	LOD = 14.2	6.5		2	85 (83 to 93)	
	Not assigned	LOD = 5.1	1.9		7	28 (8 to 51)	
	Not assigned	LOD = 6	2.6		11	58 (32 to 64)	
	Not assigned	LOD = 3.3	1.9		17	51 (14 to 63)	

$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	Cross	QTL	Scores	Variance (%)	Phenotypes	Animal chromosome	QTL peak	Reference
	ILS inbred, long	Weht1	LOD = 4.6		Interacts with Wght2	1	78	(648)
	sleep) \times ISS	Wght2	LOD = 4.5		Interacts with Wght1	4	3.2	
sheep) Wight M LOD = 3.2 (D) = 3.2 (D) = 3.2 (D) = 3.4 (D)	(inbred short	Weht3	LOD = 8.6		interacts what wight	4	52.6	
Image Projects 10 -75 Wights LOD = 0.4 19 20 KKTAY HALRE Tright LOD = 2.1 Trighteride and BW 4 59 (690,650) × KKTAYF1 D770/1 LOD = 2.3 BW candidate gave 5 78 (630,651) LGU Adapr LOD = 2.4 Adaposity (males) 1 10 (630,651) Wa2 LOD = 3.71 Late weight gain 6 6 7 (640,651) Wa2 LOD = 3.71 Late weight gain 6 6 7 (630,651) Wa2 LOD = 3.71 Cane weight gain 6 6 7 (640,751) 7 46.4 7 7 46.4 7 7 46.4 7 7 46.4 7 7 46.4 7 7 46.4 7 7 46.4 7 7 46.4 7 7 46.4 7 7 46.4 7 4.4 2.5 7	(litered short	Waht4	LOD = 3.22			5	73	
whote 100 $= 0.4$ $= 1.6$ KKT1 w (BLUb) 7[1/1] LOD $= 2.1$ Fighyceide and BW 4 59 (649.650) KKT1 w (BLUb) 2.1 LOD $= 2.3$ BW $= 1.7$ $= 4.6$ LG0 × SM01 Adip1 LOD $= 2.3$ BW $= 1.7$ $= 6.6$ LG0 × SM01 Adip2 LOD $= 3.3$ Law weigh gain 6 $= 6.7$ Wal LOD $= 3.3$ Law weigh gain 6 $= 6.7$ $= 5.8$ Wal LOD $= 3.31$ Law weigh gain 6 $= 6.7$ $= 5.8$ Adip3 LOD $= 3.31$ Adiposity $= 9$ $= 2.4$ $= 46.3$ $= 6.67$ Adip4 LOD $= 2.57$ Adiposity $= 8$ $= 3.2$ $= 8.67$ $= 6.67$ Adip5 LOD<= 2.44	sicep)	Waht5	LOD = 3.22 LOD = 7.6			11	75	
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$		W ghi J Walaté	LOD = 7.0			10	75	
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$		w ghto	LOD = 9.4			19	20	((10 (50)
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	$KK/Ia \times (BALB/c$	IglsI	LOD = 2.1		Triglyceride and BW	4	59	(649,650)
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	\times KK/Ta)F1	D17Mit218	LOD = 2.9		BW	17	42	
		Azgp1	LOD = 2.3		BW candidate gene	5	78	
	$LG/J \times SM/J$	Adip1	LOD = 2.4		Adiposity (males)	1	11	(620,651– 654)
		Wta1	LOD = 2.35		Late weight gain	4	6.5	
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$		Wta2	LOD = 3.49		Late weight gain	6	67	
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $		Adip2	LOD = 3.71		Adiposity/weight	6	46.3	
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $		Adip3	LOD = 3.71		Adiposity (males)/weight	7	46.4	
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$		A din A	IOD = 2.57		(inales)/weight	8	37	
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$		Adip4	LOD = 2.37		Adiposity	0	32	
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$		Adips	LOD = 1.84		Adiposity	9	42	
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$		Adip6	LOD = 2.69		Adiposity (males)	12	45	
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$		Adip7	LOD = 1.9		Adiposity (males)	13	1 (0 to 30)	
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $		Wta3	LOD = 2.7		Weight	14	2.5	
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$		Wta4	LOD = 2.44			17	17.4	
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$		Adip8	LOD = 2.84		Adiposity	18	20 (8 to 38)	
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	$LG/J \times SM/J$	Not assigned				7		(654)
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $		Not assigned	LOD = 3.7			7	66 (65.6 to 69)	
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$		Not assigned	LOD = 4.07			17	22.8 (17.7 to 24.2)	
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$		Not assigned	LOD = 3.68		Also epididymal, retroperitoneal, and mesenteric	1	62 (56.6 to 65)	
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$		Not assigned	LOD = 3.21	r	Also retroperitoneal, mesenteric, and leptin	8	59 (32 to 59)	
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$		Not assigned	LOD = 3.58	r	Also Retroperitoneal & mesenteric	10	63 (59 to 70)	
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$		Not assigned	LOD = 3.5		Also mesenteric and leptin	Х	69	
M16i (rapid 3- to 6-week weightScfq1LOD = 7.65.9Fat, subcutaneous1110.10 H of 1010.10 H of 106-week weightScfq2LOD = 4.45Fat, subcutaneous1525.2 (8.8 to 39.6)gain) × L6 (lowScfq3LOD = 4.13.8Fat, subcutaneous1124.9 (9.9 to 47.5)6-week weightScfq4LOD = 4.13.4Fat, subcutaneous1721.9 (0 to 34)Scfpq1LOD = 3.912Fat, subcutaneous1033.1 (20.5 to 55.3)adjusted for 10-week weightadjusted for 10-week weight1420.3 (0 to 34.5)Epfpq1LOD = 65.31420.3 (0 to 34.5)Epfpq2LOD = 3.81266.8 (52.2 to 72.7)Epfpq3LOD = 3.43.41553.4 (21.2 to 46.3)Epfq4LOD = 9.56.7284 (79.8 to 87.6)Epfq2LOD = 4.64.3297.6 (95.5 toID2.4)Epfq4LOD = 3.42.67Epfq4LOD = 3.52.51117.4 (0 to 34.9)Epfq5LOD = 3.42.6721.5 (0 to 35.9)W10q11LOD = 299.4279.6 (76.8 to 81.7)W10q10LOD = 8.34.8455.3 (41.1 to 61.8)W10q12LOD = 6.92.11719.2W10q13LOD = 5.77953.9 (44.5 to 61.4)		Not assigned	LOD = 4.99		Ĩ	11	10.9 (1.1 to 17)	
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	M16i (rapid 3- to	Scfal	LOD = 7.6	5.9	Fat subcutaneous	2	84 (81 7 to 88 9)	(655-658)
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	6 week weight	Scfq1 Scfq2	LOD = 4.0	5	Fat, subcutaneous	15	25.2(8.8 to 30.6)	(055-058)
gain× Lo (low $Sc/q3$ LOD = 4.13.8Fat, subcutaneous11 24.9 (9.8 G 4.3)6-week weight $Scfq4$ LOD = 4.13.4Fat, subcutaneous17 21.9 (0 to 34) $Scfpq1$ LOD = 3.912Fat, subcutaneous,10 33.1 (20.5 to 55.3)adjusted for 10-weekweight $Epfpq2$ LOD = 3.81266.8 (52.2 to 72.7) $Epfpq3$ LOD = 3.63.31551.1 (46.3-ter) $Epfpq4$ LOD = 9.56.7284 (79.8 to 87.6) $Epfq2$ LOD = 4.64.3297.6 (95.5 to $Epfq4$ LOD = 3.831721.9 (0 to 33.2) $Epfq4$ LOD = 3.52.51117.4 (0 to 34.9) $Epfq5$ LOD = 3.43.4297.6 (95.5 to 102.4) 102.4 101010 $Epfq4$ LOD = 3.831721.9 (0 to 33.2) $Epfq5$ LOD = 3.42.6721.5 (0 to 35.9) $W10q1$ LOD = 299.4279.6 (76.8 to 81.7) $W10q10$ LOD = 8.34.8455.3 (41.1 to 61.8) $W10q11$ LOD = 7.98628.5 (20 to 47.2) $W10q13$ LOD = 5.77953.9 (44.5 to 61.4)	$(1) \times 16$	Scjq2 Sofa3	LOD = 4.4	2 9	Fat, subcutaneous	15	23.2 (0.0 to 39.0)	
6-week weight) $Scfq4$ LOD = 4.1 3.4 Fat, subcutaneous, adjusted for 10-week weight 17 $21.9 (0 \text{ to } 34)$ $Scfpq1$ LOD = 3.912Fat, subcutaneous, adjusted for 10-week weight10 $33.1 (20.5 \text{ to } 55.3)$ $Epfpq1$ LOD = 6 5.3 14 $20.3 (0 \text{ to } 34.5)$ $Epfpq2$ LOD = 3.812 $66.8 (52.2 \text{ to } 72.7)$ $Epfpq3$ LOD = 3.6 3.3 15 $51.1 (46.3 \text{-ter})$ $Epfpq4$ LOD = 3.4 3.4 15 $33.4 (21.2 \text{ to } 46.3)$ $Epfq1$ LOD = 9.5 6.7 2 $84 (79.8 \text{ to } 87.6)$ $Epfq2$ LOD = 4.6 4.3 2 $97.6 (95.5 \text{ to } 102.4)$ $Epfq4$ LOD = 3.8317 $21.9 (0 \text{ to } 33.2)$ $Epfq4$ LOD = 3.4 2.5 11 $17.4 (0 \text{ to } 34.9)$ $Epfq4$ LOD = 3.4 2.6 7 $21.5 (0 \text{ to } 35.9)$ $W10q1$ LOD = 2.9 9.4 2 $79.6 (76.8 \text{ to } 81.7)$ $W10q10$ LOD = 7.9 8 6 $28.5 (20 \text{ to } 47.2)$ $W10q12$ LOD = 6.9 2.1 17 19.2 $W10q13$ LOD = 5.77 9 $53.9 (44.5 \text{ to } 61.4)$	g_{alll} \wedge L0 (low	SCJQS Sefe	LOD = 4.1	J.0 2.4	Fat, subcutaneous	11	24.9(9.91047.3)	
Scjpq1LOD = 3.9 12Fat, subcutateous, adjusted for 10-week weightEpfpq1LOD = 6 5.3 14 $20.3 (0 \text{ to } 34.5)$ Epfpq2LOD = 3.8 12 $66.8 (52.2 \text{ to } 72.7)$ Epfpq3LOD = 3.6 3.3 15 $51.1 (46.3 \text{-ter})$ Epfpq4LOD = 3.4 3.4 15 $33.4 (21.2 \text{ to } 46.3)$ Epfq2LOD = 4.6 4.3 2 $97.6 (95.5 \text{ to } 102.4)$ Epfq3LOD = 3.8 317 $21.9 (0 \text{ to } 33.2)$ Epfq4LOD = 3.5 2.5 11 $17.4 (0 \text{ to } 34.9)$ Epfq5LOD = 3.4 2.6 7 $21.9 (0 \text{ to } 35.9)$ Wl0q11LOD = 29 9.4 2 $79.6 (76.8 \text{ to } 81.7)$ Wl0q11LOD = 7.9 8 6 $28.5 (20 \text{ to } 72.2)$ Wl0q12LOD = 6.9 2.1 17 19.2 Wl0q13LOD = 5.7 7 9 $53.9 (44.5 \text{ to } 61.4)$	o-week weight)	ScJq4	LOD = 4.1	3.4	Fat, subcutaneous	17	21.9(0.054)	
Epfpq1 $LOD = 6$ 5.31420.3 (0 to 34.5) $Epfpq2$ $LOD = 3.8$ 1266.8 (52.2 to 72.7) $Epfpq3$ $LOD = 3.6$ 3.315 51.1 (46.3-ter) $Epfpq4$ $LOD = 3.4$ 3.415 33.4 (21.2 to 46.3) $Epfq1$ $LOD = 9.5$ 6.7284 (79.8 to 87.6) $Epfq2$ $LOD = 4.6$ 4.3297.6 (95.5 to $Epfq3$ $LOD = 3.8$ 31721.9 (0 to 33.2) $Epfq4$ $LOD = 3.5$ 2.51117.4 (0 to 34.9) $Epfq5$ $LOD = 3.4$ 2.6721.5 (0 to 35.9) $W10q1$ $LOD = 29$ 9.4279.6 (76.8 to 81.7) $W10q10$ $LOD = 8.3$ 4.8455.3 (41.1 to 61.8) $W10q11$ $LOD = 7.9$ 8628.5 (20 to 47.2) $W10q12$ $LOD = 6.9$ 2.11719.2 $W10q13$ $LOD = 5.7$ 7953.9 (44.5 to 61.4)		SCJPq1	LOD = 3.9	12	adjusted for 10-week weight	10	55.1 (20.5 10 55.5)	
Epfpq2LOD = 3.81266.8 (52.2 to 72.7) $Epfpq3$ LOD = 3.63.31551.1 (46.3-ter) $Epfpq4$ LOD = 3.43.41533.4 (21.2 to 46.3) $Epfq1$ LOD = 9.56.7284 (79.8 to 87.6) $Epfq2$ LOD = 4.64.3297.6 (95.5 to 102.4) $Epfq3$ LOD = 3.52.51117.4 (0 to 33.2) $Epfq4$ LOD = 3.42.6721.5 (0 to 35.9) $W10q1$ LOD = 299.4279.6 (76.8 to 81.7) $W10q10$ LOD = 7.98628.5 (20 to 47.2) $W10q12$ LOD = 6.92.11719.2 $W10q13$ LOD = 5.77953.9 (44.5 to 61.4)		Epfpa]	LOD = 6	5.3		14	20.3 (0 to 34.5)	
Lpfpq2LOD3.61Lod50.61.1 $Epfpq3$ LOD 3.6 3.3 15 51.1 (46.3-ter) $Epfpq4$ LOD 3.4 3.4 15 33.4 (21.2 to 46.3) $Epfq1$ LOD 9.5 6.7 2 84 (79.8 to 87.6) $Epfq2$ LOD $= 4.6$ 4.3 2 97.6 (95.5 to $Epfq3$ LOD $= 3.8$ 317 21.9 (0 to 33.2) $Epfq4$ LOD $= 3.5$ 2.5 11 17.4 (0 to 34.9) $Epfq5$ LOD $= 3.4$ 2.6 7 21.5 (0 to 35.9) $W10q1$ LOD 29 9.4 2 79.6 (76.8 to 81.7) $W10q10$ LOD $= 8.3$ 4.8 4 55.3 (41.1 to 61.8) $W10q11$ LOD $= 7.9$ 8 6 28.5 (20 to 47.2) $W10q12$ LOD $= 6.9$ 2.1 17 19.2 $W10q13$ LOD $= 5.7$ 7 9 53.9 (44.5 to 61.4)		Enfna?	LOD = 3.8	1		2	66 8 (52 2 to 72 7)	
Epfpq3 $LOD = 3.0$ 3.3 15 $31.1 (40.5401)$ $Epfpq4$ $LOD = 3.4$ 3.4 15 $33.4 (21.2 to 46.3)$ $Epfq1$ $LOD = 9.5$ 6.7 2 $84 (79.8 to 87.6)$ $Epfq2$ $LOD = 4.6$ 4.3 2 $97.6 (95.5 to 102.4)$ $Epfq3$ $LOD = 3.8$ 3 17 $21.9 (0 to 33.2)$ $Epfq4$ $LOD = 3.5$ 2.5 11 $17.4 (0 to 34.9)$ $Epfq5$ $LOD = 3.4$ 2.6 7 $21.5 (0 to 35.9)$ $W10q1$ $LOD = 29$ 9.4 2 $79.6 (76.8 to 81.7)$ $W10q10$ $LOD = 7.9$ 8 6 $28.5 (20 to 47.2)$ $W10q11$ $LOD = 7.9$ 8 6 $28.5 (20 to 47.2)$ $W10q12$ $LOD = 6.9$ 2.1 17 19.2 $W10q13$ $LOD = 5.7$ 7 9 $53.9 (44.5 to 61.4)$		Epjpq2 Epfpq3	10D - 36	3 3		15	51.1 (46.3 ter)	
Epfpq4 $LOD = 3.4$ 3.4 13 33.4 (21.2 to 40.3) $Epfq1$ $LOD = 9.5$ 6.7 2 84 (79.8 to 87.6) $Epfq2$ $LOD = 4.6$ 4.3 2 97.6 (95.5 to $Epfq3$ $LOD = 3.8$ 3 17 21.9 (0 to 33.2) $Epfq4$ $LOD = 3.5$ 2.5 11 17.4 (0 to 34.9) $Epfq5$ $LOD = 3.4$ 2.6 7 21.5 (0 to 35.9) $W10q1$ $LOD = 29$ 9.4 2 79.6 (76.8 to 81.7) $W10q10$ $LOD = 7.9$ 8 6 28.5 (20 to 47.2) $W10q11$ $LOD = 7.9$ 8 6 28.5 (20 to 47.2) $W10q12$ $LOD = 6.9$ 2.1 17 19.2 $W10q13$ $LOD = 5.7$ 7 9 53.9 (44.5 to 61.4)		Epjpq5 Enfna4	LOD = 3.0	2.4		15	31.1 (40.3 - 101)	
Epfq1 $LOD = 9.5$ 6.7 2 $84 (79.8 to 87.5)$ $Epfq2$ $LOD = 4.6$ 4.3 2 $97.6 (95.5 to 102.4)$ $Epfq3$ $LOD = 3.8$ 3 17 $21.9 (0 to 33.2)$ $Epfq4$ $LOD = 3.5$ 2.5 11 $17.4 (0 to 34.9)$ $Epfq5$ $LOD = 3.4$ 2.6 7 $21.5 (0 to 35.9)$ $W10q1$ $LOD = 29$ 9.4 2 $79.6 (76.8 to 81.7)$ $W10q10$ $LOD = 8.3$ 4.8 4 $55.3 (41.1 to 61.8)$ $W10q11$ $LOD = 7.9$ 8 6 $28.5 (20 to 47.2)$ $W10q12$ $LOD = 6.9$ 2.1 17 19.2 $W10q13$ $LOD = 5.7$ 7 9 $53.9 (44.5 to 61.4)$		Epjpq4 Evfv1	LOD = 0.4	5.4		15	33.4 (21.2 to 40.3)	
Epjq2LOD = 4.64.3297.6 (95.5 to 102.4)Epfq3LOD = 3.831721.9 (0 to 33.2)Epfq4LOD = 3.52.51117.4 (0 to 34.9)Epfq5LOD = 3.42.6721.5 (0 to 35.9)W10q1LOD = 299.4279.6 (76.8 to 81.7)W10q10LOD = 8.34.8455.3 (41.1 to 61.8)W10q11LOD = 7.98628.5 (20 to 47.2)W10q12LOD = 6.92.11719.2W10q13LOD = 5.77953.9 (44.5 to 61.4)			LOD = 9.3	0.7		2	84 (79.8 to 87.0)	
Epfq3LOD = 3.831721.9 (0 to 33.2) $Epfq4$ LOD = 3.52.51117.4 (0 to 34.9) $Epfq5$ LOD = 3.42.6721.5 (0 to 35.9) $W10q1$ LOD = 299.4279.6 (76.8 to 81.7) $W10q10$ LOD = 8.34.8455.3 (41.1 to 61.8) $W10q11$ LOD = 7.98628.5 (20 to 47.2) $W10q12$ LOD = 6.92.11719.2 $W10q13$ LOD = 5.77953.9 (44.5 to 61.4)		Epfq2	LOD = 4.6	4.3		2	97.6 (95.5 to 102.4)	
Epfq4LOD = 3.52.51117.4 (0 to 34.9) $Epfq5$ LOD = 3.42.6721.5 (0 to 35.9) $W10q1$ LOD = 299.4279.6 (76.8 to 81.7) $W10q10$ LOD = 8.34.8455.3 (41.1 to 61.8) $W10q11$ LOD = 7.98628.5 (20 to 47.2) $W10q12$ LOD = 6.92.11719.2 $W10q13$ LOD = 5.77953.9 (44.5 to 61.4)		Epfq3	LOD = 3.8	3		17	21.9 (0 to 33.2)	
Epfq5LOD = 3.42.6721.5 (0 to 35.9) $W10q1$ LOD = 299.4279.6 (76.8 to 81.7) $W10q10$ LOD = 8.34.8455.3 (41.1 to 61.8) $W10q11$ LOD = 7.98628.5 (20 to 47.2) $W10q12$ LOD = 6.92.11719.2 $W10q13$ LOD = 5.77953.9 (44.5 to 61.4)		Epfq4	LOD = 3.5	2.5		11	17.4 (0 to 34.9)	
W10q1LOD = 299.4279.6 (76.8 to 81.7) $W10q10$ LOD = 8.34.8455.3 (41.1 to 61.8) $W10q11$ LOD = 7.98628.5 (20 to 47.2) $W10q12$ LOD = 6.92.11719.2 $W10q13$ LOD = 5.77953.9 (44.5 to 61.4)		Epfq5	LOD = 3.4	2.6		7	21.5 (0 to 35.9)	
W10q10LOD = 8.34.8455.3 (41.1 to 61.8) $W10q11$ LOD = 7.98628.5 (20 to 47.2) $W10q12$ LOD = 6.92.11719.2 $W10q13$ LOD = 5.77953.9 (44.5 to 61.4)		W10q1	LOD = 29	9.4		2	79.6 (76.8 to 81.7)	
W10q11 $LOD = 7.9$ 86 $28.5 (20 to 47.2)$ $W10q12$ $LOD = 6.9$ 2.1 17 19.2 $W10q13$ $LOD = 5.7$ 7 9 $53.9 (44.5 to 61.4)$		W10q10	LOD = 8.3	4.8		4	55.3 (41.1 to 61.8)	
W10q12 $LOD = 6.9$ 2.1 17 19.2 $W10q13$ $LOD = 5.7$ 7 9 53.9 (44.5 to 61.4)		W10a11	LOD = 7.9	8		6	28.5 (20 to 47.2)	
W10q12LOD 0.7 2.1 17 17.2 W10q13LOD = 5.77953.9 (44.5 to 61.4)		W10a12	LOD = 6.9	2.1		17	19.2	
		W10q13	LOD = 5.7	7		9	53.9 (44.5 to 61.4)	

Cross	QTL	Scores	Variance (%)	Phenotypes	Animal chromosome	QTL peak	Reference
	W10q14	LOD = 5.2			8	26.4 (19.2 to 41.4)	
	W10q15	LOD = 4.8	3.1		17	30.9 (24.5 to 41.1)	
	W10q16		2.8		5	42.8 (29.4 to 61.8)	
	W10q17	LOD = 4.2	1		13	55.4	
	W10w18	LOD = 4.1	1.9		7	18.2	
	W10a2	LOD = 26.4	8.1		11	17.7 (11.3 to 24.1)	
	W10a3	LOD = 15.5	7		3	29.7 (23.7 to 40.5)	
	W10q3	LOD = 14.9	95		3	47.7 (40.5 to 54)	
	W10q4	LOD = 10.2	5.3		10	31.7 (24.8 to 42.6)	
	W10q5	LOD = 10.2 LOD = 0.7	3.0		1	56.3 (48.7 to 66.5)	
	W10q0	LOD = 9.7 LOD = 0.1	3.9		1	72.6 (66.5 to 70)	
	W10q7	LOD = 9.1 LOD = 10.2	5 2		1	72.0 (00.3 to 79) 21.7 (24.8 to 42.6)	
	W10q0	LOD = 10.2	3.5		10	51.7 (24.6 to 42.0)	
MIL V OSZDI //I	w10q9	LOD = 8.6	8.0	TT (1 C' 1'	2	50.8 (42.4 to 65.5)	((50)
$MH \times C5/BL/0J$	HIQI	LOD = 5.0	4./	$(MH \times ML)F2$ cross	1	127	(039)
	Hlq2	LOD = 3.7	3.1	Heat loss	2	71	
	Hlq3	LOD = 3.8	3.1	Heat loss	3	35	
	Hlq4	LOD = 4.7	3.9	Heat loss	3	3.9	
	Hlq5	LOD = 4.1	3.4	Heat loss	7	61	
	Fatq1	LOD = 7.4 to 8.0	5.4 to 5.9	Gonadal fat	1	62	
	Bata1	LOD = 3.96	3.3	Brown fat	1	102	
	Bata?	LOD = 3.46	2.8	Brown fat	3	55	
	Wt10a1	LOD = 4.25	3 3	Brown fut	1	25	
	Wt10a2	LOD = 4.25	3.8		3	61	
	Wt10q2	LOD = 4.70 LOD = 3.63	2.0		11	32	
	Wt2al	LOD = 5.03	2.9		11	32 72	
	W13Q1	LOD = 3.13	4.1		1	109	
	W15Q2	LOD = 10.09	0		1	108	
	WISQS	LOD = 0.28	22	Confirmed in (MUL)	1/	14	
	W <i>t</i> 0 <i>q1</i>	LOD = 4.02	3.3	ML)F2 cross	1	27	
	Wt6q2	LOD = 3.98	3.2		1	108	
	Wt6q3	LOD = 4.55	3.7		11	36	
Mhi (inbred, high	Not assigned	F = 10.47	4.9		5	73 (66-telomere)	(660)
food intake) \times	Not assigned	F = 10.48	4.7		7	49 (35 to 68)	
Lhi (inbred, low	Not assigned	F = 34.28	14.4*	Non-Mendelian	8	7 (1 to 19)	
food intake)	Not assigned	F = 7.98	3.6		9	47	
	Not assigned	F = 7.02	3.2		18	40	
NON/Lt \times (NZO/	Dbsty1	LOD = 9.36		BW	1	21 (8.3 to 43.1)	(661)
H1Lt \times NON/	Dbsty2	LOD = 3.86		Adiposity index	5	43	
Lt)F1	Dbsty3	LOD = 4.88		Adiposity index	12	48 (45 to 53)	
$NZM/B1NJ \times SM/J$	Bfq1	LOD = 3.6	36	Body fat	2	81	(662)
$NZO \times (SJL/x)$ NZO)F1	Nobq1	LOD = 3.8	16.8	BMI (females)	5	32	(663–665)
$SM/I \times A/I$	Rwa3	IOD = 4.6	6	BW at 10 weeks	8	56 (53 to 69)	(666)
51415 / 145	Bwq4 Bwq4	LOD = 4.8	6	BW at 10 weeks	18	28 (20 to 54)	(000)
$SM/I \times NZO/H11 t$	Dwq4 Oba4	LOD = 4.0	0	Inquinal fat (%) (males)	17	20(20 10 54) 87(61 to 155)	(667)
SWIJ A NZO/IIILt	Obq7 Obq7	LOD = 0.3 LOD = 6		Mesenteric fat (%)	1	28.7 (0.1 to 15.5) 28.7 (25.7 to 42)	(007)
	Oba8	IOD = 64		Retroperitoneal fat (%)	1	61 9 (63 7 to 85 1)	
	Obq9	LOD = 0.4 $LOD = 6.7$		Mesenteric fat (%)	1	88.4 (82.4 to 92.7)	
	Oba10	IOD = 64		Gonadal fat (%) (malas)	2	58 1 (50 7 to 67 4)	
	Oball	LOD = 0.4 LOD = 4.1		Gonadal fat $(\%)$ (mates)	ے ج	10(3.1 to 16.0)	
	Obg12	LOD = 4.1		Consider fat $(\%)$	5	$20(3.4 \pm 0.10.9)$	
	00q12 01-12	LOD = 4.5		Gonadai Tat (%) Maaantania $f \neq (0')$	5	29 (21.9 to 30.1)	
	Obq13	LOD = 9.3		Mesenteric fat (%)	6	20.8 (20.7 to 29.4)	
	Obq14	LOD = 9.2		Mesenteric fat (%)	6	45.5 (39.4 to 46.9)	
	Obq15	LOD = 6.6		Gonadal fat (%) (males)	7	51.4 (44.2 to 52.4)	

