Supplementary Table S1

Behavioral testing at each phenotyping site

Behavioral tests at NY site

Approximate age	Procedure
21	Rats arrive in NY (approximately 21 days old).
35	Rats housed until they are approximately 35 days of age.
49	Social behavior
51	Locomotor activity.
71	Light reinforcement
98	Reaction Time
120	Delay Discounting:
122	Rats are transferred to a different animal facility
127	Pavlovian Condition Approach
138	Conditioned cue preference
148	Rats sacrificed; DNA for genotyping and tissue samples collected.

Behavioral tests at MI site

Approximate age	Procedure
21	Rats arrive in MI (approximately 21 days old).
35	Rats housed until they are approximately 35 days of age.
42	Pavlovian Condition Approach
55	Novelty seeking
60	Cocaine contextual conditioning
75	Rats sacrificed; DNA for genotyping and tissue samples collected.

Behavioral tests at TN site

Breeders

Approximate age	Procedure
21	Rats arrive in TN (approximately 21 days old).
35	Rats housed until breeding age and then bred for 1-2 cycles
170	Rats sacrificed; DNA for genotyping and tissue samples collected.

Experimental rats

Approximate age	Procedure
0	Rats are born from the HS breeders in TN animal facility
21	Behavior test battery (locomotor, social, etc)
36	Intravenous catheter implanter
38	Nicotine self-administration test for 12 days
51	Progressive ratio
52	Extinction
55	Reinstatement
85	Rats sacrificed; DNA for genotyping and tissue samples collected.

Supplementary Table S2

Effect of a covariate was regressed out if it was significant and explained more than 2% of the variance

Phenotype	covariates
Body Weight	Age, MI
	Age, TN breeders
	Age, TN experiment
Body Length NoTail	Age, NY
	Age, TN breeders
	Age, TN experiment
	Technician JS, TN experiment
	Technician XH, TN breeders
Body Length Tail	Age, MI
	Age, NY
	Age, TN experiment
	Technician ALE, MI
	Technician MM, MI
	Technician YL, TN experiment
BMI NoTail	Age, MI
	Age, NY
	Age, TN experiment
	Technician JS, TN experiment
	Technician XH, TN breeders
BMI Tail	Age, MI
	Age, NY
	Age, TN breeders
	Age, TN experiment
	Technician ALE, MI
	Technician MM, MI
RetroFat	Age, TN breeders
	Age, TN experiment
	Technician ALE, MI
	Technician MM, MI
EpiFat	Age, TN breeders
	Age, TN experiment
	Technician AG, NY

	Technician CTA, NY
	Technician NPR, NY
ParaFat	Age, NY
	Age, TN experiment
	Technician AH, MI
	Technician KP, NY
	Technician NPR, NY
	Technician WH, TN breeders
	Technician TW, TN experiment
	Technician WH, TN experiment
Fasting Glucose	Age, NY

Supplementary Table S3

Sex specific SNP Heritability estimates

Trait	Males Heritability $\pm$ SE	Females Heritability $\pm$ SE
body weight	0.45 $\pm$ 0.04	0.47 $\pm$ 0.04
body length_Tail	0.36 $\pm$ 0.04	0.35 $\pm$ 0.04
body length_NoTail	0.26 $\pm$ 0.04	0.27 $\pm$ 0.04
BMI_Tail	0.34 $\pm$ 0.04	0.25 $\pm$ 0.04
BMI_NoTail	0.28 $\pm$ 0.04	0.18 $\pm$ 0.04
RetroFat	0.47 $\pm$ 0.04	0.43 $\pm$ 0.04
EpiFat	0.37 $\pm$ 0.03	NA
ParaFat	NA	0.38 $\pm$ 0.04
Fasting Glucose	0.21 $\pm$ 0.04	0.19 $\pm$ 0.04

Supplementary Table S4

Summary of QTLs with strain distribution pattern of the founder strains. Pleiotropic loci are highlighted in yellow. Nearby loci that were not considered pleiotropic are highlighted in grey.