Cross	QTL	Scores	Variance (%)	Phenotypes	Animal chromosome	QTL peak	Reference
(C57BL/6J \times TH)F1 \times TH and (CAST/Ei \times	Tabw Tafat Tabw2	LOD = 3.9 LOD = 3.1			7 4 6	27.8 (0 to 44) 69.8 (68 to 90) 38.5 (19.1 to 65.5)	(668,669)
TH)F1 \times TH (TallyHo) \times various							
Taval × Taval	CDF8	n < 0.001	0.0% Lass for	Fat			(670)
Rat	0DF0	p < 0.001	9.970 Less lat	Tat			(070)
$(OLETF \times BN) \times$	Dmo9	LOD = 3.5		Adiposity index	11		(671)
OLETF	Dmol	LOD = 8.2 to		BW	1		
	Dmo4	LOD = 4.4 to 5.5		Adiposity index	1		
	Dmo7p	LOD = 4.9 to 5.4		Adiposity index	7		
	Dmo6p	LOD = 3.5 to 3.6		Adiposity index	6		
	Dmo5	LOD = 3.5 to 3.6		Adiposity index	3		
	Dmo10	LOD = 3.5 to 3.6		BW	11		
BN imes GK/Nidd/gk5	Nidd/gk5 weight	LOD = 4.19	13	Weight	8		(672)
$Dahl \times MNS$	DAHL3	p = 0.00003	13	BW	3		(673)
$F344 \times OLETF$	Olep1	LOD = 5.39	6.5	Leptin	2		(674)
	Olep2	LOD = 4.49	8	Leptin	6		
$GK \times BN$	Nidd/gk6			BW	17		(675)
	Nidd/gk1			Adiposity	1		
	bw/gk1			BW	/		
$CV \times E244$	Niddm1	IOD = 3.2	22.5	BW	8 1		(676)
UK ^ F344	Weight1	LOD = 5.2 LOD = 6.2	23.3	DW	1 7		(070)
	Niddm3	LOD = 0.2 LOD = 3.0			10		
Lepr(fa)/Lepr(fa)	Ofa12	LOD = 3	8.3	BML female	12		(677)
$13M \times WKY$	Ofa1	LOD = 2.2	6.9	BMI, female	1		(0,1)
$OLETF \times BN$	Dmo1	LOD = 6	11.6	BW	1		(678)
$OLETF \times F344$	Niddm24	LOD = 3.91		Also known as Nidd6/of	1Distal	D1Rat81-D1Rat90	(679)
	Obs5	LOD = 5.1		Obs5 narrowed to 10- cM interval	14	D14Rat23- D14Wox7	(680)
$\mathrm{SHR} \times \mathrm{BB/OK}$	SHR4	LOD = 3.1	14	BW (females)	4		(681)
	SHR1	LOD = 3.3	32	BW (males)	1		
$SHR \times wild$	SHR10	LOD = 3.5		BW (males)	10		(682)
WOKW \times DA/K	Wokw1/Q1ms5	LOD = 4.5	16	BMI	5		(644,683)
ה'	Wokw1/Q1ms1	LOD = 4.9	31	30-Week BW	1		
Pig Deuleeleine M	6664.112	E = 11.0	(W7-:-1-4	4		((04)
Vorkshire	SSC4:115 SSC7	F = 11.8 F = 13.8	6.0	weight Back fat	4		(084)
TOTKSHILE	SSC1	F = 13.3 F = 11.3	4.8	Back fat	1		
	SSC5	F = 9.5	4.8	Back fat	5		
Duroc \times Berkshire	SSC2 0	F = 10.03	1.0	Back fat	2		(685)
	SSC2 30	F = 10.61		Fat (%)	2		,
	SSC2 37	F = 7.34		Weight	2		
	SSC6 110	F = 7.39		Weight	6		
Duroc, Hampshire,	PigQTL2	F = 7.9		Average back fat	7		(686,687)
Landrace \times Meishan							

						-	
Cross	QTL	Scores	Variance (%)	Phenotypes	Animal chromosome	QTL peak	Reference
Duroc, Hampshire, Landrace × Meishan	HMGA1	<i>p</i> = 0.01		Back fat	7		(669)
Large White × European wild boar	FAT1	p = 0.0001	9.7	Body fat (%)	4		(688–690)
Landrace \times Iberian	FAT1 FAT1	F = 11.1		Back fat depth	4		(691) (692)
Landrace \times Iberian	SSC6 60-100	p = 0.001		Back fat thickness	6		(693)
	SSC6 130-132/ LEPR	p = 0.001 p = 0.001		Back fat thickness, intramuscular fat (%)	6		(0)5)
Landrace × Iberian	AFABP			Fatness	4		(692)
Meishan × (Dutch Landrace × Large White)	SSC7	F = 18		Back fat thickness	7		(694,695)
Meishan \times (Dutch Landrace \times Large White	SSC2	F = 2.7		Back fat thickness	2		(694,695)
Meishan \times Duroc	SSC6 102,7- 116.7	F = 16.16	4	Weight	6		(696)
	SSC6 102,7- 116.7	F = 12.65	14	Weight, daily gain	6		
	SSC7 56.2	F = 11.45	12	Weight, daily gain	7		
	SSC7 113.3	F = 13.6	14	Fat, back fat thickness	7		
	SSCX 74,6	F = 15.79	16	Fat, intramuscular	Х		
Meishan $ imes$ Duroc	HMGA2	p = 0.01	14	Fat, back fat thickness	7		(669)
Dutch $ imes$ Meishan	SSC6q	F = 14.7	0.1 to 0.2	Intramuscular fat	6q		(465,697)
	SSC7	F = 49.4		Back fat thickness	7		
	SSC2	F = 24.1		Back fat thickness	2		
	SSC6p	F = 14.5		Intramuscular fat	6р		
	SSCX	F = 12.8	0.1 to 0.2	Intramuscular fat	Х		
Gottingen × Meishan	SSC7	F = 19.5	18	Back fat thickness	7		(698)
Large White × Meishan	BFM4			Midback fat depth	4		(699)
Meishan × Large White	SSCX 67	$p = 1.4^{e15}$		Fat thickness at the loin	X		(700)
White \times Meishan	SSC4:49-84	F = 14.9 to 15.3	3 to 4	Back fat thickness	4		(701,702)
	SSC8	F = 9.5	1 to 2	Back fat thickness	8		
	SSC/	F = 10.4 to 20.5	2 to 5	Back fat depth	1		
	5501	F = 39.4 to 94.9 E = 12.4 to	1 to 2	Weight	1		
	3303	F = 13.4 to 15.1	2 10 5	Back fat thickness	5		
	SSC6	F = 11.9	1 to 2	Back fat thickness	6		
	SSCX	F = 37.4 to 71.8		Back fat depth	Х		
White composite \times	SSC7	F = 14.7		Back fat thickness	7		(703)
Meishan	SSC1	F = 15.4		Back fat thickness	1		
	SSCX	F = 32.3		Back fat thickness	X		(70.4)
Hampshire, Landrace × Minghu	PITI	F = 3.34		42-Day weight	13		(704)
Large White × Wild Boar	IGF2q	F = 7.1	10.4	Back fat depth	2p		(634,705)

ing of crosses between two strains define only a statistical probability of a polymorphic gene residing in a defined genetic interval. Follow-up studies are necessary to confirm this likelihood. Congenic (and subcongenic) strains have been generated for some of these QTLs, supporting the existence and magnitude of some of these phenotypes. Some cases include the characterization of the Fob3 QTL (645,646). Congenic strains containing a chromosome 15 region from the lean L strain were introgressed onto the F genetic background. Interestingly the characterization of subcongenic lines suggests that Fob3 contains two contributory regions: Fob3a and Fob3b, conferring late and early onset phenotypes, respectively. Expression analysis of genes positioned within the Fob3b segment by microarray screening identifies a candidate gene, Sqle (squalene epoxidase). This gene is involved in the regulation of cholesterol biosynthesis. Interestingly, the expression of other genes of the cholesterol biosynthesis pathway mapping outside of the Fob3b region are also perturbed, suggesting that the changes in activity of this pathway may be responsible for the phenotypic differences between the F parental and the F.L<Chr15> congenic strains. Other murine QTL regions for which candidate genes have been implicated include Bw19 (Gpc3, Glypican 3) (606) and the QTL on chromosome 7 associated with adiposity (ATP10a, encodes ATPase, class V, type 10A) (706). A candidate gene for a rat QTL Niddm24 is Pnlip (encodes pancreatic lipase). The continued generation of congenic mouse strains and expression screening and single nucleotide polymorphism genotyping analysis should continue to implicate specific genes with well-characterized QTL regions.

QTLs from Cross-Breeding Experiments Other Than Rodents

Syntenic regions in humans have been picked up directly from the original papers or determined from the U.S. Livestock Genome Mapping Projects (NAGRP03). Four new chromosomes were targeted according to QTL analysis in chicken, one in pig, and one in sheep (Table 3). In a cross between Landrace and Iberian pig strains, a QTL for fatness was reported on pig chromosome 4 in the region of the AFABP gene (692) corresponding to the human fatty acidbinding protein 4 (adipocyte) gene located at 8q24. A QTL for fat was reported in a sheep Texel imes Texel cross at the growth differentiation factor 8 gene (670), which is located at 2q32.2 in humans. The main QTL region detected for fat on chicken chromosome 7 from the cross White Leghorn layer \times commercial broiler (591) corresponded to human chromosome 2q21. The cross of Rhode Island Red layer with itself produced a QTL for BW on chromosome 4 (707) corresponding to human chromosome 17q11.1-q12, whereas the White Plymouth Rock cross produced a QTL for weight on chromosome 5 (594) corresponding to human 22q13.1-q13.31

but also to 12p13-q23 reported in the cross WL \times RIR (593). Finally, a QTL for weight was reported on chicken chromosome 1 (596) that corresponds to human chromosome 21q22.

Associations with Candidate Genes

The evidence for associations between candidate genes and obesity-related phenotypes is summarized in Table 4. A total of 416 studies covering 127 candidate genes have reported significant associations. Of these, 57 studies (40 candidate genes) were published during the past year. This year's update includes 14 new candidate gene entries.

Associations with BW, BMI, Overweight, and Obesity

BW, BMI, overweight, and obesity were associated with DNA sequence variation in *ACE* (710,711), *ADIPOQ* (718–720), *ADRB2* (744), *BDNF* (814), *COMT* (822), *CYP11B2* (824), *DRD4* (836), *ENPP1* (839), *ESR1* (841), *ESR2* (841), *FOXC2* (850,851), *GAD2* (855), *GHRHR* (859), *HTR2C* (884), *LIPC* (951), *MC4R* (971), *MCHR1* (876,877), *NPY* (981), *NTRK2* (998), *NPY2R* (984), *PLIN* (1112), *PPARG* (1012,1021,1027), *PPARGC1A* (1042), *PYY* (984,1046), *RETN* (1051), *SERPINE1* (1055), *UCP1* (1084), and *VDR* (1110).

Associations with Body Composition and Fat Distribution Phenotypes

Body composition-related phenotypes (fat mass, fat-free mass, percentage body fat, sum of skinfolds) showed associations with markers in ACE (712), UCP1 (1079), LEPR (937), LIPC (951), PLIN (1113), PPARG (1021), GFPT1 (858), AR (809), DIO1 (830), IGF2 (899), FOXC2 (850), and COMT (822). Phenotypes reflecting body fat distribution [abdominal visceral and subcutaneous fat, waist-to-hip ratio (WHR), waist circumference, sagittal diameter] were associated with ACE (710), ADIPOQ (719), ADRB2 (744), APOA2 (792), FABP2 (847), LTA (964), MTTP (976), PLIN (1113), PPARG (1021), and UCP1 (1079).

Associations with Changes in BW and Body Composition

Eight studies reported associations between seven candidate genes and changes in BW and body composition. The *ADRB1* (736), *NMB* (978), and *PPARG* (1016) loci showed associations with spontaneous changes in BW and adiposity over time. Markers in the *PPARG* (1032) gene were reported to be associated with exercise training-induced weight loss, whereas sequence variation in the *APOA5* (797) and *MC4R* (972) loci modified weight loss in response to a low-fat diet and bariatric surgery, respectively. The *ADIPOQ* (721) and *LEPR* (949) loci were reported to be associated with changes in BW during a 3-year diabetes prevention trial with acarbose.

Gene	Location	Subjects	Phenotype	р	Reference
ABCC8	11p15.1	232 Cases	Obesity, morbid	0.02	(708)
ABCG5	2p21	262 Cases	BMI	0.05	(709)
ACE	17g24.1	1009 Men	BMI	0.012	(710)
	1	964 Men	Waist circumference	0.0023	(710)
		956 Subjects	Overweight (Blacks from U.S.)	0.03	(711)
		1059 Subjects	Overweight (Blacks from Nigeria)	0.04	(711)
		956 Subjects	Obesity (Blacks from U.S.)	0.02	(711)
		1059 Subjects	Obesity (Blacks from Nigeria)	0.04	(711)
		922 Subjects	Body fat (%) (physically active Health ABC subjects)	0.05	(712)
		959 Cases	Overweight	0.014	(713)
		186 Cases	BMI	0.04	(714)
ACP1	2p25	75 Cases	BMI (in children)	0.02	(715)
		265 Cases	BMI (in type 2 diabetic subjects)	0.002	(716)
ADA	20g13.12	273 Cases	BMI (in type 2 diabetic subjects)	0.0004	(717)
ADIPOO	3027	194 Subjects	BMI	0.017	(718)
	0427	811 Subjects 45 families	BMI (Hispanic families from IRAS)	0.004	(719)
		811 Subjects 45 families	Waist circumference (Hispanic families from IRAS)	0.001	(719)
		811 Subjects 45 families	Abdominal visceral fat (Hispanic families from IRAS)	0.001	(719)
		100 Subjects, 100 women	BMI (women with polycystic ovarian syndrome)	0.01	(720)
		770 Subjects	Weight change during acarbose trial (STOP-NIDDM trial cohort)	0.043	(720)
		1470 Cases	3 year increase in BMI	0.033	(722)
		4479 Cases	2 year increase in weist to hin ratio	0.033	(722)
		4479 Cases		0.01	(722)
		105 Cases	DIVII	0.05	(723)
		412 Cases	Dody weight weigt singumfanges (in Language in whites)	0.047	(724)
		415 Cases	Body weight, waist circumference (in Japanese, in wintes)	0.05	(723)
		05 Cases	DIVII PMI (in chose women)	0.02	(720)
		95 Cases	Societal abdominal diamatan (in abasa waman)	0.014	(727)
		95 Cases	Sagittal abdominal diameter (in obese women)	0.052	(727)
100121	10-24 -26	245 Cases	BIVII Skinfolda taunli ta automitu actia (in Dlaska)	0.05	(728)
ADKAZA	10q24-q20	215 Cases	Skillolds, trunk-to-extremity ratio (in blacks)	0.04	(729)
		12 Cases	Abde wind total fat	0.002	(730)
		476 Cases	Abdominal total fat	0.005	(731)
		4/6 Cases	Abdominal subcutaneous fat	0.012	(731)
		93 Cases, 49 men, 44 women	psychotic)	0.023	(732)
ADRA2B	2q11.2	166 Cases	Basal metabolic rate (in obese non-diabetics)	0.01	(733)
		126 Cases	Body weight, change, 5-year (in non-diabetics)	0.04	(734)
ADRB1	10q24-q26	931 Cases	BMI, body weight, fat mass	0.05	(735)
		760 Subjects	BMI increase during 15-year follow-up	0.018	(736)
ADRB2	5q31-q32	239 Cases	Waist-to-hip ratio	0.05	(737)
		180 Cases	BMI	0.003	(738)
		494 Cases	Body weight, increase (in men)	0.01	(739)
		141 Cases	Catecholamine-induced lipolysis in adipocytes	0.01	(740)
		247 Cases	BMI, change (in women)	0.04	(741)
		247 Cases	Fat mass, change (in women)	0.0008	(741)
		247 Cases	Body fat (%) change (in women)	0.0003	(741)
		230 Cases	Skinfolds, sum of eight (in men)	0.03	(741)
		236 Cases	Lipolysis	0.02	(742)
		508 Cases	BMI (in Japanese)	0.001	(743)
		272 Subjects	BMI (African Americans from IRAS)	0.001	(744)
		992 Subjects	BMI (whole IRAS cohort)	0.045	(744)
		992 Subjects	Waist-to-hip ratio (whole IRAS cohort)	0.0001	(744)
		948 Subjects	Abdominal visceral fat (whole IRAS cohort)	0.0001	(744)
		140 Cases	BMI, fat mass, fat cell volume	0.001	(745)
		826 Cases	BMI, obesity, waist-to-hip ratio, waist circumference, hip circumference	0.05	(746)
		366 Cases	BMI (in women)	0.01	(747)
		836 Cases	BMI, body weight, waist-to-hip ratio, waist circumference, hip circumference (in French men)	0.002	(748)

Table 4. Evidence for association between markers of candidate genes with obesity-related phenotypes

Gene	Location	Subjects	Phenotype	р	Reference
		63 Cases	BMI. fat mass	0.05	(749)
		277 Cases	BMI (in Japanese men)	0.004	(750)
		1576 Cases	BMI	0.02	(751)
		284 Cases	Leptin	0.03	(752)
		224 Cases	BMI (in men)	0.01	(731)
		24 Cases	Leptin, body weight, increase, skinfolds, sum of eight	0.03	(753)
		286 Cases	Body weight, increase	0.04	(754)
		574 Cases	BMI (in Japanese)	0.009	(755)
ADRB3	8p12-p11.2	185 Cases	Body weight, increase over 20 years, weight, current	0.007	(756)
1101100	oprie prine	313 Cases	Obesity (in those 20 to 35 years old)	0.05	(757)
		476 Cases	BMI (in men)	0.05	(758)
		553 Cases	Obesity (in Japanese children)	0.02	(759)
		179 Cases	BMI	0.006	(760)
		295 Cases	BMI	0.05	(761)
		695 Cases	BMI	0.001	(762)
		83 Cases	BMI (in coronary artery disease patients)	0.05	(763)
		211 Cases	Obesity moderate	0.02	(763)
		53 Cases	Obesity	0.02	(765)
		350 Cases	BMI	0.009	(766)
		308 Cases	BMI abdominal subcutaneous fat abdominal visceral fat	0.002	(767)
		154 Cases	Obesity (in sedentary individuals)	0.02	(768)
		154 Cases	5 year weight goin	0.05	(768)
		40 Cases	PML hin aircumferance (in women)	0.03	(709)
		56 Cases	BMI, fat mass, waist singumfannes	0.05	(770)
		128 Cases	Bivil, lat mass, waist circumetence Body weight increase over 25 years	0.03	(771)
		120 Cases	Body weight, increase over 25 years	0.01	(772)
		Cases		0.001	(773)
		63 Cases	Abdominal visceral lat	0.001	(773)
		65 Cases	Abdominal subcutaneous fat	0.001	(773)
		1675 Cases	BMI, obesity, body fat (%)	0.05	(774)
		254 Cases	Obesity, early onset	0.002	(775)
		76 Cases	Fat mass (in Thai men)	0.05	(770)
		131 Cases	Fat mass, abdominal visceral fat	0.01	(777)
		261 Cases	BMI	0.05	(778)
		979 Cases	Waist-to-hip ratio, overweight (in men >53 years old)	0.05	(779)
		802 Cases	BMI	0.02	(780)
		224 Cases	BMI (in men)	0.02	(731)
		49 Cases	BMI	0.03	(781)
		335 Cases	Waist-to-hip ratio (in women)	0.02	(782)
		47 Cases	BW (in obese children)	0.05	(783)
AGRP	16q22	183 Cases	BMI, body fat (%), fat mass (in whites)	0.003	(784)
		253 Cases	BMI	0.015	(785)
		212 Cases	Fat mass	0.028	(785)
		212 Cases	Body fat (%)	0.013	(785)
		874 Cases	Body weight	0.02	(786)
		874 Cases	BMI	0.01	(786)
		874 Cases	Fat-free mass	0.002	(786)
		874 Cases	Fat mass	0.04	(786)
AGT	1q42.2	135 Cases	Body weight, change	0.006	(787)
		316 Cases	Waist-to-hip ratio	0.007	(788)
		57 Cases	Adipocyte size	0.01	(789)
		106 Cases	Adipocyte size	0.02	(789)
		94 Cases	Fat mass (in women >42 years old)	0.008	(790)
APOA1	11q23.3	482 Cases	BMI (in type 2 diabetics)	0.048	(791)
	-	482 Cases	Waist-to-height ratio (in type 2 diabetics)	0.023	(791)
APOA2	1q23.1	122 Women	Abdominal visceral fat (white women)	0.05	(792)
	-	624 Cases	Waist circumference	0.03	(793)
APOA4	11q23.3	369 Cases	BMI	0.003	(794)
	1	375 Cases	BMI, waist-to-hip ratio (in young men)	0.004	(795)
		613 Cases	BMI, body fat (%)	0.004	(796)
APOA5	11g23	606 Subjects. 606 women	Weight loss on a 3-month low-fat diet	0.0021	(797)
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Gene	Location	Subjects	Phenotype	р	Reference
APOB	2p24.2	56 Cases	Body fat (%), abdominal fat	0.04	(798)
	•	232 Cases	BMI	0.005	(799)
		181 Cases	BMI	0.05	(800)
APOC3	11q23.1-q23.2	270 Cases	Obesity	0.05	(801)
APOD	3q26.2-qter	114 Cases	BMI	0.006	(802)
APOE	19q13.32	1775 Cases	BMI	0.01	(803)
	1	405 Cases	Fat mass	0.002	(804)
		405 Cases	Body fat (%)	0.003	(804)
		405 Cases	Lean mass	0.004	(804)
		164 Cases	Waist circumference (in women with a family history of diabetes)	0.05	(805)
		64 Cases	Body fat (%), leptin (in women)	0.02	(806)
AR	Xq11.2-q12	131 Cases	BMI	0.043	(807)
		113 Cases	Waist circumference (in women)	0.002	(808)
		294 Men	Fat-free mass	0.027	(809)
		112 Men	Fat-free mass	0.049	(809)
		106 Cases	Body fat (%)	0.01	(810)
ATP1A2	1q23.1	122 Cases	Body fat (%), respiratory quotient	0.05	(811)
	•	156 Cases	Respiratory quotient (in young adults)	0.0001	(812)
		12 Cases	Fat mass	0.01	(813)
		12 Cases	Body weight	0.05	(813)
BDNF	11p13	249 Subjects	Minimum lifetime BMI (PO trios with restricting AN)	0.019	(814)
CAPN10	2q37.3	148 Cases	adrb3 activity in adipocytes (in overweight individuals)	0.004	(815)
	1	286 Cases	BMI	0.003	(816)
CART	5q13.2	612 Cases	Waist-to-hip ratio (in men)	0.002	(817)
	- 1	528 Cases	BML obesity	0.008	(818)
CBFA2T1	8q21.3	281 Cases	BMI, body fat (%), waist circumference, hip circumference	0.0002	(819)
CCKAR	4p15.2-p15.1	1296 Cases	Leptin, body fat (%)	0.003	(820)
CNTFR	9p13.2	465 Cases	Fat-free mass	0.011	(821)
COMT	22g11.21	246 Subjects	Height (pre-/early pubertal girls)	0.001	(822)
	1	246 Subjects	Body weight (pre-/early pubertal girls)	0.009	(822)
		246 Subjects	Total lean mass (pre-/early pubertal girls)	0.004	(822)
		83 Cases	Exercise training-induced percentage body fat loss	0.05	(823)
CRHR1	17a12-a22	503 Cases	BMI	0.0083	(14)
CYP11B2	8a24 3	190 Subjects	BMI (normotensive highlanders from India)	0.002	(824)
0111102	0421.5	100 Subjects	BMI (hypertensive highlanders from India)	0.002	(824)
CYP19A1	15a21.1	125 Cases	Sagittal abdominal diameter (in women)	0.049	(825)
0111)/11	15421.1	300 Cases	BMI	0.01	(826)
		83 Cases	Exercise training-induced body fat loss	0.01	(823)
		83 Cases	Exercise training induced percentage body fat loss	0.01	(823)
CYP2D6	22q13.1	11 Cases, 11 men	BMI change percentage (white schizophrenic under anti- psychotic)	0.01	(827)
CYP7A1	8q12.1	1102 Cases	BMI	0.05	(828)
DF	19p13.3	24 Cases	Abdominal fat (in monozygotic twins)	0.05	(829)
DIO1	1p32	350 Subjects	Fat-free mass	0.03	(830)
DRD2	11g23.2	392 Cases	Body weight	0.002	(831)
		176 Cases	Obesity	0.002	(832)
		320 Cases	Energy expenditure, 24-hour, sleeping metabolic rate	0.03	(833)
		383 Cases	Skinfolds iliac skinfolds tricens	0.002	(834)
		900 Cases	Obesity	0.03	(835)
DRD4	11p15.5	128 Subjects, 128 women	Maximal lifetime BMI (women with seasonal affective disorder)	0.001	(836)
		103 Cases	Maximal lifetime BMI	0.007	(837)
ENPP1	6q23.1	293 Cases	Leptin	0.01	(838)
		1225 Cases 1205 controls	Obesity (obese children and controls)	1^{e-05}	(839)
		184 Families	Obesity	0.01	(839)
ESR1	6a25.1	108 Cases	BMI (in post-menopausal women)	0.04	(840)
	- q =0.1	295 Subjects	BMI	0.024	(841)
		551 Cases	BMI (in middle-aged women)	0.05	(842)
				0.05	(0-14)