Trait	Chr	Peak Marker (bp)	-logP	Peak Marker			Genotype of the founders at the Peak Marker								LD Interval			Genes in the LD interval (no LOC...)	Credible Set Interval		
				Reference Allele	Allele frequency	Effect size	ACI	BN	BUF	F344	M520	MR	WN	WKY	start (bp)	stop (bp)	size (Mb)		start (bp)	stop (bp)	size (Mb)
BMI_Tail	1	106,866,154	6.05	G	0.29	0.15 ± 0.03	A A	G G	G G	G G	T T	G G	G G	A A	105,730,059	109,396,142	3.67	Ano5, Gas2, Ccdc179, Nell1, Fancf, Slc17a6, Svip	105,730,059	108,187,307	2.46
RetroFat	1	160,530,456	7.51	T	0.53	-0.14 ± 0.02	C C	T T	T T	T T	T T	T T	C C	T T	157,254,290	162,857,247	5.60	Dlg2, Ccdc90b, Mir708, Tenm4, Nars2, Gab2, Kctd21, Alg8, Ndufc2, Thrsp, Ints4, Aamdc, Clns1a, Aap11, Pak1	157,254,290	162,857,247	5.60
Body Weight	1	185,730,317	7.58	C	0.74	0.16 ± 0.02	T T	C C	T T	T T	C C	C C	C C	C C	184,463,432	187,738,111	3.27	Xylt1, Sox6, Pik3c2a, Rps13, Plekha7, Nucb2	184,812,645	187,300,775	2.49
BMI_NoTail	1	187,300,775	6.72	A	0.66	0.15 ± 0.02	G G	A A	G G	G G	G G	A A	A A	G G	184,772,616	189,346,447	4.57	Gp2, Xylt1, Rps15a, Gde1, Itprip12, Sox6, Umod, Acsm2, Tmc7, Iqck, Acsm5, Pik3c2a, Coq7, Syt17, Gprc5b, Gpr139, Knop1, Pdilt, Csp110, Rps13, Clec19a, Smg1, Plekha7, Tmc5, Nucb2, Arl6ip1, Vps35l	184,816,720	189,346,447	4.53
TL	1	253,524,003	5.76	G	0.45	0.13 ± 0.03	G G	C C	G G	G G	G G	G G	C C	G G	253,082,171	254,725,734	1.64	Ears2l1, Rpp30, Kif20b, Pank1, Mir107, Htr7	253,376,067	254,725,734	1.35
ParaFat	1	280,924,549	7.22	G	0.57	0.20 ± 0.03	G G	G G	A A	G G	G G	G G	G G	A A	280,876,316	282,114,080	1.24	Fam204a, Cacul1, Grk5, Prllr, Eif3a, Ces2i, Nanos1, Prdx3, Rab11fip2	280,924,333	282,114,080	1.19
Body Weight	1	281,756,885	16.21	C	0.58	0.21 ± 0.02	C C	C C	T T	C C	C C	C C	C C	T T	280,924,333	282,114,080	1.19	Fam204a, Prllr, Cacul1	281,402,451	282,114,080	0.71
RetroFat	1	281,777,218	20.21	A	0.57	0.24 ± 0.02	A A	A A	C C	A A	A A	A A	A A	C C	280,924,333	282,114,080	1.19	Fam204a, Cacul1, Grk5, Prllr, Eif3a, Ces2i, Nanos1, Prdx3, Rab11fip2	280,924,333	282,043,175	1.12
EpiFat	1	281,802,657	14.00	C	0.56	0.29 ± 0.03	C C	C C	T T	C C	C C	C C	T T	T T	280,924,333	282,736,275	1.81	Fam45a, Fam204a, Cacul1, Grk5, Prllr, Eif3a, Ces2i, Nanos1, Prdx3, Rab11fip2, Ces2, Ces2c, Sfxn4	280,924,333	282,114,080	1.19
BMI_Tail	1	282,049,439	11.44	C	0.55	0.18 ± 0.02	C C	C C	T T	C C	C C	C C	C C	T T	280,924,333	282,736,277	1.81	Fam45a, Fam204a, Cacul1, Grk5, Prllr, Eif3a, Ces2i, Nanos1, Rab11fip2, Prdx3, Ces2, Ces2c, Sfxn4	280,924,333	282,114,080	1.19
Body Weight	2	65,816,485	6.55	A	0.91	0.20 ± 0.03	G G	A A	G G	G G	G G	G G	G G	G G	62,570,942	71,814,490	9.24	Cdh10, Cdh9, Cdh12, Drosha, Cdh6, Egf	62,570,942	71,814,490	9.24
RetroFat	3	95,389,621	13.12	A	0.44	-0.19 ± 0.02	A A	A A	A A	A A	G G	A A	A A	A A	92,336,188	97,685,154	5.35	Cdt59, Ccdc73, Prrg4, Apip, Qser1, Cstf3, Nat10, Pdhx, Immp1l, Tcp111l, Eif3m, Cat, Pamr1, Dcdc1, Abtb2, Pax6, Rcn1, Ehf, Caprin1, Dcdc5, Lmo2, Depdc7, Elf5, Dnajc24, Hipk3, Wt1, Slc1a2, Cd44, Fbxo3, Elp4	94,050,143	95,685,634	1.64
Body Length_NoTail	3	136,021,511	6.92	A	0.77	-0.16 ± 0.03	G G	A A	G G	G G	G G	G G	G G	A A	132,291,573	137,146,532	4.85	Sel1l2, Ism1, Flrt3, Smrpb2, Tasp1, Esf1, Macrod2, Sptlc3, Ndufaf5, Kif16b	132,865,862	136,625,612	3.76
Body Length_Tail	3	136,021,511	5.97	A	0.77	-0.14 ± 0.03	G G	A A	G G	G G	G G	G G	G G	A A	132,291,573	137,146,532	4.85	Sel1l2, Ism1, Flrt3, Smrpb2, Tasp1, Esf1, Macrod2, Ndufaf5, Sptlc3, Kif16b	132,779,438	137,146,532	4.37
Body Weight	3	136,021,511	7.34	A	0.77	-0.16 ± 0.02	G G	A A	G G	G G	G G	G G	G G	A A	132,291,573	137,146,532	4.85	Sel1l2, Ism1, Flrt3, Tasp1, Esf1, Macrod2, Smrpb2, Ndufaf5, Sptlc3, Kif16b	134,319,381	137,146,532	2.83
RetroFat	3	137,537,161	8.21	G	0.44	-0.15 ± 0.02	A A	A A	A A	A A	G G	A A	A A	G G	136,161,761	138,849,437	2.69	Bfsp1, Banf2, Dstn, Rbbp9, Kat14, Otor, Polr3f, Smim26, Macrod2, Snrpb2, Dzank1, Mgme1, Pcsk2, Zfp133, Dtd1, Ovol2, Kif16b	136,178,205	138,775,911	2.60
Body Weight	5	50,933,779	6.99	G	0.78	-0.16 ± 0.03	G G	G G	G G	G G	A A	G G	G G	G G	49,152,709	50,940,275	1.79	Rbp1, Stx5, Sec23b	49,156,473	50,940,275	1.78
EpiFat	6	26,266,960	7.25	G	0.59	-0.20 ± 0.03	A A	G G	G G	G G	G G	G G	G G	A A	22,684,886	28,223,800	5.54	Alk, Clip4, Wdr43, Spdya, Pyp1cb, Srd5a2, Plb1, Fosl2, Babam2, Rbks, Slc4a1ap, Supt7l, Gpn1, Gckr, Ift172, Krtcap3, Nrbp1, Ppm1g, Zfp513, Snx17, Eif2b4, Gtf3c2, Mpv17, Ucn, Trim54, Dnajc5g, Slc30a3, Cad, Atraid, Slc5a6, Prr30, Preb, Abhd1, Cgref1, Khk, Emilin1, Osr4, Agbl5, Tmem214, Mapre3, Dpysl5, Cenpa, Slc35f6, Kcnk3, Otof, Drc1, Selenoi, Adgrf3, Hadhb, Hadha, Garem2, Babom2, Hadha, Ift172, Dnajc5g, Kcnk3, Garem2, Supt7l	22,940,602	28,164,637	5.22