Gene	Location	Subjects	Phenotype	р	Reference
		551 Cases	Body fat (%) (in middle-aged women)	0.05	(842)
		551 Cases	Waist circumference (in middle-aged women)	0.05	(842)
		216 Cases	Obesity, android type	0.0002	(843)
ESR2	14q23.2	295 Subjects	BMI	0.02	(841)
FABP1	2p11	130 Cases	BMI	0.05	(844)
		130 Cases	Waist circumference	0.005	(844)
FABP2	4q27	714 Cases	BMI	0.042	(845)
		507 Cases	BMI, body fat (%)	0.01	(846)
		120 Subjects, 120 women	Total abdominal fat (white women)	0.004	(847)
		120 Subjects, 120 women	Subcutaneous abdominal fat (white women)	0.03	(847)
		395 Cases	Abdominal fat	0.008	(848)
FASN	17q25	214 Cases	Body fat (%)	0.002	(849)
		174 Cases	Respiratory quotient, 24-hour	0.04	(849)
		174 Cases	24-hour carbohydrate oxidation	0.03	(849)
FOXC2	16q22-q24	127 Cases, 127 controls	Obesity	0.027	(850)
		223 Cases, 231 controls	Obesity	0.043	(850)
		388 Subjects	BMI (Swedish type 2 diabetics)	0.03	(851)
		388 Subjects	Fat mass (Swedish type 2 diabetics)	0.04	(851)
		644 Cases	BMI	0.03	(852)
		215 Cases	Body fat (%)	0.02	(852)
		724 Cases	Waist-to-hip ratio	0.04	(853)
GAD2	10p11.23	575 Cases	Morbid obesity, eating behavior	0.0049	(854)
		575 Cases	Morbid obesity, eating behavior	0.014	(854)
		477 Cases, 614 controls	Obesity (obese children and controls)	0.043	(855)
		559 Subjects	Birth weight (obese children)	0.009	(855)
GCGR	17pter	950 Cases	Waist-to-hip ratio, waist girth, sagittal abdominal diameter	0.001	(856)
GCK	7p15.3-p15.1	58 Cases	Body weight at birth (in men)	0.002	(857)
GFPT1	2p13	164 Subjects, 164 men	Fat (%)	0.009	(858)
GHRHR	7p14	1095 Subjects, 178 families	Obesity	0.025	(859)
		1418 Subjects	Obesity (MONICA Augsburg cohort)	0.002	(859)
GHRL	3p26-p25	300 Cases	Obesity age of onset	0.003	(860)
		65 Cases	BMI (in tall obese children)	0.001	(861)
		192 Cases	Obesity (in women)	0.05	(862)
GNB3	12p13.31	737 Cases	Obesity (in men)	0.01	(863)
		294 Cases	Weight gain during pregnancy	0.006	(864)
		230 Cases	BMI (in primiparous women)	0.01	(865)
		20 Cases	Lipolysis	0.01	(866)
		111 Cases	Weight loss with sibutramine	0.0013	(867)
		213 Cases	BMI, waist circumference, hip circumference, skinfolds (in Nunavut Inuit)	0.05	(868)
		181 Cases	Body weight at birth	0.02	(869)
		130 Cases	BMI	0.001	(870)
		250 Cases	Fat mass, change, body fat, change (%)	0.006	(871)
		114 Cases	Lipolysis (subcutaneous, adrenoreceptor-mediated)	0.004	(872)
		197 Cases	BMI (in hypertensives)	0.02	(873)
		1950 Cases	BMI, body weight (in men, white, Chinese, and African)	0.001	(874)
		774 Cases	BMI	0.03	(875)
		774 Cases	Body fat (%)	0.02	(875)
		134 Cases, 80 men, 54 women	Weight change (Chinese schizophrenic under anti- psychotic)	0.003	(732)
GPR24	22q13.2	469 Cases, 1127 controls	Obesity (French obese children)	0.006	(876)
		719 Cases, 326 controls	Obesity	0.0016	(877)
GYS1	19q13.33	130 Cases	Obesity	0.03	(878)
HSD11B1	1q32-q41	263 Cases	BMI (in children)	0.005	(879)
		263 Cases	Waist circumference (in children)	0.05	(879)
		263 Cases	Waist-to-hip ratio (in children)	0.05	(879)
HSD3B1	1p11.2	132 Cases	Skinfolds, sum of six, 12-year change	0.04	(811)
HSPA1B	6p21.31	517 Cases	Obesity	0.0002	(880)
HTR1B	6q14.1	98 Cases	BMI (in women with bulimia nervosa)	0.001	(881)

Gene	Location	Subjects	Phenotype	р	Reference
HTR2A	13q14.11	276 Cases	Dietary energy, carbohydrate and alcohol intake (in obese subjects)	0.028	(882)
		264 Cases	BMI, waist-to-hip ratio, sagittal abdominal diameter	0.015	(883)
HTR2C	Xa24	293 Cases 481 controls	Obesity	0.0001	(884)
1111120	11921	224 Cases	Obesity	0.008	(885)
		117 Cases	Body weight gain anti-nsychotic-induced	0.0003	(886)
		148 Cases	Body weight loss (in teenage women)	0.0003	(887)
		580 Cases	Dody weight, loss (in teenage wonten)	0.0001	(889)
		72 Cases 45 mar 28 mars	DIVII Weicht channe (fram 58 mhite/22 African American	0.009	(000)
		73 Cases, 45 men, 28 women	schizophrenic under anti-psychotic)	0.05	(889)
		42 Cases, 34 men, eight women	BMI change 10% (white schizophrenic under anti- psychotic)	0.004	(890)
		41 Cases, 26 men, 15 women	BMI change (%) (5 white/35 African American/1 Hispanic schizophrenic under anti-psychotic)	0.05	(891)
	41 Cases, 26 men, 15 women	BMI change 7% (5 white/35 African American/1 Hispanic schizophrenic under anti-psychotic)	0.003	(891)	
		58	BMI change 9 months; white schizophrenic under anti- psychotic	0.03	(892)
		117	BMI change; Chinese schizophrenic under anti-psychotic	0.0003	(886)
		32	BMI change; Chinese schizophrenic under anti-psychotic	0.02	(893)
IDE	10a23-a25	724 Cases	BMI	0.0067	(894)
IGF1	12a23.3	502 Cases	Body fat (%) fat-free mass fat mass change	0.05	(895)
IGF2	11p15 5	2734 Cases	Body weight	0.01	(896)
1012	11010.0	1474 Cases	BMI	0.02	(897)
		427 Cases	Fat mass	0.02	(898)
		206 Women	Fat_free mass	0.05	(899)
П.6	7p21	200 Wollien 271 Cases	BMI (in men)	0.007	(900)
ILU	7.021	271 Cases	Waist circumference (in men)	0.007	(900)
		124 Cases	Fasting energy expenditure	0.012	(901)
		124 Cases	Energy expenditure during hyperingulinemic clamp	0.007	(901)
		3376 Cases	BMI	0.007	(902)
		3376 Cases	Body weight change during a 3.5 year follow up	0.027	(902)
		242 Cases	Eat frag mass	0.03	(902)
		571 Cases	DMI	0.02	(903)
		195 Cases	DMI	0.009	(904)
		465 Cases	DMI	0.005	(903)
II (D	1-22	184 Cases	BMI Obseits (in menue)	0.03	(905)
ILOK	1922	184 Cases	Obesity (in women)	0.05	(906)
		700 Cases	BMI	0.003	(907)
		700 Cases	BMI	0.001	(907)
		700 Cases	BMI	0.004	(907)
		700 Cases	BMI	0.02	(907)
		700 Cases	BMI	0.02	(907)
INS	11p15.5	758 Cases	Body weight	0.009	(908)
		2734 Cases	Body weight	0.001	(896)
		431 Cases	BMI	0.043	(909)
		431 Cases	Waist circumference	0.015	(909)
		238 Cases	Obesity	0.05	(910)
		1152 Cases	BMI	0.0002	(911)
		1207 Cases	Body weight	0.02	(912)
		1207 Cases	BMI	0.03	(912)
		1207 Cases	Waist circumference	0.03	(912)
		52 Cases	Waist-to-hip ratio (in obese women)	0.005	(913)
INSR	19p13.3-p13.2	75 Cases	Obesity (in hypertensives)	0.05	(914)
IRS1	2q36.3	304 Cases	BMI	0.001	(915)
		304 Cases	Waist-to-hip ratio	0.001	(915)
		156 Cases	Leptin (in obese subjects)	0.03	(916)
		1748 Cases	BMI (in African Americans)	0.04	(917)
IRS2	13q34	233 Cases	BMI	0.02	(918)
	-	233 Cases	Body fat (%)	0.01	(918)
		233 Cases	Waist circumference	0.004	(918)
Gene	Location	Subjects	Phenotype	р	Reference
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LDLR	19p13.2	83 Cases	BMI (in normotensives)	0.008	(919)
	1	131 Cases	BMI, skinfolds, subscapular, skinfolds, triceps, arm fat	0.001	(920)
			index		
		270 Cases	Obesity	0.02	(921)
		84 Cases	BMI (in hypertensives)	0.004	(922)
		112 Cases	BMI (in hypertensives)	0.04	(923)
LEP	7q31.3	103 Cases	BMI, body weight	0.005	(924)
		395 Cases	Leptin	0.02	(925)
		39 Cases	Leptin secretion	0.05	(926)
		738 Cases	Obesity	0.011	(927)
		738 Cases	BMI	0.028	(927)
		233 Cases	Leptin (in obese women)	0.02	(928)
		211 Cases	Obesity (in women)	0.05	(929)
		117 Cases	Leptin	0.04	(930)
		168 Cases	Body weight, decrease	0.006	(931)
		84 Cases	Body weight	0.05	(932)
		73 Cases, 55 men, 18 women	BMI change 9 months (white schizophrenic under anti- psychotic)	0.03	(892)
		128 Cases, 38 controls, 61 men 67 women	BMI change (Chinese schizophrenic under anti-psychotic)	0.003	(933)
		128 Cases, 38 controls, 61 men, 67 women	Abdominal subcutaneous fat change (Chinese schizophrenic under anti-psychotic)	0.009	(933)
LEPR	1n31	502 Cases	BML fat mass	0.005	(934)
	1901	308 Cases	Fat-free mass	0.03	(935)
		335 Cases	BML body weight fat mass (in women)	0.01	(936)
		103 Subjects	Body fat (%)	0.02	(937)
		405 Cases	Fat mass	0.015	(938)
		405 Cases	Lean mass	0.002	(938)
		179 Cases	BMI fat mass body weight loss (in overweight women)	0.002	(939)
		336 Cases	Overweight/obesity	0.000	(940)
		220 Cases	Lentin BMI fat mass (in post-menonausal women)	0.0001	(941)
		267 Cases	BMI sagittal abdominal diameter	0.04	(942)
		600 Cases	BMI > 25	0.04	(942)
		130 Cases	Obesity extreme (in children)	0.007	(944)
		268 Cases	Energy expenditure 24-hour	0.02	(945)
		184 Cases	A dipocyte size, subcutaneous abdominal	0.02	(945)
		20 Cases	Rody fat (%)	0.02	(945)
		20 Cases	Abdominal total fat, abdominal subsutaneous fat	0.003	(940)
		02 Cases		0.03	(947)
		118 Cases	BMI BMI shange during 2 year follow up (STOP NIDDM trial	0.01	(948)
		770 Subjects	cohort)	0.009	(949)
		770 Subjects	Waist circumference change during 3-year follow-up (STOP-NIDDM trial cohort)	0.006	(949)
LIPC	15q21–23	230 Cases	BMI	0.002	(950)
		234 Cases	Waist circumference	0.002	(950)
		231 Cases	Abdominal visceral fat	0.03	(950)
		1070 Subjects	BMI	0.02	(951)
		1070 Subjects	Body fat (%)	0.03	(951)
LIPE	19q13.2	257 Cases	BMI, body fat (%), fat mass, skinfolds, sum of eight (in white and black women)	0.005	(952)
		117 Cases	Waist-to-hip ratio, lipolysis	0.02	(953)
		405 Cases	Obesity (in women)	0.05	(954)
		405 Cases	Body fat (%) (in women)	0.05	(954)
		380 Cases	Obesity	0.002	(955)
		110 Cases	BMI (in women)	0.012	(956)
LMNA	1q23.1	48 Cases	Leptin, lipodystrophy, leptin-to-BMI ratio	0.05	(957)
		306 Cases	Leptin, BMI, waist-to-hip ratio (in Canadian Oji-Cree)	0.05	(958)
		47 Cases	Familial partial lipodystrophy	0.0001	(959)
		186 Cases	BMI, body weight, waist circumference, skinfolds,	0.002	(960)
			subscapular		

Gene	Location	Subjects	Phenotype	р	Reference
LPL	8p21.3	587 Cases	BMI (in women)	0.02	(758)
	1	249 Cases	Body fat (%), fat mass, BMI, change (in white women)	0.01	(961)
		236 Cases	BMI	0.05	(962)
LRPAP1	4p16.3	235 Cases	Abdominal obesity	0.045	(963)
LTA	6p21.3	5630 Subjects	Waist circumference	0.009	(964)
MACS2	16p12.3	1976 Cases	BMI	0.009	(965)
	I	1976 Cases	Waist-to-hip ratio	0.0011	(965)
MAOA	Xp11.4-p11.3	50 Cases	BMI > 35	0.005	(966)
MC3R	20q13.2-q13.3	314 Cases	BMI, body fat (%), fat-free mass, fat mass, respiratory quotient (in normal-weight and overweight individuals)	0.0005	(967)
		244 Cases	Leptin (in morbidly obese subjects)	0.05	(968)
MC4R	18q22	156 Cases	BMI, body fat (%), fat-free mass, fat mass (in women)	0.003	(969)
		520 Cases	Obesity	0.017	(970)
		1135 Cases	Obesity (in children and adolescents)	0.006	(33)
		332 Subjects	BMI (offspring of the Quebec Family Study)	0.002	(971)
		426 Cases	Severe obesity	0.04	(38)
		174 Subjects	Weight loss after bariatric surgery (severely obese patients undergoing bariatric surgery)	0.003	(972)
		268 Cases	BMI, waist-to-hip ratio	0.023	(973)
		229 Cases	Resting energy expenditure	0.007	(974)
MC5R	18q22	156 Cases	BMI, body fat (%), fat-free mass, fat mass (in women)	0.002	(969)
MED12	Xq13.1	68 Cases	Obesity	0.001	(975)
MTTP	4q24	258 Subjects	Abdominal visceral fat	0.005	(976)
NCOA3	20q13.13	301 Cases	BMI (in post-menopausal women with breast cancer)	0.01	(977)
NMB	15q25	291 Subjects	6-year change in BMI	0.037	(978)
		291 Subjects	6-year change in waist circumference	0.018	(978)
		291 Subjects	6-year change in percentage body fat	0.017	(978)
NPR3	5p14-p13	787 Cases	BMI	0.048	(979)
		787 Cases	Waist-to-hip ratio	0.022	(979)
NPY	7p15.1	595 Cases	BMI, waist-to-hip ratio	0.03	(980)
		907 Subjects	BMI (non-obese Swedish subjects)	0.005	(981)
		369 Cases	Body weight at birth	0.03	(982)
NPY2R	4q31	952 Cases	BMI	0.017	(983)
		952 Cases	Waist-to-hip ratio	0.013	(983)
		100 Cases, 67 controls, 167 men	Severe obesity (male Pima Indians)	0.002	(984)
NPY5R	4q31-q32	74 Cases	Obesity (in Pima Indians)	0.05	(985)
NR0B2	1p35.3	294 Cases	Body weight at birth	0.05	(986)
		809 Cases	BMI (in 7-year-olds)	0.05	(986)
		809 Cases	Waist circumference (in 7-year-olds)	0.01	(986)
		305 Cases	BMI (in women)	0.05	(986)
		217 Cases	Obesity, early onset	0.009	(987)
NR3C1	5q31	51 Cases	Abdominal visceral fat (in lean subjects)	0.003	(988)
		279 Cases	BMI (in obese subjects)	0.04	(989)
		135 Cases	Waist-to-hip ratio (in men)	0.01	(990)
		262 Cases	Leptin, BMI, waist-to-hip ratio, waist circumference	0.001	(991)
		369 Cases	Overweight (in type 2 diabetics)	0.003	(992)
		83 Cases	Skinfolds, sum of (in girls)	0.01	(993)
		480 Cases	Abdominal visceral fat	0.001	(994)
		12 Cases	Body weight, gain	0.01	(995)
		1963 Cases	BMI	0.002	(996)
		1963 Cases	Waist-to-hip ratio	0.02	(996)
		370 Cases	BMI	0.05	(996)
		337 Cases	Lean mass	0.02	(997)
NTRK2		164 Subjects	Minimum lifetime BMI (Spanish eating disorder patients)	0.001	(998)
PGR	11q22.2	301 Cases	BMI (in post-menopausal women with breast cancer)	0.005	(977)
PLIN	15q26	117 Cases	Lipolysis in adipocytes (in obese women)	0.0008	(999)
	-	1538 Cases	BMI	0.004	(1000)
		1538 Cases	BMI	0.004	(1000)
		351 Subjects, 351 women	Body fat (%)	0.016	(1113)

Gene	Location	Subjects	Phenotype	р	Reference
		351 Subjects, 351 women	Body fat (%)	0.014	(1113)
		351 Subjects, 351 women	Waist circumference	0.02	(1113)
		351 Subjects, 351 women	Waist circumference	0.045	(1113)
		123 Cases, 623 controls	Obesity (Malays from Singapore)	0.05	(1112)
		77 Cases, 521 controls	Obesity (Indians from Singapore)	0.05	(1112)
PNMT	17q21.2	149 Cases	Weight loss (in women)	0.006	(1002)
POMC	2p22-p21	75 Cases	Leptin (in obese children)	0.03	(860)
		337 Cases	Leptin (in Mexican Americans)	0.001	(1003)
		118 Cases	Leptin (in lean subjects)	0.003	(1004)
PON1	7q21.3	114 Cases	BMI	0.045	(1005)
PON2	7q21.3	100 Cases	Body weight at birth (in Trinidadian neonates and South Asians)	0.05	(1006)
PPARA	22q13.31	698 Cases	BMI	0.023	(1007)
		570 Cases	Body fat (%)	0.028	(1007)
		154 Cases	BMI (in type 2 diabetics)	0.02	(1008)
PPARD	6p21.2-p21.1	178 Cases	BMI	0.03	(1009)
		179 Cases	BMI	0.04	(1009)
PPARG	3p25	414 Cases	BMI	0.039	(1010)
		921 Cases	Leptin, BMI, waist circumference (in Mexican Americans)	0.02	(1011)
		203 Subjects	BMI (Javanese non-diabetics)	0.0016	(1012)
		333 Cases	BMI (in the middle-aged)	0.03	(1012)
		973 Cases	BMI (in the elderly)	0.02	(1013)
		422 Cases	BMI	0.03	(1014)
		752 Cases	BML change (in obese men)	0.002	(1017)
		869 Cases	BML change (in lean men)	0.008	(1015)
		1954 Subjects	BMI over 15 years (whites of the CARDIA study)	0.01	(1016)
		1954 Subjects	Waist circumference over 15 years (whites of the CARDIA study)	0.01	(1016)
		1844 Subjects	BMI over 15 years (Blacks of the CARDIA study)	0.05	(1016)
		464 Cases	BML obesity	0.01	(1017)
		619 Cases	BMI	0.04	(1018)
		41 Cases	BMI	0.02	(1019)
		41 Cases	Fat mass	0.02	(1019)
		451 Cases	BMI (in overweight Blacks)	0.02	(1020)
		451 Cases	Waist-to-hip ratio (in overweight Blacks)	0.01	(1020)
		451 Cases	Waist circumference (in overweight Blacks)	0.004	(1020)
		1051 Subjects	BMI	0.012	(1021)
		1051 Subjects	Waist-to-hip ratio	0.001	(1021)
		1051 Subjects	Fat mass	0.003	(1021)
		1051 Subjects	Body fat (%)	0.025	(1021)
		228 Cases	Obesity, morbid	0.02	(1022)
		119 Cases	Weight, increase, 10-year	0.009	(1023)
		225 Cases	Weight, decrease, 3-year	0.04	(1024)
		140 Cases	BMI	0.05	(1025)
		838 Cases	BMI, body weight, waist circumference, height	0.002	(1026)
		1133 Subjects	BMI	0.036	(1027)
		820 Cases	Leptin (in obese subjects)	0.001	(1028)
		183 Cases	Lipid oxidation. 24-hour	0.03	(1029)
		183 Cases	Lipid balance, 24-hour	0.02	(1029)
		70 Cases	Weight, increase	0.01	(1030)
		100 Cases	BMI	0.0012	(1031)
		29 Subjects	Endurance training-induced weight loss (healthy offspring of type 2 diabetics)	0.05	(1032)
		311 Cases	Ponderal index at hirth	0.007	(1033)
		311 Cases	Body weight gain	0.007	(1033)
		121 Cases	RMI	0.001	(1033)
		714 Cases	BMI	0.03	(1034)
		596 Cases	Fat mass	0.04	(1035)
		685 Cases	La mass Waist circumfaranca	0.009	(1033)
		JOJ Cases	waist encumerence	0.05	(1055)

Gene	Location	Subjects	Phenotype	р	Reference
		501 Cases	Abdominal visceral fat	0.01	(1035)
		501 Cases	Abdominal subcutaneous fat	0.001	(1035)
		268 Cases	BMI	0.022	(1036)
		3080 Cases	BMI	0.037	(1037)
		3080 Cases	BMI	0.036	(1037)
		375 Cases	Obesity, severe, with early onset	0.05	(1038)
		141 Cases	BMI, body weight, fat mass, waist circumference, lean body mass, hip circumference	0.002	(1039)
PPARGC1/	A 4p15.31	467 Cases	Fat mass (in Austrian women)	0.005	(1040)
	- Prese	467 Cases	BMI (in Austrian women)	0.006	(1040)
		467 Cases	Waist circumference (in Austrian women)	0.01	(1040)
		467 Cases	Hip circumference (in Austrian women)	0.03	(1040)
		201 Cases	Adipocyte size (in Pima Indians)	0.04	(1041)
		165 Cases	Lipid oxidation, 24-hour (in Pima Indians)	0.03	(1041)
		165 Cases	Lipid balance, 24-hour (in Pima Indians)	0.004	(1041)
		156 Subjects	BMI	0.031	(1042)
PTPN1	20a13 1-a13 2	1553 Cases	BMI	0.0146	(1043)
1 11 101	20415.1 415.2	1553 Cases	BMI	0.0140	(1043)
		257 Cases	BMI	0.010	(1043)
DTDDE	1p34	580 Cases	BMI	0.03	(1045)
I II KI	1004	580 Cases	Waist sizeumfaranza	0.03	(1045)
DVV	17-21 1	100 Cases 67 controls 167	Source obesity (male Dime Indians)	0.01	(1043)
F I I	17421.1	men	Severe obesity (male Finia indians)	0.001	(964)
		6022 Subjects	Overweight	0.018	(1046)
RETN	19p13.2	777 Cases	Body weight	0.005	(1047)
		777 Cases	Waist circumference	0.001	(1047)
		777 Cases	BMI	0.019	(1047)
		773 Cases	Waist circumference	0.026	(1047)
		411 Cases	BMI, obesity	0.0097	(1048)
		814 Cases	BMI	0.01	(1049)
		814 Cases	Waist circumference	0.048	(1049)
		12 Cases	Overfeeding-induced increase in abdominal visceral fat	0.033	(1050)
		320 Subjects, 320 women	BMI (women with polycystic ovary syndrome)	0.02	(1051)
SAH	16p13.11	4059 Cases	BMI	0.0066	(1052)
SCARB1	12q24.31	288 Cases	BMI (in healthy lean women)	0.004	(1053)
		228 Cases	Obesity, morbid	0.002	(1022)
SERPINE1	7q21.3-q22	1098 Cases	Abdominal subcutaneous fat	0.0265	(1054)
		472 Women	BMI (women from the Quebec Family Study cohort)	0.009	(1055)
		505 Cases	Obesity	0.002	(1056)
SGK	6q23	263 Cases	BMI	0.008	(1057)
SLC6A14	Xq23-q24	1267 Cases	Obesity	0.0001	(1058)
	* *	1267 Cases	Obesity, eating behavior	0.013	(1058)
		299 Cases	Obesity	0.0002	(1059)
		1805 Cases	Obesity	0.003	(1059)
SLC6A3	5p15.33	90 Cases	Obesity (in black smokers)	0.006	(1060)
SORBS1	10q24.1	770 Cases	Obesity	0.05	(1061)
	1	114 Cases	BMI	0.008	(1005)
SREBF1	17p11.2	807 Cases	Obesity	0.038	(1062)
	.1	807 Cases	Obesity	0.006	(1062)
TCF1	12a24.31	203 Cases	BMI (in young early onset diabetics)	0.0024	(1063)
TGFB1	19a13.31	405 Cases	Lean mass	0.002	(804)
10121	19410101	284 Cases	BMI (in Swedish men)	0.05	(1064)
		284 Cases	Sagittal abdominal diameter (in Swedish men)	0.05	(1064)
тн	11n15 5	2734 Cases	Body weight	0.0014	(896)
TNF	6n21 3	176 Cases	BMI	0.0014	(1065)
T 1 41.	0421.0	170 Cases	BMI	0.01	(1066)
		157 Cases	Body fot (%)	0.01	(1066)
		159 Cases	Douy rat (70) Waist circumference	0.05	(1066)
		139 Cases	Waist airoumforence (in women)	0.03	(1000)
			waist circumference (in women) $\mathbf{D}_{\mathbf{r}} = f_{\mathbf{r}} f_{\mathbf{r}} f_{\mathbf{r}} (\mathbf{r}')$	0.04	(1067)
		38 Cases	BODY TAT (%)	0.02	(1068)

Gene	Location	Subjects	Phenotype	р	Reference
		1351 Cases	BMI	0.004	(1069)
		378 Cases	BMI, body fat (%) (in women)	0.02	(1070)
		1047 Cases	Obesity	0.04	(1071)
		363 Cases	BMI	0.01	(1072)
		110 Cases	Obesity	0.02	(1073)
TNFRSF1B	1p36.21	217 Cases	Leptin, BMI	0.05	(1074)
UBL5	19p13.3	396 Cases	Fat mass	0.026	(1075)
	1	396 Cases	Body fat (%)	0.001	(1075)
		396 Cases	Waist-to-hip ratio	0.034	(1075)
UCP1	4q28-q31	163 Cases	Body weight, decrease, BMI, decrease	0.05	(1076)
	1 1	526 Cases	BMI (in overweight women)	0.02	(1077)
		162 Cases	Waist-to-hip ratio	0.003	(1078)
		387 Subjects	Waist-to-hip ratio	0.008	(1079)
		387 Subjects	Body fat (%)	0.014	(1079)
		113 Cases	Body weight (in Japanese women)	0.001	(1080)
		99 Cases	Body weight, change (in pre-menopausal women)	0.048	(1081)
		22 Cases	High-fat meal-induced thermogenesis	0.01	(1082)
		123 Cases	Fat, increase (in high-weight gainers)	0.05	(1083)
		172 Subjects, 172 women	Obesity	0.002	(1084)
		24 Cases	Body weight, resting metabolic rate	0.05	(1085)
UCP2	11q13.3	60 Cases	Energy expenditure, 24-hour, spontaneous physical activity, 24-hour, sleeping spontaneous physical activity, respiratory quotient, 24-hour non-protein, fat ovidation 24 hour	0.005	(1086)
		220 Cases	BMI (in South Indian women)	0.02	(1087)
		701 Cases	BMI (III South Indian women)	0.02	(1087)
		506 Cases	Obesity	0.03	(1088)
		S90 Cases	Obesity	0.007	(1088)
		040 Cases	Obesity	0.002	(1089)
		147 Cases	Desting anargy expanditure	0.000	(1090)
		147 Cases	Chaose evidetion rate at rest	0.03	(1091)
		147 Cases	Linid evidetion rate at rest	0.02	(1091)
		147 Cases	Chasity	0.02	(1091)
		41 Cases	Body weight, increase, fat mass, increase (in peritoneal dialysis patients)	0.01	(1092) (1093)
		82 Cases	BMI, metabolic rate, 24-hour sleeping (in those >45 years old)	0.007	(1094)
		63 Cases	BMI	0.028	(1095)
		105 Cases	BMI, body fat (%), body weight, fat mass, overweight (%), skinfolds, sum of four	0.001	(1096)
UCP3	11q13	120 Cases	BMI, respiratory quotient, lean body mass, respiratory quotient, non-protein, fat oxidation (in African Americans)	0.008	(1097)
		116 Cases	Waist-to-hip ratio (in South Indian women, in European women)	0.03	(1098)
		722 Cases	Fat mass	0.004	(1099)
		722 Cases	Lean mass	0.013	(1099)
		722 Cases	BMI	0.023	(1099)
		722 Cases	Body fat (%)	0.049	(1099)
		419 Cases	BMI	0.004	(1100)
		73 Cases	Resting energy expenditure (in Black women)	0.01	(1101)
		734 Cases	Leptin, BMI, body fat (%), fat mass, skinfolds, sum of six	0.0005	(1102)
		393 Cases	Skinfolds, sum of eight	0.01	(1103)
		434 Cases	BMI	0.01	(1104)
		401 Cases	BMI (in morbidly obese subjects)	0.0037	(1105)
		382 Cases	Body weight, BMI, current, BMI, maximum	0.02	(1106)
		24 Cases	Body weight, resting metabolic rate	0.01	(1085)
		64 Cases	Leptin, body fat (%) (in women)	0.03	(806)
VDR	12q13.11	153 Cases	Fat mass	0.05	(1107)
		153 Cases	Body weight	0.05	(1107)

Gene	Location	Subjects	Phenotype	р	Reference
		588 Cases	BMI	0.009	(1108)
		302 Cases	BMI	0.01	(1109)
		302 Cases	Fat-free mass	0.002	(1109)
		260 Women	BMI	0.042	(1110)
		309 Cases	BMI (in early onset type 2 diabetics)	0.0058	(1111)

Negative Associations with Obesity-Related Phenotypes

In addition to the positive studies summarized above, we identified 92 studies dealing with 58 genes in which there was no evidence of associations between DNA sequence variations and obesity-related phenotypes. Among these studies, the most frequent ones were those pertaining to markers of *PPARG* (1012,1114-1126) (14 studies), ADIPOQ (1127-1130), ADRB3 (1084,1121,1131,1132), IL6 (1129,1133-1135) (four studies each), and ESR1 (1136-1138) (three studies). Other markers yielding negative findings were those related to ACE (710,1032), ACTN (1139), ADIPOR1 (1140), ADIPOR2 (1140), ADRB1 (1132), ADRB2 (1132), AGER (1141), AHSG (1142), APOA4 (1143), APOE (1144,1145), AR (1146), BDNF (1147), CASQ1 (1148), COL1A1 (1134), CRP (1149), ENPP1 (1150), FABP2 (1151), GNAS (1152), GNB3 (1152,1153), GPR40 (1154), H6PD (1155), HSD11B1 (1155,1156), ICAM1 (1157), IGF1 (1158), IL6R (1159), INS (1160,1161), KCNJ11 (1120), KL (1146), LEP (1129), LEPR (1162), LIPC (1163), LPL (1164), LTA (964), MKKS (1165), MT-DLOOP (1166), MTHFR (1167), MTTP (1168), NOS3 (1169,1170), NPY (1171), NR0B2 (1172), PARD6A (1173), PLIN (1174), PPARGC1A (1115,1175), PRDM2 (1176), PTPN1 (1177), SCD (1178), SELE (1179), TAS2R38 (1180), TNF (1181), UCP1 (1084), UCP2 (1182,1183), UCP3 (1182,1184), and VDR (1134,1185).