RetroFat	6	28,148,338	19.50	G	0.65	-0.26 ± 0.02	G G	G G	G G	G G	G G	G G	G G	A A	25,954,450	28,752,109	2.80	Cenpo, Axsl2, Zfp512, Krtcap3, Agbl5, Tcf23, Dnajc27, Zfp513, Tmem214, Trnaa-agc6, Emilin1, Slc35f6, Mapre3, Drc1, Preb, Rab10, Ppm1g, Trim54, Snx17, Gpn1, Nrbp1, Ncoa1, Prr30, Trnay-gua3, Adcy3, Atraid, Abhd1, Khk, Slc5a6, Cib4, Ost4, Cad, Cenpa, Kif3c6 Rbks, Efr3b, Gckr, Gtf3c2, Dnmt3a, Ucn, Eif2b4, Hadhb, Pomc, Ptrhd1, Slc4a1ap, Dtnb, Adgrf3, Slc30a3, Selenoi, Mrpl33, Otof,	26,844,333	28,707,142	1.86
Body Length_Tail	6	137,745,191	5.89	C	0.54	-0.12 ± 0.02	T T	C C	C C	C C	C C	C C	C C	T T	136,769,305	138,087,183	1.32	Tmem179, Mta1, Cdca4, Crip2, Ahnak2, Brf1, Cep170b, Adssl1, Gpr132, Clba1, Pld4, Tedc1, Siva1, Tmem121, Akt1, Zbtb42, Ighe,	137,264,981	138,087,183	0.82
Body Weight	7	24,886,476	7.29	G	0.07	0.26 ± 0.04	G G	G G	C C	G G	G G	G G	G G	G G	24,869,890	25,213,445	0.34	Nudt14, Tex22, Inf2, Jag2, Pacs2, Btbd6, Crip1	24,869,890	25,144,762	0.27
Body Weight	7	36,497,588	9.77	C	0.14	-0.24 ± 0.03	C C	C C	G G	C C	G G	C C	G G	C C	34,119,928	36,522,260	2.40	Usp44, Rpl3113, Hal, Mir331, Vezt, Ndufa12, Ptxnc1, Snrpf, Elk3, Lta4h, Ntn4, Trnad-guc2, Cradd, Amdhd1, Fgd6, Tmcc3, Socs2,	34,156,704	36,517,726	2.36
Body Length_NoTail	7	36,517,726	7.88	T	0.12	-0.25 ± 0.04	T T	T T	C C	T T	C C	T T	C C	T T	34,119,928	36,522,260	2.40	Lta4h, Hal, Amdhd1, Snrpf, Ntn4, Usp44, Metap2, Mir331, Vezt, Fgd6, Nr2c1, Ndufa12, Tmcc3, Cradd, Socs2	34,156,704	36,522,260	2.37
Body Length_Tail	7	36,517,726	14.37	T	0.12	-0.33 ± 0.04	T T	T T	C C	T T	C C	T T	C C	T T	34,119,928	36,522,260	2.40	Metap2, Nr2c1, Ccdc38, Cep83	34,903,746	36,522,260	1.62
TL	7	36,526,715	6.10	A	0.37	0.14 ± 0.03	A A	A A	A A	A A	A A	A A	A A	G G	36,289,478	36,765,903	0.48	Nud54,Mrpl42,Ube2n,Socs2,Cradd	36,349,309	36,554,099	0.20