Drug-Induced BW Gain and Obesity

Unintentional weight gain and weight loss are potential side effects associated with several pharmacological therapies. In previous editions of the human obesity gene map, these studies were summarized within the association studies section. However, because the number of reports addressing the contribution of DNA sequence variation in specific candidate genes to the drug-induced weight changes has increased, these studies will be reviewed in a specific section from now on.

Drug-induced weight gain and obesity have been observed after insulin therapy in patients with type 1 or 2 diabetes; in psychiatric therapy using anti-psychotics, antidepressants, or mood stabilizers; in neurological treatments with anti-epileptic drugs; and in hypertension or steroid hormone therapies (for review, see 1186). Drug-induced weight changes could range from a loss of weight to a gain of >50 kg in patients on anti-epileptic, anti-depressant, or anti-psychotic medication (1186). Because modest weight losses of 5% to 10% of initial BW are clinically significant (1187), it is clear that even modest weight gain is an undesirable side-effect of drugs.

Response to anti-psychotic treatment is considered to be a complex trait in which many genes, each with a small effect, are expected to play a role (1188). Few genes have yet to be studied in relation to BW gain under anti-psychotics (Table 4). The functional -759C>T variant (1189) in the serotonin receptor 2C gene (HTR2C) was studied in Chinese anti-psychotic-naïve schizophrenic patients. Carriers of the -759T variant showed three times lower antipsychotic-induced weight gain than those not carrying the Tallele (886). This result was confirmed in anti-psychoticnaïve Chinese men (893) but not in a third sample of anti-psychotic-resistant Chinese (1190). However, in a group of anti-psychotic-resistant African-American, white, and Hispanic individuals, the association of the -759T variant with a smaller weight gain was confirmed recently (891), as in anti-psychotic-naïve whites (892). In contrast, Basile et al. (889) reported that carriers of the -759T allele gained more weight than non-carriers in a mixed population of anti-psychotic-resistant white and African-American patients. A Cys23Ser variant of the HTR2C locus showed no association with BW gain in clozapine-treated anti-psychotic-naïve or resistant schizophrenics of white or African American descent (1191-1193).

A significant effect of the cytochrome P450, subfamily IID, polypeptide 6 (CYP2D6) genotypes on the percentage change of BMI was reported in white men taking olanzapine and carrying the poor *4 and intermediate *1/*3 metabolizer genotypes (827,1194). On the other hand, no association with BW changes in African Americans and whites taking clozapine was observed with a dinucleotide repeat polymorphism of the cytochrome P450 subfamily I, polypeptide 2 (CYP1A2) gene (1191). Chinese anti-psychotic-naïve schizophrenic homozygotes for the A allele of the -2548A>G polymorphism of the LEP gene showed higher changes in BW than patients carrying A/G and G/G genotypes (933). An opposite result was observed in antipsychotic-naïve whites showing a higher BMI change in homozygotes for the G allele (892). In two recent studies on Chinese schizophrenic patients treated with clozapine, the

G/G homozygotes of the -1291C>G variant of the adrenergic $\alpha 2A$ receptor (ADRA2A) locus showed a 3 times greater weight gain than the C/C genotype (732). Furthermore, a 2 to 3 times greater weight gain was reported in the TT genotype of the GNB3 825C>T variant in contrast to carriers of the C allele (1195). Negative results were reported previously for these two genes (1191,1196). Finally, 12 genes showed negative results with anti-psychotic-induced weight changes. Those were the tumor necrosis factor α (1191), the seroton in 1A and 2A receptors, the histamine H1 and H2 receptors, the β 3 and α 1a-adrenergic receptors (1191,1192,1196,1197), the serotonin transporter and the serotonin receptor 6 (1192), the dopamine receptor 4 (1198), the cytochrome P450 1A2 (CYP1A2), which is different from the CYP2D6 that had shown some association, and the 25-kDa synaptosomal-associated protein (1199).

Treatment with lithium has long been recognized to be associated with adverse metabolic effects, notably weight gain (1200). No evidence for an association has been observed between two polymorphisms (+35A>G in intron 3 and +7T>G in intron 10) in the α subunit of the olfactory G-protein G_{olf} gene and weight gain in response to lithium treatment (1201). The combination of glitazones with insulin may favor weight gain due to enhanced adipogenesis. Patients with the PPARG Pro12Ala genotype show a better response to rosiglitazone treatment than those with the Pro12Pro genotype do, with no difference in weight or BMI (1202).

Human QTLs

Linkage Studies

Linkage studies with obesity-related phenotypes are summarized in Table 5. During the past year, 11 linkage studies were published: nine genome scans, one bivariate linkage analysis of metabolic syndrome phenotypes with markers on chromosome 7q (1203), and a meta-analysis of genomewide linkage studies for BMI (1204).

Two genome scans for eating-related phenotypes were reported last year. The first was a genome scan for total caloric and macronutrient intakes assessed from a food frequency questionnaire in 816 subjects from the San Antonio Family Heart Study (1235). Evidence of linkage was found on chromosome 2p22-p21 near marker D2S1346 for total caloric intake and intakes of fat, saturated fat, and protein (LOD scores ranging from 2.09 to 2.62). The second was a genome scan of eating behaviors assessed from the Three-Factor Eating questionnaire in 660 subjects from the Quebec Family Study (978). Evidence of linkage was found on chromosomes 15q21-q23 (LIPC), 15q24-q25 (D15S206), and 17q22-q24 (D17S1306, D17S1290, D17S1351) for susceptibility to hunger and on chromosome 19p13 (D19S215) for disinhibition.

A genome-wide linkage analysis of obesity associated with the use of anti-psychotics in patients treated for psychoses was performed in 508 subjects from 21 multigenerational kindreds (1258). Obesity diagnosed from medical files was found to be 2.5 times more prevalent in patients treated with anti-psychotics than in untreated family members. Linkage with obesity and a set of 470 microsatellite markers was tested only in pedigrees with at least two occurrences of obesity. Evidence of linkage with obesity was found on chromosomes 6p23 (D6S260; LOD = 1.72), 8q22-q23 (D8S1136; LOD = 1.93), 9q34 (D9S282; LOD = 1.71), and 12q23.1-q24.23 (D12S1279-D12S366; LOD = 2.74).

Four genome scans reporting linkages with BMI and body fatness phenotype were published during the past year. In a study performed in West African families with type 2 diabetes (1236), linkage analysis of BMI and body composition assessed by bioelectric impedance revealed evidence of three QTLs affecting body fatness chromosomes 2p16p13.3 (D2S2739-D2S441), 4q24 (D4S1647-D4S2623), and 5q14.3 (D5S1725). All linkages with BMI showed LOD scores below 1.7 (1236). A second genome scan for loci linked to BMI and percentage body fat assessed from bioelectric impedance was conducted in 3383 subjects from 1124 hypertensive African-American and white families (1227). Linkage to BMI and percentage body fat was tested separately in men and women and also in the combined sample. In the combined sample, evidence of linkage was found on chromosome 3q13.33 for BMI (LOD = 2.8) and on chromosome 12q24.3 for percentage body fat (LOD = 3.3). QTLs influencing both BMI and percentage body fat were found over a broad region [102 to 200 centimorgans (cM)] on chromosome 3 in men (3p12.2, 3q13.33, 3q26.33, and 3q27.3). Evidence of linkage with percentage body fat was also found on chromosomes 7q36.1 (LOD = 1.8), 15q25.3 (LOD = 3.0), and 18p11.22-p11.23 (LOD = 1.7) in men. In women, QTLs affecting percentage body fat were found on chromosomes 2p24.2 (LOD = 1.8), 12q24-q24.32(LOD = 3.8), and 21q21.2 (LOD = 1.8), whereas linkage with BMI was found on chromosome 11p13 (LOD = 1.8). The third study was undertaken in a European-American sample of 1297 subjects from 260 families with the aim of detecting imprinted genetic loci influencing obesity-related traits (1224). Parent-specific linkage analyses of overweight $(BMI \ge 27)$, obesity $(BMI \ge 30)$, and obesity-related quantitative traits [BMI, percentage body fat, and waist circumference (WC)] were performed with 391 microsatellite markers. Several QTLs influencing obesity were uncovered: a paternal effect for BMI and WC on 2p25.1, a maternal effect for percentage body fat on 3p24, a paternal effect for BMI on 3q12.3, a maternal effect for obesity on 9q22.33, a maternal effect for overweight on 10p12.2, a paternal effect for percentage body fat on 11q12 and 11q13.3, a maternal effect for BMI and WC on 12q24.21, a maternal effect for overweight on 13q13.3, and a paternal effect for BMI and WC on 13q31.3. The fourth scan was

Cono/monkon	Location	Dopulation	Dhanatymas	Saana	Doforonco
Gene/marker	Location	ropulation	r nenotypes	Score	Kelefence
D1S468	1p36.32	1249 sibpairs, >10,000 relative pairs	BMI	LOD = 2.75	(1205)
		758 subjects, 53 pedigrees	BMI	LOD = 2.32	(1206)
		994 subjects, 37 pedigrees	BMI	LOD = 2.5	(1207)
D1S508	1p36.23-p36.22	994 subjects, 37 pedigrees	BMI	LOD = 2.2	(1207)
PGD	1p36.22	>168 pairs	Skinfolds, suprailiac	p = 0.03	(1208)
D1S552	1p36.13	893 sibpairs	BMI (in whites)	LOD = 2.03	(1209)
ATCT051	1p36	320 subjects, 154 families	BMI	MLS = 2.14	(1210)
D1S3721	1n34.1	157 subjects 7 families	BMI (in whites)	p = 0.0099	(1211)
D1S193	1p34.1	202 to 251 pairs, 137 sibships of adult brothers and sisters	BMI	p = 0.03	(1212)
D1\$197	1p33	202 to 251 pairs, 137 sibships of adult brothers and sisters	Insulin level, fasting	p = 0.05	(1212)
D1S200	1p32.2	202 to 251 pairs, 137 sibships of adult brothers and sisters	Fat mass BMI	p = 0.009 p = 0.04	(1212)
D1S476	1p32.2	202 to 251 pairs, 137 sibships of	Insulin level, integrated, after oral glucose	p = 0.02	(1212)
		adult brothers and sisters	DMI		
			BMI	p = 0.03	
			Fat mass	p = 0.02	
			Skinfolds, sum of six	p = 0.02	
LEPR-IVS16CTTT	1p31.2	268 to 324 pairs	Fat-free mass	p = 0.007	(935)
			Fat mass	p = 0.03	
LEPR-IVS3CA	1p31.2	268 to 324 pairs	BMI	p = 0.04	(935)
			Fat mass	p = 0.04	
			Skinfolds, sum of six	p = 0.02	
			Fat-free mass	p = 0.05	
LEPR-0223R	1n31.2	268 to 324 pairs	Fat mass	p = 0.005	(935)
	100112	200 to 221 pairs	BMI	p = 0.020	(200)
			Skinfolds sum of six	p = 0.02 n = 0.04	
				p = 0.04	
D101//5	1 01 1	100 11 10 1	Fat-free mass	p = 0.05	(1010)
D181665	1p31.1	198 subjects, 18 pedigrees	Leptin	LOD = 3.4	(1213)
D18550	1p31.1	236 pairs	Respiratory quotient, 24-hour (in Pima Indians)	LOD = 2.8	(1214)
D1S2737	1p31.1	342 families	Trends in BMI from childhood to adulthood	LOD = 2.2	(1215)
LEPR	1p31	302 subjects, 57 families, 545 sibpairs	Blood glucose, fasting (in Mexican Americans) Blood pressure diastolic (in Mexican	p = 0.018 p = 0.003	(1216)
5161/01		514 II - 00 0 II - 015	Americans)	p 0.000	(1017)
D1\$1631	1p21.2	514 subjects, 99 families, 347	Total energy intake	p = 0.0002	(1217)
		sibships	Carbohydrate intake	p = 0.0026	
			Fat intake	$p = 2^{e-05}$	
AMPD1	1p13.2	514 subjects, 99 families, 347 sibships	Total energy intake Fat intake	p = 0.0005 $p = 6^{e-05}$	(1217)
D1S2726	1p12	342 families	Trends in BMI from childhood to adulthood	LOD = 2.5	(1215)
D1S534	1p11.2	769 subjects, 182 families	BMI (in Africans)	LOD = 2.24	(1218)
	I	514 subjects, 99 families, 347	Total energy intake	p = 0.0008	(1217)
		sibships	Fat intake	p = 0.00038	
		521 subjects 156 families	Abdominal subcutaneous fat	I OD = 2.3	(1219)
S100A1	1q21	514 subjects, 99 families, 347 sibships	Fat intake	p = 0.001	(1217)
D1S1679	1q21–1q22	3027 subjects, 401 families, 317 sibships	BMI (National Heart, Lung, and Blood Institute Family Heart Study)	LOD = 1.8	(1220)
D1S394	1q21.1	514 subjects, 99 families, 347 sibships	Fat intake	p = 0.00081	(1217)
ATP1A2	1q23.1	582 subjects, 171 families, 289 pairs	Respiratory quotient	p = 0.02	(812)
		295 subjects, 164 families	Adipocyte size	LOD = 1.7	(1221)
D1S194-D1S196	1q23.1-q23.2	897 subjects, 179 families, 2127 relative pairs	Waist circumference	MLS = 3.71	(1222)
ATP1B1	1q23.3	94 pairs	Respiratory quotient	p = 0.04	(811)

Table 5. Evidence for the presence of linkage with obesity-related phenotypes

Table	5.	(continued)
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Gene/marker	Location	Population	Phenotypes	Score	Reference
D1S222	1q31.1	514 dubjects, 99 families, 347	Fat intake	p = 0.0002	(1217)
D1S456	1q32.1	313 subjects, 126 families, 99 sibships	Protein intake (%) (in Blacks)	p = 0.0021	(1217)
D1S517	1q43	313 subjects, 126 families, 99 sibships	Sucrose intake (in Blacks)	p = 0.0018	(1217)
D1S204	1q44	313 subjects, 126 families, 99 sibships	Sucrose intake (in Blacks)	p = 0.0054	(1217)
D2S2976	2p25.3	2086 subjects, 330 pedigrees	Waist circumference	LOD = 2.06	(1223)
D2S2952	2p25.1	1297 subjects, 260 families	Waist circumference, paternal	LOD = 2	(1224)
D2S1400	2p25.1	1297 subjects, 260 families	BMI, paternal	LOD = 2.45	(1224)
ACP1	2p25	300 pairs	BMI	p = 0.004	(1225)
		>168 pairs	Skinfolds, triceps	p = 0.02	(1208)
D2S1360	2p24.2	1297 subjects, 260 families	BMI	LOD = 1.7	(1226)
	r	3383 subjects, 1124 families	Body fat (%) (women)	LOD = 1.8	(1227)
D2S2337	2p24.1	264 sibpairs	Leptin (in French whites)	LOD = 2	(1228)
D2S165	2p23.3	1100 subjects, 170 families	Adiponectin (in Northern Europeans)	LOD = 2.7	(1229)
	-r	264 pairs	Leptin	LOD = 2.4	(1230)
D2S367	2p23.1	1100 subjects, 170 families	Adiponectin (in Northern Europeans)	LOD = 2.7	(1229)
525007	-p=011	264 pairs	Leptin	LOD = 2.7	(1230)
D2S1788	2n22 3	5000 relative pairs	Leptin	LOD = 4.9	(1231)
D201700	2922.0	sooo lelaite pails	Fat mass	LOD = 2.8	(1231)
		337 subjects	Lentin	LOD = 7.5	(1003)
		1778 sibshins	BMI	n = 0.0006	(1232)
		349 subjects 66 pedigrees	BMI (in whites)	p = 0.0000 LOD = 3.08	(1232)
		720 subjects, 230 families	Lentin	n = 0.008	(1233)
		720 subjects, 250 families	BMI	p = 0.008 n = 0.008	(1254)
D2\$1346	$2n22_{-}n21$	816 subjects 12 families	Total energy intake	p = 0.008	(1235)
D251540	2p22-p21	oro subjects, 42 fammes	Protein intake	LOD = 2 LOD = 2.22	(1255)
			Fat intake	LOD = 2.22 LOD = 2.00	
			Saturated fat intake	LOD = 2.07 LOD = 2.62	
D2\$1356	$2n22_{-}n21$	1778 sibships	BMI	n = 0.0004	(1232)
D2S1350	2p22-p21 2p16-3	1778 sibships	BMI	p = 0.0004 p = 0.0004	(1232)
D2S1732	2p10.5 2p16	321 relative pairs	Body fat $(\%)$	p = 0.0004	(1232)
D2S2730 D2S441	2p10 2p16 $2p13$ 3	321 relative pairs	Eat mass	LOD = 3.5	(1236)
D2S441	2p10-2p13.3	453 subjects 00 families	Abdominal subcutaneous fat	LOD = 2.30 LOD = 1.88	(1230)
IGKC	2p15.5 2p11.2	>168 pairs	Skinfolds, tricens	LOD = 1.00 n = 0.03	(1237) (1208)
D2S293-D2S383	2q12.2-2q14.3	430 subjects, 27 sibpairs, 27	BMI	p = 0.03 LOD = 2.9	(1208)
D2S160	2q13	1249 sibpairs, >10,000 relative	BMI	LOD = 2.56	(1205)
D20410	2-14.1	pairs	Waint simon frances	LOD = 2	(1002)
D25410 D25247	2q14.1	2080 subjects, 550 pedigrees	DMI	LOD = 2	(1223)
D23347	2414.5	1249 slopans, >10,000 relative	Divit Dody fot (%)	LOD = 4.04	(1203)
		pans	Fot mass	LOD = 1.91	
		759 subjects 52 padigroop	Fat mass	LOD = 2.03 LOD = 2.42	(1206)
D201224	2-21.2	452 subjects, 55 pedigrees	DIVII Abdominal viaconal fat	LOD = 3.42	(1200)
D251554	2421.5	453 subjects, 99 families	Abdominal visceral fat	LOD = 1.97	(1257)
D251399	2q23.3	455 subjects, 99 families	Addominal visceral fat $\mathbf{PMI} > 00$ th mercentile	LOD = 2.3	(1237)
D25112-D25390	2q35.2-2q36.5	506 subjects, 115 pedigrees	BMI $> 991n$ percentile	LOD = 2.73	(1239)
D20424	0.25	452 1 4 00 6 11	Bivit > 97th percentile	LOD = 2.08	(1007)
D25434	2q35	453 subjects, 99 families	Abdominal Visceral fat	LOD = 2.5	(1237)
D2S1363-D2S1279	2q35-2q36.3	2467 subjects, 387 families	BMI	LOD = 2.4	(1240)
			waist-to-nip ratio	LOD = 1.72	
D202207	2.06.2		Subscapular skinfold	LOD = 2.55	(1210)
D382387	3p26.3	320 subjects, 154 families	BMI	MLS = 3.67	(1210)
Dagiaso		215 subjects, 105 families	Abdominal subcutaneous fat	LOD = 2.16	(1237)
D3S1259	3p25.2	1055 pairs	BMI	LOD = 2	(1241)
D3S3608	3p25.2	624 subjects, 28 families	Eating behavior, restraint (in Old Order Amish)	LOD = 2.5	(1242)
D3S2403	3p24	1297 subjects, 260 families	Body fat (%), maternal	LOD = 2.2	(1224)

Gene/marker	Location	Population	Phenotypes	Score	Reference
D3S3038	3p24.3	893 sibpairs	BMI, paternal effect (in whites)	p = 0.0065, LOD = 1.77	(1209)
D3S2432	3p22.3	377 pairs	Body fat (%) (in Pima Indians)	LOD = 2	(1243)
D3S1768	3p22.2	580 families	BMI	LOD = 3.4	(1244)
Chr3p-region	3p14	1848 subjects, 279 pedigrees	BMI	LOD = 1.9	(1245)
	• • • •		BMI and systolic blood pressure	LOD = 2.13	()
			BMI and diastolic blood pressure	LOD = 2.36	
D3\$2406	3n12 2	3383 subjects 1124 families	BMI (men)	LOD = 2	(1227)
D3S2400	3a12.2	1207 subjects, 260 families	BMI paternal	LOD = 3.66	(1227)
D333043	5412.5	1297 subjects, 260 families	DMI > 20	LOD = 5.00 NDI = 1.99	(1224)
			$\text{DIVII} \ge 30$	NPL = 1.00	(1240)
		1297 subjects, 260 families	$BMI \ge 30$	NPL = 1.88	(1226)
Chr3q-region	3q13.3	1848 subjects, 279 pedigrees	BMI and systolic blood pressure and diastolic blood pressure (trivariate)	LOD = 2.59	(1245)
ATA28H11	3q13.33	3383 subjects, 1124 families	BMI (men)	LOD = 2.3	(1227)
	*		Body fat (%) (men)	LOD = 2.6	
			BMI (men and women)	LOD = 2.8	
D3S1764	3a22.1	596 subjects, 158 families	Factor central obesity	MLS = 2.61	(1247)
	- 1	1055 pairs	BMI	IOD = 34	(1241)
D3S1744	3a23	1778 sibships	BMI	n = 0.0009	(1232)
D3S3053	3925	1778 sibships	BMI	p = 0.0005 p = 0.0015	(1232)
D333033	2~26.22	2200 subjects 507 femilies	DMI	p = 0.0013	(1232)
D552427	5420.55	2209 subjects, 507 families		LOD = 3.5	(1246)
			waist circumference	LOD = 2.4	(1007)
		3383 subjects, 1124 families	BMI (men)	LOD = 1.7	(1227)
		545 subjects, 128 families	BMI (in African Americans)	LOD = 4.3	(1249)
		1055 pairs	BMI	LOD = 3.4	(1241)
		618 subjects, 202 families	BMI	LOD = 1.8	(1250)
D3S3676	3q26.33	545 subjects, 128 families	BMI (in African Americans)	LOD = 4.3	(1249)
D3S1262	3q27.3	3383 subjects, 1124 families	Body fat (%) (men)	LOD = 2.4	(1227)
D3S1311	3q29	215 subjects, 105 families	Abdominal subcutaneous fat	LOD = 2.5	(1237)
D4S912	4p16.1	430 subjects, 27 sibpairs, 27 pedigrees	BMI	LOD = 4.5	(1238)
D4S2639	4p15.32	994 subjects, 37 pedigrees	BMI	LOD = 2.2	(1207)
D4S2289	4n15.31	994 subjects 37 pedigrees	BMI	LOD = 2.6	(1207)
D4S2397	4n15.2	521 subjects 156 families	Abdominal subcutaneous fat	LOD = 2.4	(1219)
D4\$3350	4p15.1	994 subjects 37 pedigrees	BMI	IOD = 9.2	(1207)
D453530	4p15.1	994 subjects, 37 pedigrees	BMI	MIS = 6.1	(1207)
D452032	4p13.1	004 subjects, 37 pedigrees	BMI	I OD = 3.4	(1207)
D451027	4p15 4a12	004 subjects, 37 pedigrees	DMI	LOD = 3.4	(1207)
D453019	4412	1240 sibration $> 10,000$ relation	DMI	LOD = 2.1	(1207)
D481592	4q12	pairs pairs	BMI	LOD = 2.29	(1205)
D4S3248	4q13.1	994 subjects, 37 pedigrees	BMI	LOD = 2	(1207)
D4S1647	4q24	59 pedigrees, 277 sibships	BMI	LOD = 2.63	(1251)
D4S1647-D4S2623	4q24-4q25	321 sibpairs	Body fat (%)	LOD = 2.39	(1236)
D4S1644	4q28.3	1297 subjects, 260 families	BMI	LOD = 1.71	(1226)
	1	1297 subjects, 260 families	BMI	LOD = 1.71	(1246)
D4S2417	4q31.1	893 sibpairs	BMI, paternal effect (in whites)	p = 0.005, I OD = 1.84	(1209)
		521 subjects 156 families	Abdominal subcutaneous fat	IOD = 1.8	(1219)
GVDA	4a31.1	160 pairs	Skinfolds, trunk to extremity ratio	LOD = 1.0 n = 0.02	(1217)
D481620	4431.1	202 sibrairs	DML motornal affact (in whitea)	p = 0.02	(1232)
D431629	4q32.1	893 siopairs	BMI, maternal effect (in whites)	p = 0.005, LOD = 1.89	(1209)
D4S406	4q34.1	447 subjects, 109 pedigrees	BMI > 35	LOD = 2.55	(1253)
D4S2431	4q34.1	215 subjects, 105 families	Abdominal subcutaneous fat	LOD = 2.3	(1237)
D5S817	5p15.2	1100 subjects, 170 families	Adiponectin (in Northern Europeans)	LOD = 4.1	(1229)
	I.	618 subjects, 202 families	BMI	LOD = 1.9	(1250)
D5S426	5p13.3	264 pairs	Leptin	LOD = 2.9	(1230)
D5S2489	5n13 2	1526 pairs	BMI (in Pima Indians)	LOD = 1.7	(1250)
ISL1	5a11.2	226 pairs	Obesity	n = 0.03	(1257)
1,521	5911.2		Lentin	p = 0.0004	(1200)
			DMI	p = 0.0004	
			DIVII	p = 0.0004	

Gene/marker	Location	Population	Phenotypes	Score	Reference
D5S407	5q11.2	1249 sibpairs, >10,000 relative	Fat-free mass	LOD = 1.59	(1205)
D5S2500	5q12.1	1526 pairs	BMI (in Pima Indians)	LOD = 1.7	(1254)
D5S1725	5q14.3	321 sibpairs	Fat mass	LOD = 2.25	(1236)
	1	1	Body fat (%)	LOD = 2.56	
D5S1463	5a14.3	447 subjects, 109 pedigrees	BMI > 27	LOD = 2.68	(1253)
D5S1453	5q21.3	342 families	Trends in BMI from childhood to adulthood	LOD = 2	(1215)
D5S1505	5q23.1	342 families	Long-term burden in BMI	LOD = 2.2	(1215)
D5S658	5q31.3	453 subjects, 99 families	Abdominal subcutaneous fat	LOD = 2.06	(1237)
	1	5	Abdominal total fat	LOD = 1.84	
NR3C1	5q31	88 pairs	BMI	p = 0.009	(1256)
D5S1480	5q32	453 subjects, 99 families	Abdominal total fat	LOD = 2.1	(1237)
D5S820-D5S1456	5q33.2-5q35.1	729 subjects, 275 families	Abdominal subcutaneous fat	MLS = 2.64	(1210)
D5S1471	5q35.1	893 sibpairs	BMI (in whites)	p = 0.0006,	(1209)
	1	*		LOD = 2.48	· · · ·
D5S211	5q35.2	3027 subjects, 401 families, 317 sibships	BMI (National Heart, Lung, and Blood Institute Family Heart Study)	LOD = 1.8	(1220)
		2072 subjects, 407 families	Factor central obesity	MLS = 1.87	(1247)
D5S408	5q35.3	157 subjects, 7 families	BMI (in whites)	p = 0.0039	(1211)
SE30	6p25.1	803 subjects, 192 families	BMI	LOD = 2.13	(1257)
	-	596 subjects, 158 families	Factor central obesity	MLS = 2.07	(1247)
D6S2434	6p23	596 subjects, 158 families	Factor central obesity	MLS = 1.94	(1247)
D6S260	6p23	508 subjects, 21 families	Obesity under anti-psychotics	LOD = 1.72	(1258)
D6S1959	6p22.3-p22.2	618 subjects, 202 families	Body fat (%)	LOD = 2.7	(1250)
D6S276	6p22.1	624 subjects, 28 families	Eating behavior, restraint (in Old Order Amish)	LOD = 2.3	(1242)
BF	6p21.31	>168 pairs	Skinfolds, subscapular Skinfolds, triceps	p = 0.01 p = 0.01	(1208)
			Skinfolds, suprailiac	p = 0.01	
GLO1	6p21.3-p21.1	>168 pairs	Body weight	p = 0.004	(1259)
			Skinfolds, suprailiac	p = 0.004	
TNF	6p21.3	>255 pairs, 304 sibpairs	Body fat (%) (in Pima Indians)	p = 0.002	(1072)
D6S271	6p21.1	1199 pairs	Leptin	LOD = 2.1	(1260)
D6S462	6q22.31	447 subjects, 109 pedigrees	BMI > 35	LOD = 2.49	(1253)
D6S462-D6S441	6q22.31-6q23.2	506 subjects, 115 pedigrees	BMI > 97th percentile	LOD = 3.27	(1239)
			BMI > 95th percentile	LOD = 3.13	
D6S1009	6q23.3	2086 subjects, 330 pedigrees	Waist circumference	LOD = 3.3	(1223)
		330 pedigrees, 1702 sibships	BMI	LOD = 2.79	(1261)
D6S403	6q23.3	261 subjects, 27 pedigrees	(BMI, leptin, fasting specific insulin) (in Mexican Americans)	LOD = 4.2	(1262)
D6S1003	6q24.1	261 subjects, 27 pedigrees	(BMI, leptin, fasting specific insulin) (in Mexican Americans)	LOD = 4.2	(1262)
D6S264	6q27	261 subjects, 27 pedigrees	(Systolic blood pressure, diastolic blood pressure) (in Mexican Americans)	LOD = 4.9	(1262)
D6S281	6q27	1249 sibpairs, >10,000 relative	BMI	LOD = 1.77	(1205)
		pairs	Fat mass	LOD = 2.02	
D7S2477	7p22.3	349 subjects, 66 pedigrees	BMI (in whites)	LOD = 2.53	(1233)
D7S1819	7p22.2	349 subjects, 66 pedigrees	BMI (in whites)	LOD = 2.53	(1233)
D7S2557	7p21.2	342 families	Long-term burden in BMI	LOD = 2.9	(1215)
D7S3051	7p21.1	1055 pairs	BMI	LOD = 2.7	(1241)
D7S1802	7p15.3	803 subjects, 192 families	BMI	LOD = 2.4	(1257)
NPY	7p15.1	302 subjects, 57 families, 545	Obesity (in Mexican Americans)	p = 0.042	(1216)
		sibpairs	Body weight (in Mexican Americans)	p = 0.02	
			Abdominal circumference (in Mexican Americans)	p = 0.031	
			Hip circumference (in Mexican Americans)	p = 0.012	
			Diastolic blood pressure (in Mexican Americans)	p = 0.005	
			Body mass, body size (in Mexican	p = 0.048	

Gene/marker	Location	Population	Phenotypes	Score	Reference
D7S1808	7p15.1	336 sibpairs, 609 relative pairs	Fat-free mass	LOD = 2.72	(1263)
D7S817	7p14.3	769 subjects, 182 families	BMI (in Africans)	LOD = 3.83	(1218)
D7S484	7p14.2	342 families	Long-term burden in BMI	LOD = 2.4	(1215)
D7S1818	7p12.3	342 families	Trends in BMI from childhood to adulthood	LOD = 2.2	(1215)
D7S506-D7S653	7p11.2-7q11.22	430 subjects, 27 sibpairs, 27 pedigrees	BMI	LOD = 1.9	(1238)
D7S3046	7q11.22	514 subjects, 99 families, 347 sibships	Protein intake (%)	p = 0.0012	(1217)
D7S653	7q11.22	440 subjects, 27 families	Bivariate BMI: high-density lipoprotein	MLS = 3.86	(1203)
			Bivariate BMI: triglycerides	MLS = 4.21	
			Bivariate waist circumference: high-density lipoprotein	MLS = 3.47	
			Bivariate waist circumference: triglycerides	MLS = 3.74	
			Bivariate BMI: insulin	MLS = 2.44	
			Bivariate waist circumference: insulin	MLS = 1.86	
			Bivariate BMI: waist circumference	MLS = 2.98	
D7S653-D7S479	7q11.22-7q22.1	440 subjects, 27 families	BMI	MLS = 2.4	(1203)
			Waist circumference	MLS = 2	
D7S821	7q21.3	1297 subjects, 260 families	$BMI \ge 35$	NPL = 1.93	(1226)
D7S479	7q22.1	261 subjects, 27 pedigrees	High-density lipoprotein, in triglycerides (in Mexican Americans)	LOD = 3.2	(1262)
D7S1799	7q22.1	1297 subjects, 260 families	$BMI \ge 35$	NPL = 2.25	(1226)
	1	1297 subjects, 260 families	BMI > 27	NPL = 2.52	(1246)
			BMI > 30	NPL = 2.04	()
			BMI > 35	NPL = 2.25	
D7S692	7q22.3	1020 subjects, 200 families	BMI (in whites)	p = 0.0002, LOD = 2.75	(1264)
D7S523	7q31.1	1020 subjects, 200 families	BMI (in whites)	p = 0.0009, LOD = 2.11	(1264)
D7S471	7q31.1	261 subjects, 27 pedigrees	High-density lipoprotein, in triglycerides (in Mexican Americans)	LOD = 2.11 $LOD = 3.2$	(1262)
LEP	7q31.3	302 subjects, 57 families, 545	Waist-to-hip ratio (in Mexican Americans)	p = 0.01	(1216)
		sibpairs	Cholesterol, total (in Mexican Americans)	p = 0.03	
			Cholesterol, high-density lipoprotein (in Mexican Americans)	p = 0.026	
		47 pairs, 47 healthy female/female dizygotic twins	body fat	p = 0.008	(1265)
D7S2847	7q31.31	1055 pairs	BMI	LOD = 2.4	(1241)
D7S680	7q32.2	60 pairs	BMI	p = 0.002	(1266)
D7S514	7q32.2	60 pairs	BMI	p = 0.002	(1266)
	1	545 pairs	BMI (in Mexican Americans)	p = 0.0001	(1267)
		1	Skinfolds, extremity (in Mexican Americans)	p = 0.0001	
			Waist circumference (in Mexican Americans)	p = 0.0001	
			Fat mass (in Mexican Americans)	p = 0.0001	
D7S504	7q32.2	46 pairs, 103 affected sibpairs	BMI (in African Americans)	p = 0.001	(1268)
	1	78 families, 59 pairs	BMI	p = 0.04	(1269)
D7S1875	7q32.2	302 subjects, 57 families, 545 sibpairs	Waist-to-hip ratio (in Mexican Americans)	p = 0.009	(1216)
		521 subjects, 156 families	Abdominal subcutaneous fat	LOD = 2	(1219)
		88 trios (index probands and both parents)	BMI (in German children and adolescents)	p = 0.04	(1270)
D7S530	7q32.3	60 pairs	BMI	p = 0.002	(1266)
D7S1804	7q32.3	3027 subjects, 401 families, 317 sibships	BMI (National Heart, Lung, and Blood Institute Family Heart Study)	MLS = 4.9, p < 0.00001	(1220)
D7S640	7q33	672 subjects, 28 pedigrees	Leptin (in Old Order Amish)	LOD = 1.9 adjusted for	(1271)
D7S495	7q34	545 pairs	BMI (in Mexican Americans) Skinfolds, extremity (in Mexican Americans)	p = 0.0001 p = 0.0001	(1267)

Gene/marker	Location	Population	Phenotypes	Score	Reference
			Fat mass (in Mexican Americans) Waist circumference (in Mexican Americans)	p = 0.0001 p = 0.0001	
D7S1824	7q34	157 subjects, 7 families	BMI (in whites)	p = 0.0008	(1211)
KEL	7q35	160 pairs	BMI	p = 0.0001	(1252)
	1. 1.	Ī	Skinfolds, sum of six	p = 0.0001	
D7S2195	7a35	157 subjects, 7 families	BMI (in whites)	p = 0.001	(1211)
D7S3068	7q35	157 subjects, 7 families	BMI (in whites)	p = 0.004	(1211)
D7S636	7q36.1	672 subjects, 28 pedigrees	Leptin (in Old Order Amish)	LOD = 1.9 adjusted for BMI	(1271)
D7S3070	7q36.1	3383 subjects, 1124 families	Body fat (%) (men)	LOD = 1.8	1227)
		215 subjects, 105 families	Abdominal total fat training response	LOD = 2.5	(1237)
Chromosome 8 region	8pter-p23.3	2814 subjects, 505 families	BMI	$p = 4.6^{e^{-05}}$	(1204)
D8S264	8p23.3	2072 subjects, 407 families	Factor central obesity	MLS = 1.92	(1247)
D8S277	8p23.1	893 sibpairs	BMI, paternal effect (in whites)	p = 0.003, LOD = 1.98	(1209)
GATA151F02	8p22	769 subjects, 182 families	BMI (in Africans)	LOD = 2.34	(1218)
D8S549	8p22	1249 sibpairs, >10,000 relative pairs	Fat mass	LOD = 1.95	(1205)
D8S282	8p21.3	994 subjects, 37 pedigrees	BMI	LOD = 2	(1207)
D8S1121	8p11.23	470 subjects, 10 families	BMI	p = 0.0001, MLS = 3.21	(1272)
D8S1110	8q11.22	5000 sibpairs	Leptin	LOD = 2.2	(1231)
D8S1110-D8S1113	8q11.22-8q12.1	729 subjects, 275 families	Abdominal subcutaneous fat	MLS = 2.24	(1210)
D8S1113	8q12.1	893 sibpairs	BMI (in whites)	p = 0.0013, LOD = 2.05	(1209)
D8S2324	8q13.3	1297 subjects, 260 families	$BMI \ge 35$ $BMI \ge 35$	NPL = 1.9 $NPL = 1.9$	(1226)
GATA8B01	8a21 3	59 pedigrees 277 sibships	BMI = 55 BMI	IOD = 2.56	(1240) (1251)
D8\$1136	8q21.5 8q22.3	508 subjects 21 families	Obesity	MIS = 1.93	(1251)
D8S556	8q23.1	500 subjects, 21 families 522 subjects, 99 families, 364 sibnairs	BMI (in whites)	LOD = 2	(1253)
D8S1132	8a23 1	157 subjects 7 families	BMI (in whites)	n = 0.005	(1211)
D8S1179	8q25.1 8q24 11	729 subjects 275 families	Waist-to-hip ratio	MLS = 2.06	(1211)
D9S910	9a22 33	1297 subjects 260 families	BMI > 30 maternal	LOD = 2.00	(1210) (1224)
275710	9422.55	1297 subjects, 260 families	BMI = 30, material BMI > 30	NPL = 2.09	(1221) (1246)
		1297 subjects, 260 families	BMI > 30 BMI > 30	NPL = 2.09	(1210)
D9S1122	9a21-a22	521 subjects 156 families	Abdominal subcutaneous fat	LOD = 2.4	(1220) (1219)
D9S257	9a22 422	521 subjects, 156 families	Abdominal subcutaneous fat	LOD = 2.4	(1219)
D9S299-D9S930	9q31-9q31	430 subjects, 27 sibpairs, 27 pedigrees	BMI	LOD = 2.1	(1238)
ORM1	9a33.1	>168 pairs	Skinfolds, suprailiac	p = 0.03	(1208)
D9S282	9a34	508 subjects, 21 families	Obesity under anti-psychotics	LOD = 1.71	(1258)
AK1	9a34.13	>168 pairs	Skinfolds, suprailiac	p = 0.01	(1208)
D9S158	9q34.3	522 subjects, 99 families, 364	BMI (in whites)	LOD = 2.3	(1273)
D10S1435	10p15.3	522 subjects 99 families 364	BMI (in whites)	LOD = 2.7	(1273)
21001100	TopToto	sibnairs	Fat mass (in whites)	LOD = 2.7	(12/0)
		1526 pairs	BMI (in Pima Indians)	LOD = 1.7	(1254)
D10S189	10p15.1	522 subjects, 99 families, 364 sibpairs	BMI (in whites)	MLS = 2.7, SEGPATH	(1273)
			Fat mass (in whites)	MLS = 1	
		1526 pairs	BMI (in Pima Indians)	LOD = 1.7	(1254)
D10S1423	10p12.33	893 sibpairs	BMI, paternal effect (in whites)	p = 0.005, LOD = 1.89	(1209)
D10S582	10p12.31	667 subjects, 244 families	Obesity (in whites and African Americans)	NPL = 2.68	(1274)
		862 subjects, 170 families	Obesity (in African Americans, in European Americans)	p = 0.0005	(1275)

Gene/marker	Location	Population	Phenotypes	Score	Reference
D10S197	10p12.2	1297 subjects, 260 families	BMI \geq 27, maternal	LOD = 2.71	(1224)
	*	264 pairs	Obesity	LOD = 4.9	(1230)
		369 subjects, 89 families	Obesity (in white children and adolescents)	LOD = 2.24	(1276)
D10S204	10p12.1	386 subjects, 93 families	Obesity	LOD = 2.5	(1277)
D10S193	10p12.1	386 subjects, 93 families	Obesity	LOD = 2.5	(1277)
D10S208	10p11.23	667 subjects, 244 families	Obesity (in whites and African Americans)	NPL = 2.68	(1274)
		862 subjects, 170 families	Obesity (in African Americans, in European Americans)	p = 0.0005	(1275)
D10S1781	10p11.2	386 subjects, 93 families	Obesity	LOD = 2.5	(1277)
SHGC-31480	10p11.23	386 subjects, 93 families	Obesity	LOD = 2.5	(1277)
D10S220	10q21.1	672 subjects, 28 pedigrees	Leptin (in Old Order Amish)	LOD = 2.7	(1271)
D10S107	10q21.1	862 subjects, 170 families	Obesity (in African Americans, in European Americans)	p = 0.0005	(1275)
D10S1646	10q22.1	667 subjects, 244 families	Waist circumference (in whites and African Americans)	LOD = 2.5	(1274)
			BMI (in whites and African Americans)	NPL = 2.24	
D10S535	10q22.3	667 subjects, 244 families	Waist circumference (in whites and African Americans)	LOD = 2.5	(1274)
			BMI (in whites and African Americans)	NPL = 2.24	
D10S1267	10q24.32	447 subjects, 109 pedigrees	BMI > 27	LOD = 2.47	(1253)
D10S1679	10q26.13	667 subjects, 244 families	Waist-to-hip ratio (in whites and African Americans)	NPL = 2.22	(1274)
			Obesity (in whites and African Americans)	NPL = 2.25	
D10S1656	10q26.2	667 subjects, 244 families	Waist-to-hip ratio (in whites and African Americans)	NPL = 2.22	(1274)
			Obesity (in whites and African Americans)	NPL = 2.25	
Chr10q-region	10q26.3	1848 subjects, 279 pedigrees	BMI	LOD = 1.98	(1245)
			BMI and systolic blood pressure	LOD = 2.55	
			BMI and diastolic blood pressure	LOD = 3.2	
			BMI and systolic blood pressure and diastolic blood pressure	LOD = 4.09	
D10S212	10q26.3	59 pedigrees, 277 sibships	BMI	LOD = 2.08	(1251)
	1	198 subjects, 18 pedigrees	BMI	LOD = 3.3	(1213)
D11S984-D11S988	11p15.5- 11p15.5	430 subjects, 27 sibpairs, 27 pedigrees	BMI	LOD = 2.5	(1238)
CCKBR	11p15.4	226 pairs	Leptin	p = 0.01	(1255)
C11P15 3	11p15.2	215 subjects, 105 families	Abdominal subcutaneous fat	LOD = 1.85	(1237)
D11S419	11p15.2	67 pairs	BMI (in French whites)	p = 0.003	(708)
ATA34E08	11p13	3383 subjects, 1124 families	BMI (Women)	LOD = 1.8	(1227)
	1	215 subjects, 105 families	Abdominal subcutaneous fat	LOD = 1.75	(1237)
D11S1993	11a12	1297 subjects, 260 families	Body fat (%), paternal	LOD = 2.21	(1224)
D11S1313	11a12.1	369 subjects 89 families	Obesity (in white children and adolescents)	LOD = 1.65	(1276)
D11S2006-	11012.13-	729 subjects, 275 families	Abdominal visceral fat	MLS = 2.36	(1210)
D11S2371	11013.3	· _ /			()
D11S916	11q13.3	640 subjects, 240 relative pairs, 155 pedigrees	Resting metabolic rate	p = 0.006	(1278)
D11S2371	11a13.3	1297 subjects, 260 families	Body fat (%), paternal	LOD = 2	(1224)
D11S1321	11a13.3	640 subjects, 240 relative pairs.	Resting metabolic rate	p = 0.02	(1278)
		155 pedigrees	Body fat (%) Fat mass	p = 0.04 p = 0.02	()
D11S911	11q13.4	640 subjects, 240 relative pairs, 155 pedigrees	Resting metabolic rate	$p = 2^{e-06}$	(1278)
D11S2002	11q13.3	1510 subjects, 509 families	Factor central obesity	MLS = 2.19	(1247)
D11S940- D11S2000	11q22-11q22.3	562 subjects, 178 families	BMI	LOD = 2.5	(1279)
D11S2000	11g22.3	769 subjects, 182 families	BMI (in Africans)	LOD = 3.35	(1218)
		277 siblings	Body fat (%) (in Pima Indians)	p = 0.0028	(1243)
		157 subjects. 7 families	BMI (in whites)	p = 0.0079	(1210)
D1182366	11a23.1	277 siblings	Body fat (%) (in Pima Indians)	p = 0.0009	(1243)
D11S1998	11a23.3	1526 pairs	BMI (in Pima Indians)	LOD = 2.7	(1254)
	11920.0	1020 Puilo		200 2.1	(1204)

Gene/marker	Location	Population	Phenotypes	Score	Reference
D118976	11q23.3	236 pairs	Energy expenditure, 24-hour (in Pima Indians)	LOD = 2	(1214)
D11S4464	11q24.1	430 subjects, 27 sibpairs, 27 pedigrees	BMI	LOD = 2.3	(1238)
		1526 pairs	BMI (in Pima Indians)	LOD = 2.7	(1254)
		1778 sibships	BMI	n = 0.0023	(1232)
		004 subjects 37 pedigrees	BMI	p = 0.0023	(1232)
D115024	11024.2	004 subjects, 37 pedigrees	DMI	LOD = 2.6	(1207)
D115954	11q24.2	994 subjects, 37 pedigrees	DIVII	LOD = 2.0	(1207)
D115912	11q24.3	siblings	BMI	LOD = 3.6	(1280)
		1778 sibships	BMI	p = 0.0003	(1232)
		994 subjects, 37 pedigrees	BMI	LOD = 2.7	(1207)
D11S2359	11q25	1778 sibships	BMI	p = 0.0012	(1232)
GATA49D12N	12p13.31	1297 subjects, 260 families	$BMI \ge 27$	NPL = 2.12	(1226)
(D3S2395)		893 sibpairs	BMI, paternal effect (in whites)	p = 0.006, LOD = 1.83	(1209)
		1297 subjects, 260 families	$BMI \ge 27$	NPL = 2.12	(1246)
D12S391	12n13 2	342 families	Trends in BMI from childhood to adulthood	LOD = 2.9	(1215)
D1253042	12p13.2	522 subjects 90 families 364	BMI (in whites)	MIS = 2.1	(1273)
D1201042	12012.1	sibnoire	Est mass (in whites)	MLS = 1.2	(1275)
D126207	10-12 12 10-15	720 aukieste 275 families	Valiet to his setie	MLS = 1.2	(1210)
D128297- D1281294	12q13.13-12q15	729 subjects, 275 families	waist-to-nip ratio	MLS = 2.67	(1210)
D12S83	12q13.3	1249 sibpairs, >10,000 relative pairs	Fat-free mass	LOD = 1.79	(1205)
D12S1691	12q14.1	514 subjects, 99 families, 347 sibships	Fat intake	p = 0.0013	(1217)
D12S1052	12q21	729 subjects, 275 families	Waist-to-hip ratio	MLS = 2.6	(1210)
		349 subjects, 66 pedigrees	BMI (in whites)	LOD = 3.41	(1233)
D12S1052- D12S1064	12q21-12q21.33	729 subjects, 275 families	Waist-to-hip ratio	MLS = 2.91	(1210)
D12S1064	12a21.33	342 families	Trends in BMI from childhood to adulthood	LOD = 2.1	(1215)
51251001	12921100	349 subjects 66 pedigrees	BMI (in whites)	LOD = 3.41	(1233)
DAU	12022 024 2	1207 subjects, 00 pedigrees	DMI (m wines) DMI > 20	NDI = 1.02	(1235)
PAH-D12S2070	12q22-q24.2 12q22-q24.2- 12q24.21	729 subjects, 275 families	Waist-to-hip ratio	MLS = 2.48	(1240) (1210)
D12PAH	12023 1	342 families	Trends in BMI from childhood to adulthood	IOD = 23	(1215)
DIZIAII	12423.1	342 fammes	Long term hurden in BMI	LOD = 2.5 LOD = 3	(1215)
		1207	DMI > 20	LOD = 3	(1000)
D10070 D10010//	10,00,1	1297 subjects, 260 families	$BMI \ge 30$	NPL = 1.92	(1220)
D128/9-D1281366	12q23.1- 12q24.23	508 subjects, 21 families	Obesity under anti-psychotics	MLS = 2.74	(1258)
IGF1	12q23.3	521 subjects, 156 families	Abdominal subcutaneous fat	LOD = 1.9	(1219)
		502 subjects, 99 families, 352	Abdominal visceral fat (in whites)	p = 0.02	(895)
		pairs, 190 parents, 312 offspring	Fat-free mass (in whites)	p = 0.0002	
D12S1339	12q24.2	1297 subjects, 260 families	Body fat (%)	LOD = 4.08	(1246)
D12S2070	12q24.21	514 subjects, 99 families, 347 sibships	Fat intake (%)	p = 0.002	(1217)
		1297 subjects, 260 families	BMI, maternal Waist circumference, maternal	MLS = 4.01 MLS = 3.69	(1224)
		1207 subjects 260 families	Pody for (\mathcal{O}_{i})	$I_{OD} = 2.70$	(1226)
			Body fat (%)	LOD = 3.79	(1220)
		1297 subjects, 260 families	BMI	LOD = 3.57	(1246)
			Waist circumference	LOD = 3.05	
D12S395- D12S2078	12q24-12q24.32	3383 subjects, 1124 families	Body fat (%) (women)	LOD = 3.8	(1227)
D12S2078	12q24.32	521 subjects, 156 families	Abdominal subcutaneous fat	LOD = 2.9	(1219)
D12S2078- D12S1045	12q24.32- 12q24.33	3383 subjects, 1124 families	Body fat (%) (men and women)	LOD = 3.3	(1227)
D12S1045	12q24.33	521 subjects, 156 families	Abdominal subcutaneous fat	LOD = 2.9	(1219)
D12S1638	12024.33	59 pedigrees 277 sibships	BMI	LOD = 1.94	(1251)
D13S175	13a12 11	580 families	BMI	LOD = 3.3	(1231)
1301/3	13412.11	Job fammes	DIVIL	LOD = 3.3	(1244)

Gene/marker	Location	Population	Phenotypes	Score	Reference
D13S221	13q12.13	580 families	BMI	LOD = 3.3	(1244)
D13S1493	13q13.2	1297 subjects, 260 families	$BMI \ge 40$	NPL = 2.03	(1226)
		3383 subjects, 1124 families	BMI and blood pressure response to postural change	LOD = 3.2	(1281)
D13S894	13q13.3	1297 subjects, 260 families	BMI \geq 27, maternal	LOD = 2.34	(1224)
	•	1297 subjects, 260 families	$BMI \ge 40$	NPL = 2.63	(1226)
		1297 subjects, 260 families	$BMI \ge 27$	NPL = 1.88	(1246)
ESD	13q14.11	160 pairs	Body fat (%)	p = 0.04	(1252)
	•		Skinfolds, sum of six	p = 0.04	
D13S257	13q14.2	3027 subjects, 401 families, 317 sibships	BMI (National Heart, Lung, and Blood Institute Family Heart Study)	MLS = 3.2 p = 0.00006	(1220)
D13S1807	13q21.1	1297 subjects, 260 families	BMI	LOD = 2.67	(1226)
D13S800	13q21.32	342 families	Trends in BMI from childhood to adulthood	LOD = 2	(1215)
	-	1297 subjects, 260 families	BMI	LOD = 2.7	(1226)
		1297 subjects, 260 families	BMI	LOD = 2.7	(1246)
D13S793	13q31.3	1297 subjects, 260 families	BMI, paternal	LOD = 4.79	(1224)
	1	0	Waist circumference, paternal	LOD = 3.11	
		1297 subjects, 260 families	BMI	LOD = 2.78	(1226)
		1312 subjects, 696 families	Factor central obesity	MLS = 2.17	(1247)
D13S779	13q32.2	1297 subjects, 260 families	BMI	LOD = 2.82	(1226)
	1	1312 subjects, 696 families	Factor central obesity	MLS = 2.67	(1247)
		1297 subjects, 260 families	BMI	LOD = 2.82	(1246)
			Waist circumference	LOD = 1.8	
D13S285	13a34	330 pedigrees, 1702 sibships	Obesity before age 35	p = 0.001	(1282)
		521 subjects, 156 families	Abdominal subcutaneous fat	LOD = 1.9	(1219)
D14S742	14a11.2	522 subjects 99 families 364	Fat mass (in whites)	MLS = 1.7	(1273)
DINGTE	1.41.12	sibnairs	BMI (in whites)	MLS = 2.2	(12/0)
		893 sibnairs	BMI (in whites)	n = 0.002	(1209)
		ovo slopano		LOD = 1.95	(120))
D14S283	14q11.2	522 subjects, 99 families, 364	Fat mass (in whites)	p = 0.0006	(1273)
	1	sibpairs	Leptin (in whites)	p = 0.003	
		1	Fat mass (in whites)	MLS = 2	
			BMI (in whites)	MLS = 1.8	
D14S1280	14q11.2	522 subjects, 99 families, 364	Fat-free mass (in whites)	MLS = 1.1	(1273)
	1	sibpairs	BMI (in whites)	MLS = 2.4	
D14S608	14q12	1100 subjects, 170 families	Adiponectin (in Northern Europeans)	LOD = 3.2	(1229)
D14S599	14q13.1	1100 subjects, 170 families	Adiponectin (in Northern Europeans)	LOD = 3.2	(1229)
D14S276	14q22.2	672 subjects, 28 pedigrees	Waist circumference (in Old Order Amish)	LOD = 1.8	(1271)
D14S588	14q24.1	215 subjects, 105 families	Abdominal subcutaneous fat	LOD = 2.4	(1237)
D14S74	14q24.3	672 subjects, 28 pedigrees	Leptin (in Old Order Amish)	LOD = 2.5	(1271)
D14S280	14a32.12	672 subjects, 28 pedigrees	Leptin (in Old Order Amish)	LOD = 2.5	(1271)
D14S617	14q32.12	1055 pairs	BMI	LOD = 2.2	(1241)
D15S128-D15S513	15a12-15a15.1	506 subjects, 115 pedigrees	Age adiposity rebound	LOD = 2.53	(1239)
D15S1232	15q13.3	3027 subjects, 401 families, 317 sibships	BMI (National Heart, Lung, and Blood Institute Family Heart Study)	LOD = 1.7	(1220)
D15S641	15g15.2	478 subjects, 10 families	asp levels	LOD = 2.1	(1283)
			asp and high-density lipoprotein 2a- cholesterol	LOD = 3.2	()
LIPC	15q21-23	660 subjects, 202 families, 315 sibpairs, 274 men, 386 women	Eating behavior, hunger	LOD = 1.76	(978)
D15S206	15q24-q25	660 subjects, 202 families, 315 sibpairs, 274 men, 386 women	Eating behavior, hunger	LOD = 3	(978)
D15S655	15q25.3	3383 subjects, 1124 families	Body fat (%) (men)	LOD = 3	(1227)
D15S652	15q26.1	336 sibpairs, 609 relative pairs	Fat-free mass	LOD = 3.56	(1263)
D15S657	15q26.2	336 sibpairs, 609 relative pairs	Fat-free mass	LOD = 2	(1263)
D16S510	16p13.3	672 subjects, 28 pedigrees	Leptin (in Old Order Amish)	LOD = 1.7	(1271)
			BMI (in Old Order Amish)	LOD = 1.7	
D16S404	16p13.2	893 sibpairs	BMI (in whites)	p = 0.00025, LOD = 3.12	(1209)