Body Length_Tail	8	118,711,320	5.72	A	0.67	0.13 ± 0.02	A A	A A	A A	A A	A A	A A	A A	G G	116,614,891	119,781,444	3.17	Pth1r, Myl3, Actl11, Usp19, Wdr6, Camp, Setd2, Prss46, Prss45, Qrich1, Gpx1, Cdc25a, Mst1, Pfkfb4, Nme6, Celsr3, Ptpn23, Inka1, Qars, Klhdc8b, P4htm, Epm2aip1, Slc26a6, Map4, Lzf, Lrrfip2, Traip, Mir3555, Mir191, Trank1, Ccdc71, Prss44, Rbm6, Mst1r, Fbxw12, Ccdc12, Mon1a, Prss50, Ip6k1, Rtp3, Ndufgf3, Cspg5, Impdh2, Smarcc1, Ccdc51, Tnes1, Ccrl2, Atrip, Tdgf1, Gmppb, Prss42, Arik2os, Apeh, Uba7, Als2cl, Klhl18, Amigo3, Dkz30, Ngp, Dclk3, Nicn1, Kif9, Rnf133, Mir425, Mlh1, Ip6k2, Rhoa, Camkv, Bsn, Nradd, Arih2, Nbeal2, Cdhr4, Elp6, Ccdc36, Prkar2a, Dalrd3, Amt, Nckipsd, Usp4, Dag1, Scap, Lrrc2, Spink8, Uqcrc1, Mir7111, Un2, Col7a1, Shisa5, Tmie, Lamb2, Slc25a20, Tma7, Ptxnb1, Tcta, Tmem89	117,632,634	119,768,313	2.14
Body Length_Tail	9	65,078,205	6.81	C	0.76	0.16 ± 0.03	T T	C C	C C	T T	T T	T T	T T	T T	64,013,585	65,670,399	1.66	Ndufb3, Aox4, Aox3, Cuxp8, Als2cr12, Tyw5, Mars2, Orc2, Kctd18, Aox1, Ppil3, Fam126b, Aox2, Sgo2, Clk1, Maip1, Spats2l, Cflar, Nif3l1, Bzw1	64,063,377	65,670,399	1.61
BMI_Tail	10	84,080,794	8.21	G	0.57	-0.16 ± 0.02	A A	G G	G G	G G	A A	G G	A A	G G	83,442,285	85,006,252	1.56	Snf8, Hoxb4, Oxbp7, Hoxb9, Mir10a, Cdk5rap3, Hoxb5os, Atp5mc1, Scrn2, Phb, Sp2, Mir196c, Hoxb5, Hoxb7, Hoxb6, Gngt2, Pnpo, Hoxb13, Gip, B4galnt2, Ttll6, Ube2z, Lrrc46, Nfe2l1, Abi3, Prr15l, Hoxb2, Hoxb8, Mrpl10, Hoxb3, Skap1, Hoxb1, Snx11,	83,442,285	84,604,288	1.16
TL	10	84,263,936	9.38	T	0.57	0.18 ± 0.03	C C	T T	C C	T T	C C	T T	C C	T T	83,442,285	85,006,252	1.56	Snf8, Hoxb4, Oxbp7, Hoxb9, Mir10a, Cdk5rap3, Hoxb5os, Atp5mc1, Scrn2, Phb, Sp2, Mir196c, Hoxb5, Hoxb7, Hoxb6, Gngt2, Pnpo, Hoxb13, Gip, B4galnt2, Ttll6, Ube2z, Lrrc46, Nfe2l1, Abi3, Prr15l, Hoxb2, Hoxb8, Mrpl10, Hoxb3, Skap1, Hoxb1, Snx11,	83,777,266	84,604,288	0.83
Body Length_Tail	10	85,082,795	7.37	G	0.72	0.17 ± 0.03	G G	C C	G G	C C	G G	C C	C C	G G	84,902,901	85,239,899	0.34	Osbpl7, Tbx21, Npepps, Sp2, Scrn2, Lrrc46, Mrpl10, Tbkbp1, Kpnb1, Sp6	85,063,786	85,239,899	0.18
BMI_NoTail	10	96,804,258	7.66	T	0.48	-0.16 ± 0.02	T T	C C	C C	T T	T T	T T	T T	C C	96,561,667	98,097,621	1.54	Prkca, Apoh, Caz112, Axin2, Rpl-1, Mif, Rex9, Gna13, Gpa-12, Amz2, Slc16a6, Arsg, Wipi1, Prkar1a, Kin-2, Fam20a	96,561,667	98,097,621	1.54
Fasting Glucose	10	109,944,213	6.33	A	0.75	-0.18 ± 0.03	G G	A A	A A	T T	T T	A A	T T	C C	108,350,175	110,315,359	1.97	Ccdc40, Gaa, Eif4a3, Nptx1, Rptor, Chmp6, Baiap2, Aatk, Mir3065, Mir338, Cep131, Mir3594, Mir3562, Tepsin, Ndufaf8, Actg1, Fscn2, Nploc4, Oxld1, Ccdc137, Hgs, Mrpl12, Slc25a10, Gcgr, Mcrip1, Pyp1r27, P4hb, Arhgdia, Alyref, Anapc11, Npb, Pcyt2, Sirt7, Mafg, Pycr1, Myadml2, Notum, Lrrc45, Dcxr, Rfng, Gps1, Dus1l, Fasn, Slc16a3, Csnk1d, Cd7, Sectm1b, Sectm1a, Tex19.2	108,362,930	110,315,359	1.95
Body Weight	10	111,010,289	6.10	T	0.41	0.13 ± 0.02	C C	T T	T T	C C	C C	C C	C C	C C	110,664,101	111,022,246	0.36	Tbcd, Znf750, B3gntl1, Metrnl	110,912,475	111,022,246	0.11
Body Length_Tail	11	2,199,384	8.94	C	0.18	-0.22 ± 0.03	T T	C C	T T	T T	T T	T T	T T	C C	846,435	5,587,624	4.74	Stxbp2, Kl, Snapc2, Rfc3, Higd2al1, Cd209f, Xab2, Cers4, Vom2r-ps90, Retn, Ctxn1, Dppa1-ps1, Camsap3, Elav1l, Pcp2, Lrrc8e, Evi5l, Cd209e, Vom2r60, Insr, Clec4g, Fcer2, Arkgef18, Prr36, Fry, Clec4m, Tex45, Rn5s, Trappc5, Vom2r-ps97, Vom2r58, Ccl25, Cd209c, Vom2r-ps91, Map2k7, Pet100, Cd209, Tgfbr3l, Cd209a, Mcoln1, Pnpla6, Timm44, Zfp358, Stard13, Vom2r-ps96, Vom2r...	874,769	1,365,748	0.49
Body Weight	12	5,738,696	9.12	C	0.59	0.16 ± 0.02	C C	C C	C C	T T	T T	T T	T T	C C	4,938,015	6,078,451	1.14	Rxfp2, Zfp958, Fry, Vom2r58, Vom2r-ps91, Lnc001	5,557,587	6,054,407	0.50
RetroFat	12	5,782,829	7.12	T	0.73	0.14 ± 0.02	C C	T T	C C	C C	G G	C C	C C	T T	455,837	6,259,634	5.80	Rxfp2, Zar1l, Pds5b, N4bp2l2, Zfp958, Stxbp2, Kl, Snapc2, Rfc3, Higd2al1, Cd209f, Brca2, Xab2, Cers4, Vom2r-ps90, Retn, Ctxn1, Dppa1-ps1, Camsap3, Elavi1, Pcp2, Lrrc8e, Evi5l, Cd209e, Vom2r60, Insr, Clec4g, Fcer2, Arhgef18, Prr36, Fry, Clec4m, LOC688432, Tex45, Rn5s, Trappc5, Vom2r-ps97, Vom2r58, Ccl25, Cd209c, Vom2r-ps91, Map2k7, Pet100, Cd209, Tgfbr3l, Cd209a, Mcoln1, Pnpla6, Timm44, Zfp358, Stard13, Vom2r-ps96, Vom2r-ps95, Vom2r-ps94, Mcemp1, Vom2r59, Pex11a, Lnc001	455,837	6,259,634	5.80
Body Length_NoTail	12	6,239,515	6.26	A	0.52	0.13 ± 0.02	A A	A A	A A	G G	G G	G G	G G	A A	6,078,237	7,035,028	0.96	Osbpl7, Rxfp2, Mednip, Hnpb1, Trnan-gua11, Tex26, B3glct, Alox5ap, Wdr95	6,078,237	7,035,028	0.96