$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	Gene/marker	Location	Population	Phenotypes	Score	Reference
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	D16S764	16p13.12	893 sibpairs	BMI (in whites)	p = 0.0006, LOD = 2.45	(1209)
	D16S3253	16q12.2	330 pedigrees, 1702 sibships	BMI	LOD = 3.21	(1261)
$ \begin{array}{l l l l l l l l l l l l l l l l l l l $	D16S415-D16S420	16q12.2- 16q24.1	506 subjects, 115 pedigrees	Age adiposity rebound	LOD = 2.54	(1239)
D16525 [6q21 199 spics Leptin LOD = 2 (1260) D165422 D16342 D179.13 506 subjects, 115 perigence BMI DD = 2.5 (1239) D1751308 17p1.3. 78 subjects, 107 lamilies Adponenti unversame LOD = 2.7 (128) D1751308 17p1.3. 478 subjects, 107 lamilies Adponenti (in Northern Europeans) LOD = 2.7 (128) D1751308 17p1.2. 470 subjects, 107 lamilies Adponenti (in Northern Europeans) LOD = 2.5 (124) D1751293 17q1.2. 470 subjects, 107 lamilies BMI LOD = 2.2 (127) D1751200 17q2.3.2 660 subjects, 202 families BMI MLS = 2.26 (078) S171305 17q2.3.2 660 subjects, 202 families BMI MLS = 2.2 (1210) D1751290 17q2.3.2 660 subjects, 202 families BMI MLS = 2.2 (1210) D1751341 17q2.3.2-q25.1 477 subjects, 100 perigrave BMI MLS = 2.2 (1210) D1751340 17q2.3.2-q25.1 477 subjects, 100 pe	D16S2620	16q21	1055 pairs	BMI	LOD = 2.6	(1241)
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	D16S265	16q21	1199 pairs	Leptin	LOD = 2	(1260)
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	D16S422	16q23.3	995 subjects, 153 families	Resting energy expenditure	LOD = 2.96	(1284)
$ \begin{tabular}{ c c c c c c c c c c c c c c c c c c c$	D17S849-D17S799	17p13-17p13	506 subjects, 115 pedigrees	BMI > 95th percentile	LOD = 2.25	(1239)
$ \begin{array}{llllllllllllllllllllllllllllllllllll$	D17S1308	17p13.3	729 subjects, 275 families	Abdominal subcutaneous fat	MLS = 2.06	(1210)
$ \begin{array}{llllllllllllllllllllllllllllllllllll$	D17S1303	17p13.1	478 subjects, 10 families	asp levels	LOD = 2.7	(1283)
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	D17S947	17p12	1100 subjects, 170 families	Adiponectin (in Northern Europeans)	LOD = 1.7	(1229)
$ \begin{split} \begin{tabular}{ c c c c c c } \mbox{bias} bias bias bias bias bias bias bias bias$			2209 subjects, 507 families	Leptin	LOD = 5	(1248)
$ \begin{array}{llllllllllllllllllllllllllllllllllll$			1055 pairs	BMI	LOD = 2.5	(1241)
$ \begin{array}{llllllllllllllllllllllllllllllllllll$	D17S1293	17q11.2	470 subjects, 10 families	BMI	p = 0.001	(1272)
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	D17S2180	17q21.32	521 subjects, 156 families	Abdominal subcutaneous fat	LOD = 2.2	(1219)
$ \begin{array}{llllllllllllllllllllllllllllllllllll$	D17S1306	17q22	660 subjects, 202 families, 315 sibpairs, 274 men, 386 women	Eating behavior, hunger	MLS = 2.06	(978)
$\begin{array}{l c c c c c c c c c c c c c c c c c c c$	D17S1290	17q23.2	660 subjects, 202 families, 315 sibpairs, 274 men, 386 women	Eating behavior, hunger	MLS = 2.45	(978)
$\begin{array}{ c c c c c c c c c c c c c c c c c c c$			729 subjects, 275 families	BMI	MLS = 2.76	(1210)
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$			521 subjects, 156 families	Abdominal subcutaneous fat	LOD = 2.2	(1219)
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	D17S944	17q23.3-q25.1	447 subjects, 109 pedigrees	BMI > 35	LOD = 3.16	(1253)
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	D17S1351	17q23-q24	660 subjects, 202 families, 315 sibpairs, 274 men, 386 women	Eating behavior, hunger	LOD = 1.75	(978)
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	D17S1301	17q25.2	521 subjects, 156 families	Abdominal subcutaneous fat	LOD = 2.2	(1219)
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	D18S481	18p11.3	342 families	Trends in BMI from childhood to adulthood	LOD = 2	(1215)
$ \begin{array}{llllllllllllllllllllllllllllllllllll$	D18S843-D18S53	18p11.22- 18p11.23	3383 subjects, 1124 families	Body fat (%) (men)	LOD = 1.7	(1227)
Skinfolds, sum of six $p = 0.005$ Fat mass $p = 0.001$ Body fat (%)D18S87718q12.1336 sibpairs, 609 relative pairsFat-free mass $p = 0.002$ Fat-free massD18S85318q12.3336 sibpairs, 609 relative pairsFat-free massLOD = 3.6(1263) LOD = 2.3D18S53518q12.3336 sibpairs, 609 relative pairsFat-free massLOD = 3.6(1263) LOD = 3.58D18S85818q21.313383 subjects, 1124 familiesBMI and blood pressure response to postural changeLOD = 2.4(1285) (1263)D18S115518q22289 pairsRespiratory quotient $p = 0.004$ (969) (969)D19S71419p13.3404 subjectsRespiratory quotient $p = 0.002$ (1273) (1286) (adult baboons)LDLR19p13.2522 subjects, 99 families, 364 sibpairs, 274 men, 386 women sibpairs, 274 men, 386 womenSkinfolds, sum of eight (in whites) $p = 0.002$ (1273) (1273) Body fat (%) (in whites) $p = 0.001$ D19S21519p13606 subjects, 115 pedigrees sibpairs, 274 men, 386 women 	MC5R	18p11.21	289 pairs	BMI	p = 0.001	(969)
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$		I	L	Skinfolds, sum of six	p = 0.005	. ,
Body fat (%) $p = 0.02$ Pat-free mass $p = 0.008$ Resting metabolic rate $p = 0.002$ D18S877 18q12.1 336 sibpairs, 609 relative pairs Fat-free mass LOD = 3.6 (1263) D18S858 18q21.3 336 sibpairs, 609 relative pairs Fat-free mass LOD = 3.6 (1263) D18S858 18q21.31 3383 subjects, 1124 families BMI and blood pressure response to postural change LOD = 2.4 (1281) D18S1155 18q22 289 pairs Respiratory quotient $p = 0.04$ (969) D19S714 19p13.3 404 subjects Respiratory quotient $p = 0.002$ (1273) LDLR 19p13.2 522 subjects, 99 families, 364 Skinfolds, sum of cight (in whites) $p = 0.002$ (1273) D19S215 19p13 506 subjects, 115 pedigrees Age adiposity rebound LOD = 2.13 (1239) D19S215 19p13 506 subjects, 102 families SMI > 35 LOD = 1.97 (1276) D19S418 19q13.143 347 subjects, 109 pedigrees BMI > 35 LOD = 3.21 (128				Fat mass	p = 0.001	
Fat-free mass $p = 0.008$ Resting metabolic rate $p = 0.002$ D18S87718q12.1336 sibpairs, 609 relative pairsBody fat (%) (in Pima Indians)LOD = 2.3(1214)D18S53518q12.3336 sibpairs, 609 relative pairsFat-free massLOD = 3.58(1263)D18S85818q21.31338 subjects, 1124 familiesBMI and blood pressure response to posturalLOD = 2.6(1281)D18S15518q21.32367 subjects, 166 families, 193Obesity (in Finns)LOD = 2.4(1285)D18S15518q22289 pairsRespiratory quotient $p = 0.04$ (969)D19S71419p13.3404 subjectsResistin mRNA levels in adipose tissueLOD = 3.84(1286) (adult baboons)LDLR19p13.2522 subjects, 99 families, 364 sibpairsSkinfolds, sum of eight (in whites) $p = 0.009$ (1273)D19S21419p13.19q13.11506 subjects, 115 pedigrees sibpairs, 274 men, 386 womenBMI > 35LOD = 3.21(1239)D19S41819q13.41,3330 pedigrees, 1702 sibshipsObesity fin white children and adolescents)LOD = 1.97(1276)D19S25419q13.43330 pedigrees, 1702 sibshipsObesity before age 35 $p = 0.001$ (1282)D20S48220p12.2893 sibpairsBMI (in whites) $p = 4.6e^{-05}$, (1209) LOD = 3.55LOD = 3.55D20S48420p12.11724 subjects, 1202 familiesBMI (in whites) $p = 4.6e^{-05}$, (1209) LOD = 3.64				Body fat (%)	p = 0.02	
D18S87718q12.1 236 pairs336 sibpairs, 609 relative pairs 236 pairsResting metabolic rate $p = 0.002$ D18S85718q12.3 336 sibpairs, 609 relative pairs 1018S858160 = 2.3 1263)(1263)D18S85818q21.313383 subjects, 1124 familiesBody fat (%) (in Pima Indians)LOD = 2.6 LOD = 2.6(1281) (1281)D18S15518q21.32367 subjects, 166 families, 193 pairsObesity (in Finns)LOD = 2.4(1285) (1285)D18S115518q22289 pairs pairsRespiratory quotient (adult baboons) $p = 0.04$ (069)(069)D19S71419p13.3404 subjects sibpairsRespiratory quotient (adult baboons) $p = 0.002$ (1273)(1273) pairsLDLR19p13.2522 subjects, 99 families, 364 sibpairsSkinfolds, sum of eight (in whites) pairs $p = 0.0002$ (1273)(1239)D19S21519p13660 subjects, 115 pedigrees sibpairs, 274 men, 386 women sibpairs, 274 men, 386 womenBMI > 35LOD = 3.21 (1253)(1253)D19S41819q13.43300 pedigrees, 1702 sibships op 13BMI > 35LOD = 3.21 (1253)(1253)D19S25419q13.43300 pedigrees, 1702 sibships op 13Obesity before age 35 op 20016 $p = 0.001$ (1282)D20S85120p12.2893 sibpairsBMI (in whites) p = 4.6c^{-05}, (1209) LOD = 4.08 $p = 4.6c^{-05},(1209)$ LOD = 4.08D20S86420p12.11724 subjects, 1202 families Factor central obesityMLS = 1.97 MLS = 1.97(1247)				Fat-free mass	p = 0.008	
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$				Resting metabolic rate	p = 0.002	
236 pairsBody fat (%) (in Pima Indians)LOD = 2.3(1214)D18S53518q12.3336 sibpairs, 609 relative pairsFat-free massLOD = 3.58(1263)D18S85818q21.313383 subjects, 1124 familiesBMI and blood pressure response to postural changeLOD = 2.6(1281)D18S115518q21.32367 subjects, 166 families, 193 pairsObesity (in Finns)LOD = 2.4(1285)MC4R18q22289 pairsRespiratory quotient $p = 0.04$ (969)D19S71419p13.3404 subjectsResistin mRNA levels in adipose tissue (adult baboons) $D = 0.002$ (1273)LDLR19p13.2522 subjects, 99 families, 364 sibpairsSkinfolds, sum of eight (in whites) Body fat (%) (in whites) $p = 0.002$ (1273)D19S21519p13666 subjects, 115 pedigrees sibpairs, 274 men, 386 women sibpairs, 274 men, 386 womenBMI > 35LOD = 3.21(1253)D19S24419q13.11369 subjects, 89 families sibpairsObesity (in white children and adolescents)LOD = 1.8(978)D19S25419q13.43447 subjects, 109 pedigrees subjertsBMI > 35LOD = 3.21(1253)D20S82220p13893 sibpairsBMI (in whites) $p = 0.00016$, (1282)(129)D20S85120p12.2893 sibpairsBMI (in whites) $p = 4.6^{e-0.5}$, (1209) LOD = 4.08D20S60420p12.11724 subjects, 1202 familiesFactor central obesityMLS = 1.97(1247)	D18S877	18q12.1	336 sibpairs, 609 relative pairs	Fat-free mass	LOD = 3.6	(1263)
D18853518q12.3336 sibpairs, 609 relative pairs and sibpairs, 609 relative pairs and sibpairs, 1124 familiesFat-free mass harfree massLOD = 3.58(1263) LOD = 2.6D18858818q21.313383 subjects, 1124 familiesBMI and blood pressure response to postural changeLOD = 2.6(1281)D188515518q21.32367 subjects, 166 families, 193 pairsObesity (in Finns)LOD = 2.4(1285)MC4R18q22289 pairsRespiratory quotient $p = 0.04$ (969)D19571419p13.3404 subjectsRespiratory quotient $p = 0.002$ (1273)LDLR19p13.2522 subjects, 99 families, 364 sibpairsSkinfolds, sum of eight (in whites) $p = 0.002$ (1273)D198221-D19841419p13-19q13.11506 subjects, 202 families, 315 sibpairs, 274 men, 386 womenEating behavior, disinhibitionLOD = 1.8(978)D19821419q13.3300 pedigreesBMI > 35LOD = 1.97(1276)D19824419q13.43330 pedigrees, 1702 sibshipsObesity (in white children and adolescents)LOD = 1.97(1276)D19824220p13893 sibpairsBMI (in whites) $p = 0.0001$ (1282)D20858120p12.2893 sibpairsBMI (in whites) $p = 4.6^{e-05}$, LOD = 4.08 $p = 4.6^{e-05}$, LOD = 4.08D20860420p12.11724 subjects, 1202 familiesFactor central obesityMLS = 2.46(1247)		1	236 pairs	Body fat (%) (in Pima Indians)	LOD = 2.3	(1214)
D18S85818q21.313383 subjects, 1124 familiesBMI and blood pressure response to postural changeLOD = 2.6(1281)D18S115518q21.32367 subjects, 166 families, 193 pairsObesity (in Finns)LOD = 2.4(1285) changeMC4R18q22289 pairsRespiratory quotient $p = 0.04$ (969)D19S71419p13.3404 subjectsResistin mRNA levels in adipose tissue (adult baboons)LOD = 3.84(1286) (1287)LDLR19p13.2522 subjects, 99 families, 364 sibpairsSkinfolds, sum of eight (in whites) p = 0.0009 $p = 0.0009$ (1273) p = 0.0009D19S221-D19S41419p13-19q13.11506 subjects, 115 pedigrees sibpairs, 274 men, 386 womenAge adiposity reboundLOD = 2.13(1239) D19S414D19S41819q13.3-q13.43447 subjects, 109 pedigrees sibpairs, 274 men, 386 womenBMI > 35LOD = 3.21(1253) D20S482D19S41419q13.13369 subjects, 1702 sibships B93 sibpairsObesity (in white children and adolescents)LOD = 1.97 p = 0.001(1282) LOD = 3.55D20S85120p12.2893 sibpairsBMI (in whites) $p = 4.6^{e-05}$, LOD = 4.08D20S86420p12.11724 subjects, 1202 familiesFactor central obesityMLS = 1.97 MLS = 2.46D20S60420p12.11724 subjects, 1202 familiesFactor central obesityMLS = 2.46	D18S535	18q12.3	336 sibpairs, 609 relative pairs	Fat-free mass	LOD = 3.58	(1263)
D18S115518q21.32367 subjects, 166 families, 193 pairsObesity (in Finns)LOD = 2.4(1285) (1285)MC4R18q22289 pairsRespiratory quotient $p = 0.04$ (969)D19S71419p13.3404 subjectsResistin mRNA levels in adipose tissue (adult babons)LOD = 3.84(1286) (2011)LDLR19p13.2522 subjects, 99 families, 364Skinfolds, sum of eight (in whites) $p = 0.002$ (1273) Body fat (%) (in whites)D19S21-D19S41419p13-19q13.11506 subjects, 115 pedigrees sibpairsAge adiposity reboundLOD = 2.13(1239) LOD = 1.8D19S21519p13660 subjects, 202 families, 315 sibpairs, 274 men, 386 womenBMI > 35LOD = 3.21(1253)D19S41819q13.3-q13.43447 subjects, 109 pedigrees sibpairsBMI > 35LOD = 3.21(1253)D19S41419q13.11369 subjects, 89 families obesity (in white children and adolescents)LOD = 1.97(1276)D19S25419q13.43330 pedigrees, 1702 sibships BMI (in whites)Desity before age 35 $p = 0.0016$, (1209) LOD = 3.55D20S85120p12.2893 sibpairsBMI (in whites) $p = 4.6^{e^{-05}}$, (1209) LOD = 4.08T24 subjects, 1202 familiesFactor central obesityMLS = 1.97(1247)D20S60420p12.11724 subjects, 1202 familiesFactor central obesityMLS = 2.46(1247)	D18S858	18q21.31	3383 subjects, 1124 families	BMI and blood pressure response to postural change	LOD = 2.6	(1281)
MC4R18q22289 pairsRespiratory quotient $p = 0.04$ (969)D19571419p13.3404 subjectsResistin mRNA levels in adipose tissue (adult baboons)LOD = 3.84(1286)LDLR19p13.2522 subjects, 99 families, 364Skinfolds, sum of eight (in whites) $p = 0.002$ (1273)sibpairsLeptin (in whites) $p = 0.009$ $p = 0.009$ 1295221-D19S41419p13-19q13.11506 subjects, 115 pedigreesAge adiposity reboundLOD = 2.13(1239)D19S21519p13660 subjects, 202 families, 315Eating behavior, disinhibitionLOD = 1.8(978)D19S41819q13.3-q13.43447 subjects, 109 pedigreesBMI > 35LOD = 3.21(1253)D19S41419q13.11369 subjects, 89 familiesObesity in white children and adolescents)LOD = 1.97(1276)D19S25419q13.43330 pedigrees, 1702 sibshipsObesity before age 35 $p = 0.0001$ (1282)D20S48220p13893 sibpairsBMI (in whites) $p = 4.6e^{-05}$, (1209)LOD = 4.08LOD = 4.08LOD = 4.08LOD = 4.08D20S60420p12.11724 subjects, 1202 familiesFactor central obesityMLS = 1.97(1247)	D18S1155	18q21.32	367 subjects, 166 families, 193	Obesity (in Finns)	LOD = 2.4	(1285)
D19S71419p13.3404 subjectsResistin mRNA levels in adipose tissue (adult baboons)LOD = 3.84(1286)LDLR19p13.2522 subjects, 99 families, 364 sibpairsSkinfolds, sum of eight (in whites) $p = 0.002$ (1273)D19S211-D19S41419p13-19q13.11506 subjects, 115 pedigrees sibpairs, 274 men, 386 womenAge adiposity reboundLOD = 2.13(1239)D19S41819q13.3-q13.43447 subjects, 109 pedigrees sibpairs, 274 men, 386 womenBMI > 35LOD = 3.21(1253)D19S41419q13.11369 subjects, 89 families objects, 89 familiesObesity (in white children and adolescents)LOD = 1.97(1276)D19S25419q13.43330 pedigrees, 1702 sibships Obesity before age 35De 0.001(1282)D20S85120p12.2893 sibpairsBMI (in whites) $p = 4.6^{e-05}$, (1209) LOD = 4.08D20S60420p12.11724 subjects, 1202 familiesFactor central obesityMLS = 1.97(1247)D20S60420p12.11724 subjects, 1202 familiesFactor central obesityMLS = 2.46(1247)	MC4R	18a22	289 pairs	Respiratory quotient	p = 0.04	(969)
LDLR19p13.2522 subjects, 99 families, 364 sibpairsSkinfolds, sum of eight (in whites) $p = 0.002$ (1273)D19S221-D19S41419p13-19q13.11506 subjects, 115 pedigrees of subjects, 202 families, 315Age adiposity reboundLOD = 2.13(1239)D19S21519p13660 subjects, 202 families, 315 sibpairs, 274 men, 386 womenEating behavior, disinhibitionLOD = 1.8(978)D19S41819q13.3-q13.43447 subjects, 109 pedigreesBMI > 35LOD = 3.21(1253)D19S25419q13.43330 pedigrees, 1702 sibshipsObesity before age 35 $p = 0.0011$ (1282)D20S48220p13893 sibpairsBMI (in whites) $p = 4.6^{e^{-05}}$, (1209)LOD = 3.55D20S85120p12.2893 sibpairsBMI (in whites) $p = 4.6^{e^{-05}}$, (1209)LOD = 4.081724 subjects, 1202 familiesFactor central obesityMLS = 1.97(1247)D20S60420p12.11724 subjects, 1202 familiesFactor central obesityMLS = 2.46(1247)	D19S714	19p13.3	404 subjects	Resistin mRNA levels in adipose tissue (adult baboons)	LOD = 3.84	(1286)
sibpairsLeptin (in whites) $p = 0.0009$ Body fat (%) (in whites) $p = 0.009$ D19S221-D19S41419p13-19q13.11506 subjects, 115 pedigreesAge adiposity reboundLOD = 2.13(1239)D19S21519p13660 subjects, 202 families, 315 sibpairs, 274 men, 386 womenEating behavior, disinhibitionLOD = 1.8(978)D19S41819q13.3-q13.43447 subjects, 109 pedigreesBMI > 35LOD = 3.21(1253)D19S41419q13.11369 subjects, 89 familiesObesity (in white children and adolescents)LOD = 1.97(1276)D19S25419q13.43330 pedigrees, 1702 sibshipsObesity before age 35 $p = 0.0001$ (1282)D20S48220p13893 sibpairsBMI (in whites) $p = 4.6^{e-05}$, (1209)LOD = 3.55D20S85120p12.2893 sibpairsBMI (in whites) $p = 4.6^{e-05}$, (1209)LOD = 4.08T724 subjects, 1202 familiesFactor central obesityMLS = 1.97(1247)D20S60420p12.11724 subjects, 1202 familiesFactor central obesityMLS = 2.46(1247)	LDLR	19p13.2	522 subjects, 99 families, 364	Skinfolds, sum of eight (in whites)	p = 0.002	(1273)
D195221-D19541419p13-19q13.11506 subjects, 115 pedigrees sobjects, 202 families, 315 sibpairs, 274 men, 386 womenBody fat (%) (in whites) $p = 0.009$ D19521519p13660 subjects, 202 families, 315 sibpairs, 274 men, 386 womenEating behavior, disinhibitionLOD = 2.13 LOD = 1.8(1239)D19541819q13.3-q13.43447 subjects, 109 pedigreesBMI > 35LOD = 3.21 Obesity (in white children and adolescents)LOD = 1.97 (1276)(1253)D19525419q13.43330 pedigrees, 1702 sibships BM3 sibpairsObesity before age 35 BMI (in whites) $p = 0.0001$ LOD = 3.55(1209) LOD = 3.55D20585120p12.2893 sibpairsBMI (in whites) $p = 4.6^{e-05}$, LOD = 4.08(1209) LOD = 4.08D20560420p12.11724 subjects, 1202 familiesFactor central obesityMLS = 1.97 MLS = 2.46(1247)		1	sibpairs	Leptin (in whites)	p = 0.0009	
D19S221-D19S41419p13-19q13.11506 subjects, 115 pedigrees sibpairs, 274 men, 386 womenAge adiposity reboundLOD = 2.13(1239)D19S21519p13660 subjects, 202 families, 315 sibpairs, 274 men, 386 womenEating behavior, disinhibitionLOD = 1.8(978)D19S41819q13.3-q13.43447 subjects, 109 pedigreesBMI > 35LOD = 3.21(1253)D19S41419q13.11369 subjects, 89 familiesObesity (in white children and adolescents)LOD = 1.97(1276)D19S25419q13.43330 pedigrees, 1702 sibshipsObesity before age 35 $p = 0.001$ (1282)D20S48220p13893 sibpairsBMI (in whites) $p = 4.6^{e-05}$, (1209)LOD = 3.55D20S85120p12.2893 sibpairsBMI (in whites) $p = 4.6^{e-05}$, (1209)LOD = 4.08T724 subjects, 1202 familiesFactor central obesityMLS = 1.97(1247)D20S60420p12.11724 subjects, 1202 familiesFactor central obesityMLS = 2.46(1247)			L	Body fat (%) (in whites)	p = 0.009	
D19S21519p13660 subjects, 202 families, 315 sibpairs, 274 men, 386 womenEating behavior, disinhibitionLOD = 1.8(978)D19S41819q13.3-q13.43447 subjects, 109 pedigreesBMI > 35LOD = 3.21(1253)D19S41419q13.11369 subjects, 89 familiesObesity (in white children and adolescents)LOD = 1.97(1276)D19S25419q13.43330 pedigrees, 1702 sibshipsObesity before age 35 $p = 0.001$ (1282)D20S48220p13893 sibpairsBMI (in whites) $p = 0.00016$, (1209)LOD = 3.55D20S85120p12.2893 sibpairsBMI (in whites) $p = 4.6^{e-05}$, (1209)LOD = 4.08T724 subjects, 1202 familiesFactor central obesityMLS = 1.97(1247)D20S60420p12.11724 subjects, 1202 familiesFactor central obesityMLS = 2.46(1247)	D19S221-D19S414	19p13-19q13.11	506 subjects, 115 pedigrees	Age adiposity rebound	LOD = 2.13	(1239)
D19S418 19q13.3-q13.43 447 subjects, 109 pedigrees BMI > 35 LOD = 3.21 (1253) D19S414 19q13.11 369 subjects, 89 families Obesity (in white children and adolescents) LOD = 1.97 (1276) D19S254 19q13.43 330 pedigrees, 1702 sibships Obesity before age 35 $p = 0.001$ (1282) D20S482 20p13 893 sibpairs BMI (in whites) $p = 0.00016$, (1209) LOD = 3.55 D20S851 20p12.2 893 sibpairs BMI (in whites) $p = 4.6^{e-05}$, (1209) LOD = 4.08 T224 subjects, 1202 families Factor central obesity MLS = 1.97 (1247) D20S604 20p12.1 1724 subjects, 1202 families Factor central obesity MLS = 2.46 (1247)	D19S215	19p13	660 subjects, 202 families, 315 sibpairs, 274 men, 386 women	Eating behavior, disinhibition	LOD = 1.8	(978)
D19S414 19q13.11 369 subjects, 89 families Obesity (in white children and adolescents) LOD = 1.97 (1276) D19S254 19q13.43 330 pedigrees, 1702 sibships Obesity before age 35 $p = 0.001$ (1282) D20S482 20p13 893 sibpairs BMI (in whites) $p = 0.00016$, (1209) LOD = 3.55 D20S851 20p12.2 893 sibpairs BMI (in whites) $p = 4.6^{e-05}$, (1209) LOD = 4.08 D20S604 20p12.1 1724 subjects, 1202 families Factor central obesity MLS = 1.97 (1247)	D19S418	19q13.3-q13.43	447 subjects, 109 pedigrees	BMI > 35	LOD = 3.21	(1253)
D19S254 19q13.43 330 pedigrees, 1702 sibships Obesity before age 35 $p = 0.001$ (1282) D20S482 20p13 893 sibpairs BMI (in whites) $p = 0.0016$ (1209) D20S851 20p12.2 893 sibpairs BMI (in whites) $p = 4.6^{e-05}$, (1209) LOD = 4.08 1724 subjects, 1202 families Factor central obesity MLS = 1.97 (1247) D20S604 20p12.1 1724 subjects, 1202 families Factor central obesity MLS = 2.46 (1247)	D19S414	19q13.11	369 subjects, 89 families	Obesity (in white children and adolescents)	LOD = 1.97	(1276)
D20S482 20p13 893 sibpairs BMI (in whites) $p = 0.00016$, (1209) LOD = 3.55 D20S851 20p12.2 893 sibpairs BMI (in whites) $p = 4.6^{e-05}$, (1209) LOD = 4.08 1724 subjects, 1202 families Factor central obesity MLS = 1.97 (1247) D20S604 20p12.1 1724 subjects, 1202 families Factor central obesity MLS = 2.46 (1247)	D19S254	19q13.43	330 pedigrees, 1702 sibships	Obesity before age 35	p = 0.001	(1282)
D20S851 20p12.2 893 sibpairs BMI (in whites) $p = 4.6^{e^{-05}}$, (1209) (1209) LOD = 4.08 1724 subjects, 1202 families Factor central obesity MLS = 1.97 (1247) D20S604 20p12.1 1724 subjects, 1202 families Factor central obesity MLS = 2.46 (1247)	D20S482	20p13	893 sibpairs	BMI (in whites)	p = 0.00016, LOD = 3.55	(1209)
1724 subjects, 1202 familiesFactor central obesityMLS = 1.97(1247)D20S60420p12.11724 subjects, 1202 familiesFactor central obesityMLS = 2.46(1247)	D20S851	20p12.2	893 sibpairs	BMI (in whites)	$p = 4.6^{e-05},$ LOD = 4.08	(1209)
D20S604 20p12.1 1724 subjects, 1202 families Factor central obesity $MLS = 2.46$ (1247)			1724 subjects, 1202 families	Factor central obesity	MLS = 1.97	(1247)
	D20S604	20p12.1	1724 subjects, 1202 families	Factor central obesity	MLS = 2.46	(1247)

Gene/marker	Location	Population	Phenotypes	Score	Reference
D20S601	20q11.22- q11.23	236 pairs	Respiratory quotient, 24-hour (in Pima Indians)	LOD = 3	(1214)
D20S478	20q12	994 subjects, 37 pedigrees	BMI	LOD = 2	(1207)
D20S438	20a12	1711 subjects, 103 pedigrees	BMI (in Utah pedigrees)	LOD = 3.5	(1287)
	1	994 subjects, 37 pedigrees	BMI	LOD = 2	(1207)
D20S465	20q12	994 subjects, 37 pedigrees	BMI	LOD = 2	(1207)
D20S107	20a12	513 subjects, 92 families, 423	BMI	LOD = 3.2	(1288)
	- 1	pairs	Body fat (%)	LOD = 3.2	
D20S476	20q13	513 subjects, 92 families, 423 pairs	BMI	LOD = 3.06	(1288)
ADA	20q13.12	160 pairs	BMI	p = 0.001	(1252)
	1		skinfolds, sum of six	p = 0.001	
D20S481	20q13.12	994 subjects, 37 pedigrees	BMI	LOD = 2.2	(1207)
D20S17	20q13.12	650 subjects, 258 pairs, 152 pedigrees	Body fat (%)	p = 0.0078	(662)
D20S178	20q13.13	667 subjects, 244 families	Body fat (%) (in whites and African Americans)	NPL = 2.57	(1274)
D20S887	20q13.13	514 subjects, 99 families, 347 sibships	Fat intake	p = 0.0093	(1217)
D20S869	20g13.13	514 subjects, 99 families, 347	Carbohydrate intake	p = 0.0023	(1217)
		sibships	Fat intake	p = 0.0005	()
		F-	Protein intake	$p = 9^{e-05}$	
D20S857	20g13.13	514 subjects, 99 families, 347	Total energy intake	$p = 7^{e-05}$	(1217)
		sibships	Carbohydrate intake	p = 0.0008	()
		sicompo	Fat intake	p = 0.0006	
			Protein intake	p = 0.00022	
D205839	20a13.13	514 subjects 99 families 347	Total energy intake	p = 0.00014	(1217)
2200007	20410110	sibships	Carbohydrate intake	p = 0.0009	(1217)
		sicompo	Fat intake	p = 0.0019	
			Protein intake	p = 0.00041	
D20S480	20q13.13	514 subjects, 99 families, 347	Total energy intake	p = 0.0003	(1217)
	1	sibships	Carbohydrate intake	p = 0.0006	
		I I	Fat intake	p = 0.0016	
			Protein intake	p = 0.0009	
D20S211	20q13.2	513 subjects, 92 families, 423 pairs	BMI	LOD = 3.2	(1288)
		513 subjects, 92 families, 423 pairs	Body fat (%)	LOD = 3.2	(1288)
D20S876	20q13.13	514 subjects, 99 families, 347	Total energy intake	p = 0.00012	(1217)
	1	sibships	Carbohydrate intake	p = 0.001	
		1	Protein intake	p = 0.00085	
D20S120	20q13.2	650 subjects, 258 pairs, 152 pedigrees	Body fat (%)	p = 0.004	(662)
D20S149	20q13.31-qter	667 subjects, 244 families	Body fat (%) (in whites and African Americans)	NPL = 2.57	(1274)
		513 subjects 92 families 423	BMI	LOD = 3.2	(1288)
		pairs	Body fat (%)	LOD = 3.2	(1200)
D21S1442	21a21.2	3383 subjects, 1124 families	Body fat (%) (women)	LOD = 1.8	(1227)
D21S2052	21q21.3	1510 subjects, 509 families	Factor central obesity	MLS = 2.13	(1247)
D21S1440	21a22.12	1510 Subjects, 509 families	Factor central obesity	MLS = 2.13	(1247)
D21S1446	21a22.3	1297 subjects, 260 families	Body fat (%)	LOD = 4.21	(1226)
		1297 subjects, 260 families	Body fat (%)	LOD = 4.27	(1246)
D22S264	22q11.21	453 subjects. 99 families	Abdominal subcutaneous fat	LOD = 1.96	(1237)
D22S1685 (D20S608)	22q11.21	318 subjects, 10 families	Leptin	p = 0.001	(1289)
A4GALT	22a13 31	>168 pairs	Body weight	p = 0.03	(1208)
DXS8099	Xp22.13	994 subjects 37 nedigrees	BMI	LOD = 2.6	(1200)
	1.P=2.15	, i subjects, 57 pedigrees	ar a r a f a	LOD 2.0	(1207)

Table 5.	(continued)
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Gene/marker	Location	Population	Phenotypes	Score	Reference
DXS997	Xp21.3	1148 subjects, 133 families, 190 European-American families (940 members); 43 African- American families (208 members)	Waist-to hip ratio (in European Americans and African Americans)	LOD = 2.7	(1290)
DX\$1003	Xp11.3	1148 subjects, 133 families, 190 European-American families (940 members); 43 African- American families (208 members)	Waist-to-hip ratio (in European Americans and African Americans)	LOD = 2.7	(1290)
DXS1059	Xq23	994 subjects, 37 pedigrees	BMI	LOD = 2	(1207)
DXS6804	Xq23	367 subjects, 166 families, 193 pairs	Obesity (in Finns)	LOD = 3.1	(1285)
DXS1220	Xq24	184 families, 218 sibships	Obesity	MLS = 1.93	(1059)
AGTR25747C/T	Xq24	184 families, 218 sibships	Obesity	MLS = 2.3	(1059)

LOD, logarithm of odds; MLS, maximum LOD score; NPL, non-parametric linkage.

undertaken in the same sample of European American families with the aim of detecting epistatic interactions among QTLs (1226). QTLs influencing BMI were found on chromosomes 2p24.2 and 4q28.3 and over a broad region of chromosome 13q21.1-q32.2, whereas QTLs influencing percentage body fat were found on chromosomes 12q24.21 and 21q22.3. Linkages with different obesity affection status (BMI \ge 27, 30, 35, and 40) were found on chromosomes 3q12.3, 7q21.3, 7q22.1, 8q13.3, 9q22.33, 12p13.31, 12q23.1, 13q13.2, and 13q13.3. Significant evidence of interactions was found between loci on chromosome regions 2p25-p24 and 13q13-q21 (1226).

A search for genes influencing BMI, WHR, and abdominal fat assessed by computed tomography scan was undertaken in 330 subjects from 154 African-American families and in 729 subjects from 275 Hispanic-American families (1210). In the African-American families, significant linkage to BMI was found on chromosomes 1p36 (LOD = 2.14) and 3p26.3 (LOD = 3.67). In the Hispanic-American families, a QTL for BMI was found on chromosome 17q23.2 and QTLs for WHR were found on chromosomes 8q24.11, 12q13.13-q15, 12q21-q21.33, and 12q22-q24.21. QTLs for abdominal fat were found on chromosomes 5q33.2-q35.1, 8q11.22-q12.1, and 17p13.3 for abdominal subcutaneous fat and on chromosome 11q12.13-q13.3 for abdominal visceral fat. The last genome scan study was a genome-wide linkage analysis of four factors related to the metabolic syndrome derived from a factor analysis of 10 risk factors (1247). Factor analysis yielded four different metabolic syndrome factors (obesity-insulin, blood pressure, lipids-insulin, and central obesity) that were tested for linkage with 400 microsatellite markers in four different ethnic groups (blacks, whites, Hispanics, Asians). Only results with the central obesity factor are reported in Table 5. Evidence of linkage was found on chromosomes 13q31.3, 13q32.2, 20p12.2, and 20p12.1 in blacks, on chromosomes 11q13.3, 21q21.3, and 21q22.12 in whites, and on chromosomes 3q22.1, 5q35.2, 6p25.1, 6p23, and 8p23.3 in Asians. No evidence of linkage was found in Hispanics (1247).

A bivariate linkage analysis of metabolic syndrome phenotypes (BMI, WC, lipids, and insulin) with 19 markers located on chromosome 7q11.22-q22.1 performed in 440 subjects from 27 Mexican-American families revealed evidence of univariate linkage for BMI (LOD = 2.4) and WC (LOD = 2.0) between markers D7S653 and D7S479 and linkages (LOD scores ranging from 1.86 to 4.21) for most of the bivariate traits (BMI-lipids, BMI-insulin, WC-lipids, WC-insulin, BMI-WC) to a 6-cM region near marker D7S653 (1203).

Finally, a meta-analysis of genome scans that used BMI as their primary obesity phenotype and were published before July 2003 was undertaken to identify QTLs influencing obesity (1204). A total of 29 genome scans were identified from the literature; of these studies, 13 analyzed BMI as a quantitative trait. Access to detailed results was requested from the authors of the 13 studies, and information was obtained in only 5 of the 13 studies. The results from these five studies, which included a total of 2814 individuals from 505 families, were jointly analyzed using a variance component approach. For the purpose of the analysis, the genome was divided into 121 30-cM regions called bins in such a way that the first bin on chromosome 1 (1.1) includes the results of markers tested between locations 0 and 30 cM, the second bin (1.2) encompasses the 30- to 60-cM region of chromosome 1, and so on for all chromosomes. For each scan, the bins were then sorted according to the maximum LOD score in that bin, and ranks were assigned with the lowest rank assigned to the bin with the

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	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005
Single-gene mutations*				2	6	6	6	6	6	6/7	10	11
KO and Tg									38	55	166	244
Mendelian disorders with map location	8	12	13	16	16	20	24	25	33	41	49	50
Animal QTLs	7	9	24	55	67	98	115	165	168	183	221	408
Human QTLs from genome scans				3	8	14	21	33	68	139	204	317
Candidate genes with positive findings	9	10	13	21	29	40	48	58	71	90	113	127
* Number of genes, not number of r	nutations											
8												

Table 6. Evolution in the status of the Human Obesity Gene Map

highest LOD score. Within each study, the ranks were weighted according to the number of genotyped individuals in the sample, and the weighted average rank was then calculated for each bin across the five studies. The bin with the lowest weighted average rank for all studies corresponded to the region of the genome showing the most evidence of linkage across all studies retained in the metaanalysis. The results of the analysis revealed that the lowest weighted average rank was found in bin 8.1, suggesting that the best evidence of linkage to BMI across all five studies is found at the location 0 to 30 cM on chromosome 8 (8pterp23.3). Based on permutation testing, this was the only region showing significant (p = 0.0005) evidence of linkage to BMI. Interestingly, only two of the five studies retained in the meta-analysis showed suggestive evidence of linkage to BMI in that region of chromosome 8.

Conclusion

The 2005 human obesity gene map is depicted in Figure 1. The map includes >600 loci from single-gene mutations in mouse models of obesity, non-syndromic human obesity cases due to single-gene mutations, obesity-related Mendelian disorders that have been mapped, transgenic and KO mice models, QTLs from cross-breeding experiments and genome-wide scans, and genes or markers that have been shown to be associated or linked with an obesity phenotype. The map reveals that putative loci affecting obesity-related phenotypes are found on all chromosomes except Y. The number of genes and other markers associated or linked with human obesity phenotypes continues to increase, as indicated by the numbers collated in Table 6. Based on the various lines of evidence reviewed in the different sections of this report, there are now 135 different candidate genes that have been associated and/or linked with obesity-related phenotypes. The majority of the 127 candidate genes associated with obesity have been identified in association studies (Table 4). With the growing number of genes and loci indexed in the map, several genes and QTLs identified from association and genome scan studies have been replicated. We can now identify 22 different genes that have shown

associations with obesity-related phenotypes in at least five studies. Among them, those showing replications in 10 studies and more include PPARG (30 studies), ADRB3 (29), ADRB2 (20), LEPR (16), GNB3 (14), UCP3 (12), ADIPOQ (11), LEP (11), UCP2 (11), HTR2C (10), NR3C1 (10), and UCP1 (10). The number of obesity QTLs identified from genome scans now reaches 253, which include 15 QTLs that have been replicated in at least three studies. The large number of genes and loci depicted in the obesity gene map is a good indication of the complexity of the task of identifying genes associated with the susceptibility to obesity. Although several of the genes listed in this report may be false positives, it is also clear that some genes are more important than others based on the numbers of replications from independent studies. A recent meta-analysis of genetic association studies concluded that, although false positive associations are abundant in the literature, 20% to 30% of genetic associations are real and have modest effects on risk of common diseases (1291). This would suggest that perhaps as many as 20 to 30 of the obesity candidate genes identified in this report might contribute to the risk of obesity in humans. Of course, the goal remains to identify the right combination of genes and mutations that are associated with this increased risk and to determine how envi-

Figure 1: The 2005 human obesity gene map. The map includes all obesity-related genes and QTLs identified from the various lines of evidence reviewed in this article. This year's map consists of a 862-band-resolution cytogenetic map overlaid with build 35.1 of the human genome sequence available from National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov). This allows the human genes (as abbreviated in the tables and appendix and located to the right of each chromosome in this figure) to be placed at precise positions on both the sequence and the cytogenetic map. For all loci, we used the name preferred by UniSTS or Entrez Gene. The ruler to the left of each figure represents kilobasepairs. Chromosomes are drawn to scale only within a given page and not on the last page. These maps, along with information from this report, can be browsed and searched interactively at the Obesity Gene Map web site (http://obesitygene.pbrc.edu).

		Chromosome 1		0	Chro	mosome 2
	J				0.01	
- 240000	1q43 1q44	D1S204	-	240000	2q37.2 2q37.3	CAPN10 STK25
	1q42.2 1q42.3	D19517 0UDV0			2q36.3 2q37.1	D2S396 D2S206 ALPI D2S1279
-	1q42.11 1q42.12 1q42.13	AGT	3		2q36.1 2q36.2	D2S1363 IRS1
- 220000	1042.11		2	220000	2q35	D2S434 PRKAG3
	1q32.3 1q41				2q33.3 2q34	IDH1
- 200000	1q32.2	HEN D1S456 HSD11B1		200000	2q33.2	
-	1q32.1		а .	000000	2q32.3 2q33.1	
	1q31.2 1q31.3		2		2q32.1	GDF8
- 180000	1q25.2 1q25.3	D1\$222	225 543 343	180000	2q31.2 2q31.3	
-	1q24.3 1q25.1				2q31.1	6660
	1q23.3 1q24.1 1g24.2	ATP1B1	20 -		2q24.3	BBS5
- 160000	1q23.1 1q23.2	APOA2 ATP1A2 NR1I3 D1S1679 BXBG D1S194		160000	2q23.3 2q24.1 2q24.2	GPD2
	1q21.3 1q22	S100A1 IL6R LMNA FPLD2	33		2q23.1 2q23.2	0201000
-	1q21.1		8		2q22.2 2q22.3	D2S1300
- 140000				140000	2q21.2 2q21.3 2q22.1	D2S1334
-	1q11 1q12				2q21.1	D25363
- 120000	1p12 1p11.2 1p11.1	U15534 HSD3B1		120000	2q14.2 2q14.3	D2S347
-	1p13.2 1p13.1	AMPD1 NHLH2	0		2q13 2q14.1	D2S160 IL1RN D2S410
1	1p13.3	D1S1631 D1S2726 KCNA3			2q12.2 2q12.3	D2S293
- 100000	1p21.2 1p21.1	- Protocol	-	100000	2q11.2	D1S193
1	1p22.1 1p21.3				2p11.1 2q11.1	ADRA2B
-	1p22.3		10		2p11.2	FABP1 IGKC
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-	1p31.3 1p31.2	LEPR	-		2p15 2p14	D00441
60000	1p32.2	DIC1 DHCR24 D1S200 PRKAA2 D1S476		60000	2p16.2 2p16.1	
-	1p33 1p32.3	D1S197	24		2p16.3	FSHR D2S2739 D2S1352
- 40000	1p34.2 1p34.1	D1S3721 D1S193 PTPRF		40000	2p22.1 2p21	D2S1356 ABCG5
	1p35.2 1p35.1 1p34.3	COL8A2	1		2p23.1 2p22.3 2p22.2	D2S367 D2S1788 D2S1346
1	1p36.11 1p35.3	NR0B2 SDC3			2p23.3 2p23.2	D2S165
- 20000	1p36.13 1p36.12	D1S552 ATCT051		20000	2p24.2 2p24.1	APOB SDC1
	1p36.23 1p36.22 1p36.21	TNFRSF1B			2p24.3	D2S1400 LPIN1
	1p36.32 1p36.31	D1S508 H6PD PGD	20 -		2p25.2 2p25.1	D2S2952
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-	3p26.2 3p26.1	D251204			4p16.2	DAS912
	3p25.3	GHRL SLC6A1 HBH1 Dastasa BDADO			4p16.1	
	3p25.2 3p25.1	D3S3608			4p15.33	
- 20000	3p24.3	D000000		20000	4p15.32 4p15.31	D4S2639 D4S2289
	3p24.2	D3S3038 THRB			4p15.2	PPARGC1A
	3p24.1				4p15.1	CCKAH D4S2397
	3p23	D3S2432 D3S1768				D4S3350 D4S2632
40000	3p22.3 3p22.2			40000	4p14	0432032
	3p22.1 3p21.33			10000	4p13	D4S1627
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60000	3p14.3		1		1912	NMU D4S3019 D4S1592
- 00000	3p14.2			60000	4q13.1	D453248
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	3p12.3		1		4q21.1	
- 80000	3p12.2		1	80000	4q21.21	
	3p12.1		1		4q21.23 4q21.3	
	3p11.1 3q11.1		1		4q22.1	
	3q11.2	PPS2/ADL6	1		4q22.2 4q22.3	UNC5C
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	3q13.2 3q13.31	Chr3q-region DRD3			4q26	
- 120000	3q13.32 3q13.33	ATA28H11 GSK3B	-	120000	4q27	FABP2
	3q21.1 3q21.2				4q28.1	6637
	3q21.3				4q28.2	
	3q22.1 3q22.2				4420.0	
- 140000	3q22.3	D3S1764	-	140000	4q31.1	UCP1 D4S1644
-	3q24				4q31.21	GYPA D4S2417 D4S406
	3q25.1	D3S1744			4q31.22 4q31.23	
	3q25.2				4q31.3	NPY2B
- 160000	3q25.31			160000	4402.1	D4S1629
-	3q25.33 3q26.1				4q32.2 4q32.3	NPY1R NPY5R
	3q26.2	SI C242			4033	
-	3q26.31	D3S3053 GHSR			4q34.1	D4S2431
- 180000	3q26.32	D352421 D3S3676		180000	4q34.2 4q34.3	
	3q27.1				4q35.1	
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- 5p1	15.32		6		6p25.1	SE30
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- Spi	10.2	D5S817			6p24.2 6p24.1	D6S2434
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- 20000 ^{5p1}	14.3		-	20000	2.123.901.0046.0	Y
- 5p1	14.2				6p22.2	D6S276
- 5p1	13.3		3		6p22.1	
501	13.2	NPR3 AMACRD5S426			6p21.32	LTA THE D6S273 HSPA18 BE
501	13.1	DEC2490			6p21.2	GLO1 GLO1
- 40000 5p1	12	D552489	-	40000	6p21.1	D65271
- X 5p1	11		6	1	6p12.3	003271
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	1000	D5\$407	3	. 1	6p12.2 6p12.1	
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- 5q1	13.2	CART			6q13	
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80000	14.1			80000	6q14.1	HTR1B
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	15	D5S1725 D5S1463		1	6q15	D6S462
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- 100000 5q2	21.1			100000	6q16.2	SIM1
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120000		D5S1505	-	120000	6q22.2 6q22.31	
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5q3	31.1]	6q23.1 6q23.2	ENPP1
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- 140000 5q3	31.3	D5S658	-	140000	6q24.1	D6S403
- 5q3	32	D5S1480			6q24.2	D6S1003
-	33.1	ADRB2 PPARGC1B	3		6q25.1	
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- 160000 5q3	34	APPA PTTG1	-	160000	6q26	
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140000	7q34	D7S495 D7S1824	140000	8q24.23 8q24.3		140000	9q34.3 D9S158 AGPAT2
]	7q32.2 7q32.3 7q33	D7S1804 D7S640	130000	8q24.22	12453505	130000	9q34.12 9q34.13 9q34.2 DBH
-	7q31.33 7q32.1	D7S680 D7S514 D7S504 D7S1875 LEP		8q24.21	D8S1179 MYC		9q34.11 AK1
- 120000	7q31.31 7q31.32	D7S2847	120000	8q24.11 8q24.12 8q24.13		120000	9q33.2
-	7q31.2	CAV1		8q23.3			9q32 D9S930 ORM1 9q33.1
	7q22.3 7q31.1	PRKAR2B D7S692	110000	8q23.1	D8S556 D8S1132	110000	9q31.2 D95299 9q31.3
	7q22.2	SEHPINE1 VGF D7S1799		8q22.2	D8S1136		9q31.1
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-	7q21.12			8q21.2 8q21.3			9q21.33 NTRK2 9q22.1 D9S257
- 80000	7q21.11	CD36	80000	8q21.12 8q21.13	FABP4	80000	9q21.31 9q21.32
-	7q11.23	WBSCR14		8q21.11	D8S2324		9q21.12 9q21.13 9q21.2 D9S1122
	7q11.22	D7S3046	70000	8q13.1 8q13.2	CRH	70000	9q13 9q21.11
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- 40000	7p14.1		40000	8p11.23 8p11.22	ADRB3 EIF4EBP1 SFRP1	40000	9p13.2 9p13.1 9p12
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- 20000	7p15.3	D7S3051 D7S1802 IL6	20000	8p21.3	LPL D8S282 GFRA2	20000	9p22.1 9p21.3
-	7p21.2 7p21.1	D7S2557		8p22	GATA151F02 D8S549		9p22.3
]	7p22.1 7p21.3		10000	8p23.1	D8S277	10000	9p23
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-0	☐ 10p15.3		-0	□ 11p15.5	DRD4			
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1	10q11.21			11011.2	D11S1993			
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70000	10022.1	D10S1646	70000	11q13.3	GAL	ф В	SCL2	
	10422.1			11910.4	D11S916 D11S2371 UCP2 UCP3			
1	10q22.2	D10S535		11q13.5	D11S1321 D11S911			
380000	10q22.3		80000	11q14.1	D11S2002			
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100000	10q24.2		100000		PGR D115940			
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		12p12.3			0 13p11.1			14q11.1		
20	000	12012.2		20000	A 13q12.11	D13S175	20000	A 14q11.2	D110710	
		12p12.1			13q12.12				D145742 D14S283	
		12p11.23	D1001040		13q12.13	D13S221		14q12	D14S1280	
30	000	12p11.22	01231042	30000	13q12.3		30000		D145008	
	Ę	12p11.21			13q13.1 13q13.2	D13S1493		14q13.1	D14S599	
	4	12q11			13q13.3	D125804		14q13.2 14q13.3 14q21.1		
40	000	12012		40000	13q14.11	D133694	40000			
								14q21.2		
		12q13.11	VDR WNITTOP		13q14.12 13q14.13	ESD HTR2A		14q21.3		
50	000	12q13.12 12q13.13	WINTIOD	50000	13q14.2		350000	14q22.1		
		12q13.2	MMP10			D13S257 D13S1807		14q22.2	D140076	
Lŧ.		12q13.3 12q14.1	D12PAH D12S1691		13q21.1			14q22.3 14q23.1	D143270	
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		12q15	TIMORE		13q21.32			14q24.1		
70	000	12021.1		70000	13921.33		70000	14q24.2	D14S588	
			D12S1052		13q22.1	D13S800		14q24.3	DATE	
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Gene or locus	Name	Location (NCBI)
A4GALT	α 1,4-Galactosyltransferase (P1 blood group)	22q13.31
ABCA7	ATP-binding cassette, subfamily A, member 7	19p13.3
ABCC8	ATP-binding cassette, subfamily C (CFTR/MRP), member 8 (sulfonylurea receptor)	11p15.1
ABCG5	ATP-binding cassette, subfamily G (WHITE), member 5 (sterolin 1)	2p21
ACACB	Acetyl-coenzyme A carboxylase β	12q24.1
ACADVL	Acyl-coenzyme A dehydrogenase, very long chain	17p13-p11
ACE	Angiotensin I-converting enzyme (peptidyl-dipeptidase A) 1	17q24.1
ACP1	Acid phosphatase 1, soluble	2p25
ADA	Adenosine deaminase	20q13.12
ADAM12	ADAM metallopeptidase domain 12 (meltrin α)	10q26.3
ADAMTS1	A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1	21q21.2
ADCYAP1	Adenylate cyclase-activating polypeptide 1 (pituitary)	18p11
ADIPOQ	Adiponectin, C1Q, and collagen domain containing	3q27
ADRA1B	Adrenergic, α -1B-, receptor	5q23-q32
ADRA2A	Adrenergic, α -2A-, receptor	10q24-q26
ADRA2B	Adrenergic, α -2B-, receptor	2q11.2
ADRB1	Adrenergic, β -1-, receptor	10q24-q26
ADRB2	Adrenergic, β -2-, receptor, surface	5q31-q32
ADRB3	Adrenergic, β -3-, receptor	8p12-p11.2
AEBP1	AE-binding protein 1	7p13
AGPAT2	1-Acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, β) (Bernardinelli-Seip congenital lipodystrophy 1)	9q34.3
AGRP	Agouti-related protein homolog (mouse)	16q22
AGT	Angiotensinogen (serine or cysteine) proteinase inhibitor, clade A (α -1 anti-proteinase, anti-trypsin; member 8)	1q42.2
AGTR2	Angiotensin II receptor, type 2	Xq22-23
AHO2	AHO 2	15q11-q13
AHSG	α -2-HS-glycoprotein	3q27
AK1	Adenylate kinase 1	9q34.13
AKT1	v-akt Murine thymoma viral oncogene homolog 1	14q32.3
AKT2	v-akt Murine thymoma viral oncogene homolog 2	19q13.1-13.2
ALMS1	Alstrom syndrome 1	2p13
ALPI	Alkaline phosphatase, intestinal	2q37.1
AMACR	α -Methylacyl-coenzyme A racemase	5p13.2-q11.1
ANGPTL4	Angiopoietin-like 4	19p13.3
ANGPTL6	Angiopoietin-like 6	19p13.2
ANMA	Anisomastia (with obesity)	16q13-q21
APOA1	Apolipoprotein A-I	11q23.3
APOA2	Apolipoprotein A-II	1q23.1
APOA4	Apolipoprotein A-IV	11q23.3
APOA5	Apolipoprotein A-V	11q23
APOB	Apolipoprotein B [including Ag(x) antigen]	2p24.2
APOC1	Apolipoprotein C-I	19q13.2
APOC3	Apolipoprotein C-III	11q23.1-q23.2
APOD	Apolipoprotein D	3q26.2-qter
APOE	Apolipoprotein E	19q13.32
AQP7	Aquaporin 7	9p13
AR	Androgen receptor (dihydrotestosterone receptor, testicular feminization, spinal and bulbar muscular atrophy, Kennedy disease)	Xq11.2-q12
ARID5B	AT-rich interactive domain 5B (MRF1-like)	10q21.2
ARL6	ADP-ribosylation factor-like 6	3q11.2
ASIP	Agouti signaling protein, non-agouti homolog (mouse)	20q11.2-q12
ASPA	Aspartoacylase (Canavan disease)	17pter-p13
ATP12A	ATPase, H^+/K^+ transporting, non-gastric, α polypeptide	13q12.12
ATP1A2	ATPase, Na ⁺ /K ⁺ transporting, $\alpha 2$ (+) polypeptide	1q23.1
ATP1B1	ATPase, Na ⁺ /K ⁺ transporting, β 1 polypeptide	1q23.3
ATP8B1	ATPase, class I, type 8B, member 1	18q21-q22
BATF	Basic leucine zipper transcription factor, ATF-like	14q24.3
BBS1	Bardet-Biedl syndrome 1	11q13.1
BBS2	Bardet-Biedl syndrome 2	16q21