Body Length_Tail	12	43,060,205	6.27	G	0.75	-0.15 ± 0.03	G G	G G	A A	A A	A A	A A	A A	G G	42,042,283	43,190,584	1.17	Oas1g, Tbx3, Tbx5	42,062,846	43,172,537	1.11
RetroFat	13	55,021,887	7.16	C	0.67	0.14 ± 0.02	C C	C C	G G	C C	C C	C C	C C	A A	54,910,667	56,487,438	1.58	Mir3570, Mir181, Ptprc, Atpfov1g3, Nek7, Lhx9, Crb1	54,910,667	56,387,208	1.48
TL	13	109,566,014	7.04	T	0.34	0.15 ± 0.03	C C	T T	T T	T T	T T	G G	T T	C C	108,055,241	111,868,706	3.81	slc41, Angel2, Vash2, Nx1l, RGD1560186, Traf5, Smyd2, Pacc1, Dtl, Ints7, Kcnk1	108,055,241	110,373,866	2.82
Body Length_NoTail	14	26,365,986	6.54	A	0.73	-0.16 ± 0.03	G G	A A	G G	G G	G G	G G	G G	A A	25,129,356	26,478,660	1.35	Epha5	25,725,806	26,478,660	0.75
Fasting Glucose	14	86,029,588	6.27	T	0.27	-0.17 ± 0.03	T T	T T	T T	T T	T T	C C	T T	C C	82,473,632	87,575,807	5.10	Nefh, Dusp18, Zmf3, Rnf185, Patz1, Ccdc117, Kremen1, Tug1, Maea, Depdc5, Ddx56, Myl7, Pold2, Thoc5, Rhbdd3, Lzf, Slc35e4, Sec14l4, Frg2, Ccdc157, Gck, Camk2b, Nudcd3, Pla2g3, Castor1, Aehp1, Adcy1, Mrps24, Cabp7, Tcn2, Urgcp, Parb, Nkx1-1, Limk2, Spon2, Rnf215, Pisd, Tbc1d10a, Slc5a1, Dbnl, Nipsnap1, Rnr1, Myo1g, Uvssa, Hormad2, Smn, Polm, Wap, Sec14l3, Gal3st1, Osm, Pik3ip1, Selenom, Snrpg-ps1, Uqcr10, Mtmr3, Zmat5, Ctbp1, Ppia, Igfbp1, Twhah, Nf2, Ramp3, Sec14l2, H2afv, Ascc2, Tmed4, Morc2, Prr14l, Ykt6, Ap1b1, Nacad, Sfi1, Pes1, Ankrd36, Tbrg4, Ccm2, Zmiz2, Inpp5j, Xbp1, Emid1, Sf3a1, Npc1l1, Mpl1, Pgam2, Igfbp3, Eif4enif1, Eif6-ps1, Ogdh, Drg1, Ras110a, Gas2l1, Oshp2	85,206,177	86,459,891	1.25
Body Length_NoTail	16	64,014,119	6.35	G	0.55	0.13 ± 0.02	G G	G G	G G	A A	G G	G G	A A	A A	64,003,027	64,416,540	0.41	Nrg1	64,003,283	64,416,540	0.41
EpiFat	18	12,674,871	6.47	G	0.22	-0.22 ± 0.04	G G	G G	G G	G G	G G	G G	A A	G G	12,597,378	12,792,162	0.19	Klhl14	12,597,378	12,745,926	0.15
BMI_NoTail	18	25,190,274	5.78	C	0.04	-0.34 ± 0.07	C C	C C	C C	C C	T T	C C	C C	T T	23,785,532	25,418,376	1.63	Polr2d, Bin1, Svt4	23,848,600	25,364,185	1.52
TL	19	32,004,685	7.81	C	0.41	-0.15 ± 0.03	C C	C C	C C	T T	T T	C C	C C	C C	31,176,512	32,698,569	1.52	Anapc10,Mmaa,Zfp827,Abcel,Smad1,Otud4,Hhip	31,176,512	32,260,219	1.08