Appendix.	Symbols, full names, a	nd cytogenetic location of	genes and loci of the 2005 human	obesity gene map
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Gene or locus	Name	Location (NCBI)	
BBS3(ARL6)	Bardet-Biedl syndrome 3	3p13-p12	
BBS4	Bardet-Biedl syndrome 4 (myosin IXA)	15q22.3-23	
BBS5	Bardet-Biedl syndrome 5	2q31	
BBS7	Bardet-Biedl syndrome 7	4q27	
BBS8(TTC8)	Tetratricopeptide repeat domain 8	14q32.1	
BDNF	BDNF	11p13	
BF	B-factor, properdin	6p21.31	
BRS3	Bombesin-like receptor 3	Xq26-q28	
BSCL2	Bernardinelli-Seip congenital lipodystrophy 2 (seipin)	11q13	
BUB1B	BUB1 budding uninhibited by benzimidazoles 1 homolog β (yeast)	15q15	
C19orf20	Chromosome 19 open reading frame 20	19p13.3	
C3	Complement component 3	19p13.3	
CAPN10	Calpain 10	2q37.3	
CART	Cocaine- and amphetamine-regulated transcript	5q13.2	
CAV1	Caveolin 1	7q31.1	
CAV3	Caveolin 3	3p25	
CBFA2T1	Core-binding factor, runt domain, α subunit 2; translocated to, 1; cyclin D-related	8q21.3	
CBL	Cas-Br-M (murine) ecotropic retroviral transforming sequence	11q23.3	
CCKAR	Cholecystokinin A receptor	4p15.1-15.2	
CCKBR	Cholecystokinin B receptor	11p15.4	
CCND3	Cyclin D3	6p21	
CD36	CD36 antigen (collagen type I receptor, thrombospondin receptor)	7q11.2	
CDH2	Cadherin 2 (N-cadherin 1)	18q11.2	
CDKN1A	Cyclin-dependent kinase inhibitor 1A	6p21.2	
CDKN1B	p27Kip1	12p13.1-p12	
CEBPA	CCAAT/enhancer-binding protein (C/EBP), α	19q13.1	
CEBPB	C/EBP, β	20q13.13	
CEBPD	C/EBP, Δ	8p11.2-11.1	
CHM	Choroideremia (Rab escort protein 1)	Xq21.2	
CHRM3	Cholinergic receptor, muscarinic 3	1q41-q44	
CIDEA	Cell death-inducing DFFA-like effector a	18p11.21	
CLOCK	Clock homolog (mouse)	4q12	
CNR1	Cannabinoid receptor (brain)	6q14-q15	
CNTFR	Ciliary neurotrophic factor receptor	9p13.2	
COH1	Cohen syndrome 1	8q22.2	
COL8A2	Collagen, type VIII, $\alpha 2$	1p34.3	
COMT	Catechol O-methyltransferase	22q11.21	
CORIN	Corin, serine peptidase	4p13-12	
CPE	Carboxypeptidase E	4q32.3	
CPT1A	Carnitine palmitoyltransferase 1A (liver)	11q13.1-13.2	
CRH	Corticotropin-releasing hormone	8q13	
CRHR1	Corticotropin-releasing hormone receptor 1	17q12-q22	
CRHR2	Corticotropin-releasing hormone receptor 2	7p14.3	
CYB5R4	Cytochrome b5 reductase 4	6pter-q22.33	
CYP11B2	Cytochrome P450, family 11, subfamily B, polypeptide 2	8q21-q22	
CYP19A1	Cytochrome P450, family 19, subfamily A, polypeptide 1	15q21.1	
CYP2D6	Cytochrome P450, family 2, subfamily D, polypeptide 6	22q13.1	
CYP7A1	Cytochrome P450, family 7, subfamily A, polypeptide 1	8q12.1	
DBH	Dopamine β -hydroxylase (dopamine β -monooxygenase)	9q34	
DF	D component of complement (adipsin)	19p13.3	
DGATI	Diacylglycerol O-acyltransferase homolog 1 (mouse)	8q24.3	
DHCR24	24-Dehydrocholesterol reductase	1p33-31.1	
DIOI	Deiodinase, iodothyronine, type I	1p33-p32	
DLKI	Δ -Like I homolog (<i>Drosophila</i>)	14q32.3	
DNAJC3	DnaJ (Hsp40) homolog, subtamily C, member 3	13q32	
DPT	Dermatopontin	1q12-23	
DRD2	Dopamine receptor D2	11q23.2	
DRD3	Dopamine receptor D3	3q13.3	
DRD4	Dopamine receptor D4	11p15.5	
<i>EIF4EBP1</i>	Eukaryotic translation initiation factor 4E-binding protein 1	8p12	

Gene or locus	Name	Location (NCBI)
ENPP1	Ectonucleotide pyrophosphatase/phosphodiesterase 1	6q23.1
EREG	Eniregulin	4013.3
ESD	Esterase D/formylglutathione hydrolase	13a14.11
ESR1	Estrogen receptor 1	6q25.1
ESR2	Estrogen receptor 2 (ER B)	14a23.2
ESRRA	Estrogen-related receptor α	11q13
FABP1	Fatty acid-binding protein 1, liver	2p11
FABP2	Fatty acid-binding protein 2, intestinal	4g27
FABP4	Fatty acid-binding protein 4, adipocyte	8q21
FABP5	Fatty acid-binding protein 5 (psoriasis-associated)	8q21.13
FASN	Fatty acid synthase	17q25
FGF21	Fibroblast growth factor 21	19q31.1-qter
FGFR3	Fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)	4p16.3
FKHL18	Forkhead-like 18 (Drosophila)	20q11.1-11.2
FMR1	Fragile X mental retardation 1	Xq28
FOSB	FBJ murine osteosarcoma viral oncogene homolog B	19q13.32
FOXA2	Forkhead box A2	20p11
FOXC2	Forkhead box C2 (MFH-1, mesenchyme forkhead 1)	16q22-q24
FSHR	Follicle-stimulating hormone receptor	2p21
FXYD4	FXYD domain containing ion transport regulator 4	10q11.21
GABRG3	γ -Aminobutyric acid A receptor, $\gamma 3$	15q11-q12
GAD2	Glutamate decarboxylase 2 (pancreatic islets and brain, 65 kDa)	10p11.23
GAL	Galanin	11q13.2
GAMT	Guanidinoacetate N-methyltransferase	19p13.3
GAS6	Growth arrestic-specific 6	13q34
GAST	Gastrin	17q21
GCGR	Glucagon receptor	17q25
GCK	Glucokinase (hexokinase 4, maturity onset diabetes of the young 2)	7p15.3-p15.1
GDF3	Growth differentiation factor 3	12p13.1
GDF8	Growth differentiation factor 8	2q232.2
GFPT1	Glutamine-fructose-6-phosphate transaminase 1	2p13
GFRA2	GDNF family receptor $\alpha 2$	8p21
GH1	Growth hormone (GH) 1	17q22-q24
GHR	GH receptor	5p13-12
GHRH	GH-releasing hormone	20q11.2
GHRHR	GH-releasing hormone receptor	7p14
GHRL	Ghrelin, GH secretagogue receptor ligand	3р26-р25
GHSR	GH secretagogue receptor	3q26.31
GIPR	Gastric inhibitory polypeptide receptor	19q13.3
GL01	Glyoxalase I	6p21.3-p21.1
GNAS	GNAS complex locus	20q13.2-q13.3
GNB3	Guanine nucleotide-binding protein (G-protein), β polypeptide 3	12p13
GNG3	Guanine nucleotide-binding protein (G-protein), γ^3	11p11
GPAM	Glycerol-3-phosphate acyltransferase, mitochondrial	10q25.2
GPCI	Glypican I	2q35-q37
GPC3	Glypican 3	Xq26.2
GPC4	Glypican 4	Xq26.1
GPD2	Glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	2q24.1
GPHB3	Glycoprotein hormone β 5	14q23.2
GPR10	G-protein-coupled receptor 10	10q26.13
GPR109A	G-protein-coupled receptor 109A	12q24.31
GPR24 CDD25	G-protein-coupled receptor 24	22q13.3
GPK33 CDD40	Contraction coupled receptor 55	2q37.3
GPR40	G-protein-coupled receptor 40	19913.1
GPK/	O-protein-coupled receptor /	8p22-q21.13
UPAI CDM5	Chitamata macantan matahatmarin 5	3p21.3
GRMS CDM8	Chitamate receptor, metabotropic 5	11q14.5
UKMO CSV2D	Character exertises linese 2.0	/ (q31.3-q32.1)
CVDA	Orycogen synthase kinase 5 p Chroophorin A (includes MN blood group)	5q15.5 4-21.1
UIFA	Grycophorni A (includes with blood group)	4931.1

Gene or locus	Name	Location (NCBI)
GYS1	Glycogen synthase 1 (muscle)	19q13.33
H6PD	Hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	1pter-p36.13
HCRT	Hypocretin (orexin) neuropeptide precursor	17q21
HD	Huntington (Huntington disease)	4p16.3
HDC	Histidine decarboxylase	15q21-q22
HEXB	Hexosaminidase B (β polypeptide)	5q13
HMGA2	High-mobility group AT-hook 2	12q15
HRH1	Histamine receptor H1	3p25
HRH3	Histamine receptor H3	20q13.3
HSD11B1	Hydroxysteroid (11- β) dehydrogenase 1	1q32-q41
HSD11B2	Hydroxysteroid (11- β) dehydrogenase 2	16q22
HSD3B1	Hydroxy- Δ -5-steroid dehydrogenase, 3 β - and steroid Δ -isomerase 1	1p11.2
HSPA1B	Heat shock 70-kDa protein 1B	6p21.31
HTR1B	5-Hydroxytryptamine (serotonin) receptor 1B	6q14.1
HTR2A	5-Hydroxytryptamine (serotonin) receptor 2A	13q14.11
HTR2C	5-Hydroxytryptamine (serotonin) receptor 2C	Xq24
ICAM1	Intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	19p13.2
IDE	Insulin-degrading enzyme	10q23-q25
IDH1	Isocitrate dehydrogenase 1 (NADP ⁺), soluble	2q33.3
IFRD1	Interferon-related developmental regulator 1	7q22-q31
IGF1	Insulin-like growth factor 1 (somatomedin C)	12q23.3
IGF2	Insulin-like growth factor 2 (somatomedin A)	11p15.5
IGFBP6	Insulin-like growth factor-binding protein 6	12q13
IGKC	Immunoglobulin kappa constant	2p11.2
IL1RN	Interleukin 1 receptor antagonist	2q14.2
IL6	Interleukin 6 (interferon, β^2)	7p21
IL6R	Interleukin 6 receptor	1g22
INPPL1	Inositol polyphosphate phosphatase-like 1	11q23
INS	Insulin	11p15.5
INSR	Insulin receptor	19p13.3-p13.2
IPW	Imprinted in Prader-Willi syndrome	15q11.2
IRS1	Insulin receptor substrate 1	2q36.3
IRS2	Insulin receptor substrate 2	13q34
ISL1	ISL1 transcription factor, LIM/homeodomain, (islet-1)	5q11.2
KCNA3	Potassium voltage-gated channel, shaker-related subfamily, member 3	1p13.3
KCNJ11	Potassium inwardly rectifying channel, subfamily J, member 11	11p15.1
KEL	Kell blood group	7q35
KLF5	Kruppel-like factor 5 (intestinal)	13q22.1
LDLR	Low-density lipoprotein receptor (familial hypercholesterolemia)	19p13.2
LEP	Leptin (obesity homolog, mouse)	7q31.3
LEPR	Leptin receptor	1p31
LHB	Luteinizing hormone β polypeptide	19q13.32
LIPA	Lipase A, lysosomal acid, cholesterol esterase (Wolfman disease)	10q23.2-q23.3
LIPC	Lipase, hepatic	15q21-23
LIPE	Lipase, hormone-sensitive	19q13.2
LMNA	Lamin A/C	1q23.1
LPIN1	Lipin 1	2p25.1
LPL	Lipoprotein lipase	8p21.3
LRPAP1	Low-density lipoprotein receptor-related protein-associated protein 1	4p16.3
LTA	Lymphotoxin α (TNF superfamily, member 1)	6p21.3
MACS2	SAH family member, acyl-coenzyme A synthetase for fatty acids	16p12.3
MAGEL2	MAGE-like 2	15q11.2
MAOA	Monoamine oxidase A	Xp11.4-p11.3
MAPK3	Mitogen-activated protein kinase 3	6p12-p11.2
MAPK8IP1	Mitogen-activated protein kinase 8-interacting protein 1	11p11.2
MC3R	Melanocortin 3 receptor	20q13.2-q13.3
MC4R	Melanocortin 4 receptor	18q22
MC5R	Melanocortin 5 receptor	18p11.21
MECP2	Methyl CpG-binding protein 2 (Rett syndrome)	Xq28

Gene or locus	Name	Location (NCBI)
MED12	Trinucleotide repeat contain mediator of RNA polymerase II transcription, subunit 12 homolog (veast)	Xq13.1
МЕНМО	Mental retardation, epileptic seizures, hypogonadism and -genitalism, microcephaly, and obesity syndrome	Xp22.13-p21.1
MEN1	Multiple endocrine neoplasia I	11q13
MEST	Mesoderm-specific transcript homolog (mouse)	7q32
MKKS	McKusick-Kaufman syndrome	20p12
MKRN3	Makorin, ring finger protein, 3	15q11.2
MLXIPL	MLX-interacting protein-like	7q11.23
MMP11	Matrix metallopeptidase 11 (stromelysin 3)	22q11.23
MMP19	Matrix metallopeptidase 19	12q14
MRXS11	Mental retardation, X-linked, syndromic 11	Xq26-q27
MRXS7	Mental retardation, X-linked, syndromic 7	Xp11.3-q22.1
MT1A	Metallothionein 1A (functional)	16q13
MTTP	Microsomal triglyceride transfer protein	4q24
MYC	Avian myelocytomatosis viral (v-myc) oncogene homolog	8q24.12-q24.13
NCB5OR	NADPH cytochrome B5 oxidoreductase	6pter-q22.33
NCOA3	Nuclear receptor coactivator 3	20q13.13
NDN	Necdin homolog (mouse)	15q11.2
NHLH2	Nescient helix loop helix 2	1p12-p11
NMB	Neuromedin B	15q22-qter
NMU	Neuromedin U	4q12
NOS2A	Nitric oxide synthase 2A (inducible, hepatocytes)	17q11.2-12
NPB	Neuropeptide B	17q25.3
NPR3	Natriuretic peptide receptor C/guanylate cyclase C (anti-natriuretic peptide receptor C)	5p14-p13
NPY	Neuropeptide Y	7p15.1
NPY1R	Neuropeptide Y receptor Y1	4q31.3-q32
NPY2R	Neuropeptide Y receptor Y2	4q31
NPY5R	Neuropeptide Y receptor Y5	4q31-q32
NR0B2	Nuclear receptor subfamily 0, group B, member 2	1p35.3
NR1H2	nuclear receptor subfamily 1, group H, member 2	19q13.3-13.2
NR113	Nuclear receptor subfamily 1, group I, member 3	1q23.3
NR3C1	Nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	5q31
NTRK2	Neurotrophic tyrosine kinase receptor type 2	9q22.1
NTSR1	Neurotensin receptor 1 (high affinity)	20q13-20q13
OPRM1	Opioid receptor, $\mu 1$	6q24-q25
ORM1	Orosomucoid 1	9q33.1
PAH	Phenylalanine hydroxylase	12q22-q24.2
PARPI	Poly (ADP-ribose) polymerase family, member 1	1q41-q42
PAX6	Paired box gene 6 (aniridia, keratitis)	11p13
PCSKI	Proprotein convertase subtilisin/kexin type 1	5q15-q21
PCSKIN	Proprotein convertase subtilisin/kexin type 1 inhibitor	Xp11.23
PEG3	Paternally expressed 3	19q31.4
PEMI	Phosphandyletnanolamine <i>iv</i> -melnylitansferase	1/p11.2
PGD	Prosphogluconate denydrogenase	11:22.2
PGK	Progesterone receptor	11q22.2 Va26.2
ГПГ0 DIV2D1	PHD Inger protein 0 Describer protein 0	Aq20.5
PIKJKI DID5V2D	Phosphoinosinde-5-Kinase, regulatory subunit 1 (pos α) Description A proceedings to A proceedings to B by A	5q15.1 17a12
DIA2C1D	Phosphalinese A2 group IP (paperose)	17412 12a22a241
PLAZOID PLIN	Darilinin	12q25-q24.1
PISCR1	Phospholinid scramblase 1	3a23
PISCR3	Phoenholinid scramblase 3	5q25 17p13 1
PMCH	Promelonin concentrating hormone	17p13.1
PMM2	Phosphomannomutase 2	12423-424.1 16n13 2
PNMT	Phenylethanolamine N-methyltransferase	17a21.2
POMC	propriore lanocortin (adrenocorticotropin/β-lipotropin/α-melanocyte stimulating hormone/β- melanocyte stimulating hormone/β-endorphin)	2p23.3
PON1	Paraoxonase 1	7a21.3
PON2	Paraovonase 2	7021.3
1 0112	i uruonomuse 2	1421.3

Gene or locus	Name	Location (NCBI)
POR	P450 (cytochrome) oxidoreductase	7q11.2
PPARA	Peroxisome proliferative-activated receptor, α	22q13.31
PPARD	Peroxisome proliferative-activated receptor, Δ	6p21.2-p21.1
PPARG	Peroxisome proliferative-activated receptor, γ	3p25
PPARGC1A	Peroxisome proliferative-activated receptor, γ , coactivator 1 α	4p15.1-15.2
PPARGC1B	Peroxisome proliferative-activated receptor, γ , coactivator 1, β	5q32
PPP1R3A	Protein phosphatase 1, regulatory (inhibitor) subunit 3A (glycogen and sarcoplasmic reticulum- binding subunit, skeletal muscle)	7q31.1
PPP1R3C	Protein phosphatase 1, regulatory (inhibitor) subunit 3C	10q23-q24
PPY	Pancreatic polypeptide	17q21
PRKAA2	Protein kinase, AMP-activated, $\alpha 2$ catalytic subunit	1p31
PRKAG3	AMP-aprotein kinase, AMP-activated, y3 non-catalytic subunit	2q35
PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, α (tissue-specific extinguisher 1)	17q24.3
PRKAR2B	Protein kinase, cAMP-dependent, regulatory, type II, β	7q22
PRKCQ	Protein kinase C, θ	10p15
PRLHR	Prolactin-releasing hormone receptor	10q26.13
PROP1	Prophet of Pit1, paired-like homeodomain transcription factor	5q35.3
PROX1	Prospero-related homeobox 1	1q32.2-q32.3
PTPN1	Protein tyrosine phosphatase, non-receptor type 1	20q13.1-q13.2
PTPN11	Protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome 1)	12q24
PTPNS1	Protein tyrosine phosphatase, non-receptor type substrate 1	20p13
PTPRF	Protein tyrosine phosphatase, receptor type, F	1p34
PTTG1	Pituitary tumor-transforming 1	5q35.1
PWCR1	Prader-Willi syndrome critical region 1	15q11.2
PWLSX	Prader-Willi-Like Syndrome, X-linked	Xq23-q25
PYY	Peptide YY	17q21.1
RAI1	Retinoic acid induced 1	17p11.2
RASGRF1	Ras protein-specific guanine nucleotide-releasing factor 1	15q24
REN	Renin	1q32
RETN	Resistin (FIZZ3)	19p13.2
REINLB	Resistin-like β	3q13.1
RPS6KA3	Ribosomal protein S6 kinase, 90 kDa, polypeptide 3	X p22.2-p22.1
RPSOKBI	Ribosomal protein S6 kinase, 70 kDa, polypeptide 1	1/q23.2
RSCIAI	Regulatory solute carrier protein, family 1, member 1	1p30.1
	Reliniou A receptor γ	1q22-q25
SAD SCADD1	SA hypertension-associated homolog (lat)	12024 21
SCARD1	Starril aconzuma A desaturasa 1	12424.31
SDC1	Stearyi-coenzyme A desaturase i	2n24.1
SDC1	Syndecan 3 (N-syndecan)	2p24.1 1pter_p22.3
SERPINE1	Serbin pentidase inhibitor, clade E (nevin, plasminogen activator inhibitor type 1), member 1	7a21 3-a22
SERP1	Secreted frizzled-related protein 1	8n12-n11 1
SGBS2	Simpson-Golabi-Behmel syndrome, type 2	Xp22
SGK	Serum/glucocorticoid regulated kinase	6023
SH2B	SH2-B homolog	16p11.2
SIM1	Single-minded homolog 1 (Drosophila)	6q16.3-q21
SLC2A2	Solute carrier family 2 (facilitated glucose transporter), member 2	3q26.31
SLC2A4	Solute carrier family 2 (facilitated glucose transporter), member 4	17p13
SLC6A1	Solute carrier family 6 (neurotransmitter transporter, γ -aminobutyric acid), member 1	3p25-p24
SLC6A14	Solute carrier family 6 (amino acid transporter), member 14	Xq23-q24
SLC6A3	Solute carrier family 6 (neurotransmitter transporter, dopamine), member 3	5p15.33
SNRPN	Small nuclear ribonucleoprotein polypeptide N	15q12
SOAT2	Sterol O-acyltransferase 2	12q13.13
SOCS3	Suppressor of cytokine signaling 3	17q25.3
SORBS1	Sorbin and SH3 domain containing 1	10q24.1
SOX8	SRY (sex determining region Y)-box 8	16p13.3
SPARC	Secreted protein, acidic, cysteine-rich (osteonectin)	5q31.3-q32
SREBF1	Sterol regulatory element-binding transcription factor 1	17p11.2
STAT3	Signal transducer and activator of transcription 3 (acute-phase response factor)	17q21.31
STAT5B	Signal transducer and activator of transcription 5B	17q11.2

Gene or locus	Name	Location (NCBI)
STK25	Serine/threonine kinase 25 (STE20 homolog, yeast)	2q37.3
TBX3	T-box 3 (ulnar mammary syndrome)	12q24.21
TCF1	Transcription factor 1, hepatic; LF-B1, hepatic nuclear factor (HNF1), albumin proximal factor	12q24.31
TGFB1	Transforming growth factor, $\beta 1$ (Camurati-Engelmann disease)	19q13.31
TH	Tyrosine hydroxylase	11p15.5
THRA	Thyroid hormone receptor, α [erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian]	17q11.2
THRB	Thyroid hormone receptor, β [erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian]	3p24.1
TKT	Transketolase (Wernicke-Korsakoff syndrome)	3p14.3
TNF	TNF (TNF superfamily, member 2)	6p21.3
TNFRSF1B	TNF receptor superfamily, member 1B	1p36.21
TUB	Tubby homolog (mouse)	11p15.5
TXNIP	Thioredoxin-interacting protein	1q21.1
UBL5	Ubiquitin-like 5	19p13.3
UBR1	Ubiquitin protein ligase E3 component n-recognin 1	15q13
UCP1	Uncoupling protein 1 (mitochondrial, proton carrier)	4q28-q31
UCP2	Uncoupling protein 2 (mitochondrial, proton carrier)	11q13.3
UCP3	Uncoupling protein 3 (mitochondrial, proton carrier)	11q13
UNC5C	unc-5 homolog C (C. elegans)	4q21-q23
VDR	Vitamin D (1,25- dihydroxyvitamin D3) receptor	12q13.11
VGF	VGF nerve growth factor inducible	7q22
VLDLR	Very-low-density lipoprotein receptor	9p24
VSX1	Visual system homeobox 1 homolog, CHX10-like (zebrafish)	20p11.21
WBSCR14	Williams Beuren syndrome chromosome region 14	7q11.23
WNT10B	Wingless-type MMTV integration site family, member 10B	12q13
WT1	Wilms tumor 1	11p13
WTS	Wilson-Turner X-linked mental retardation syndrome	Xq21.2-q22
ZFP36	Zinc finger protein 36, C3H type, homolog (mouse)	19q13.1