Supplementary Table S5. Variant annotation and SDP for 153 potentially damaging coding variants identified for 18 QTLs . Yellow highlights indicate coding variants in which the SDP matches that of the peak marker at the QTL.

Trait	Peak.Marker	SNP in LD with Peak Marker	ref	alt	effect	impact	gene	Transcript.ID	cDNA.position	SNP.change	Amino.acid.change	ACI	BN	BUF	F344	M520	MR	WN	WKY
Fasting Glucose	chr10:109944213	chr10:108582280	C	G	missense_variant	MODERATE	Rnf213	ENSRNOT00000044983.5	9502	c.9502C>G	p.His3168Asp	GG	CC	GG	GG	GG	GG	GG	GG
		chr10:108582544	T	C	missense_variant	MODERATE	Rnf213	ENSRNOT00000044983.5	9766	c.9766T>C	p.Trp3256Arg	CC	TT	CC	CC	CC	CC	CC	CC
		chr10:108604073	G	C	missense_variant	MODERATE	Rnf213	ENSRNOT00000044983.5	12263	c.12263G>C	p.Ser4088Thr	CC	GG	CC	CC	CC	CC	CC	CC
		chr10:109244743	T	C	missense_variant	MODERATE	Cep131	ENSRNOT00000005977.6	2802	c.2729A>G	p.Asn910Ser	CC	TT	CC	CC	CC	CC	CC	CC
		chr10:109251307	A	G	missense_variant	MODERATE	Cep131	ENSRNOT00000005977.6	1311	c.1238T>C	p.Leu413Pro	GG	AA	GG	GG	GG	GG	GG	GG
		chr10:109264307	T	C	missense_variant	MODERATE	Cep131	ENSRNOT00000005977.6	125	c.52A>G	p.Met18Val	CC	TT	CC	CC	CC	CC	CC	CC
		chr10:109286225	G	A	missense_variant	MODERATE	Slc38a10	ENSRNOT00000006225.8	2491	c.2231C>T	p.Ala744Val	AA	GG	AA	AA	AA	AA	AA	AA
		chr10:109296990	A	G	missense_variant	MODERATE	Slc38a10	ENSRNOT00000006225.8	1528	c.1268T>C	p.Val423Ala	GG	AA	GG	GG	GG	GG	GG	GG
		chr10:109549959	C	G	missense_variant	MODERATE	Faap100	ENSRNOT00000054974.4	697	c.695G>C	p.Ser232Thr	GG	CC	GG	GG	GG	GG	GG	GG
		chr10:109550184	T	C	missense_variant	MODERATE	Faap100	ENSRNOT00000054974.4	472	c.470A>G	p.His157Arg	CC	TT	CC	CC	CC	CC	CC	CC
		chr10:110252682	T	C	missense_variant	MODERATE	Sectm1b	ENSRNOT00000054932.4	405	c.235A>G	p.Lys79Glu	CC	TT	CC	CC	CC	CC	CC	CC
Body Length_Tail	chr12:2199384	chr12:2001010	C	A	missense_variant	MODERATE	Pex11g	ENSRNOT00000037564.4	569	c.520G>T	p.Val174Leu	CC	CC	CC	AA	AA	AA	AA	CC
Tail Length	chr13:109566014	chr13:108143993	T	A	missense_variant	MODERATE	Cenpf	ENSRNOT00000004525.6	13	c.6071A>T	p.Asn2024Ile	AA	TT	TT	TT	TT	AA	TT	AA
		chr13:108147187	C	T	missense_variant	MODERATE	Cenpf	ENSRNOT00000004525.6	12	c.4382G>A	p.Gly1461Glu	TT	CC	CC	CC	CC	TT	CC	TT
		chr13:108148751	G	A	missense_variant	MODERATE	Cenpf	ENSRNOT00000004525.6	12	c.2818C>T	p.Leu940Phe	AA	GG	GG	GG	GG	AA	GG	AA
		chr13:108149351	C	T	missense_variant	MODERATE	Cenpf	ENSRNOT00000004525.6	12	c.2218G>A	p.Val740Ile	TT	CC	CC	CC	CC	TT	CC	TT
		chr13:108444314	A	G	missense_variant	MODERATE	LOC498308	ENSRNOT00000048200.1	7	c.569T>C	p.Val190Ala	GG	AA	AA	AA	AA	GG	AA	AA
		chr13:108444439	T	G	missense_variant	MODERATE	LOC498308	ENSRNOT00000048200.1	6	c.556A>C	p.Thr186Pro	GG	TT	TT	TT	TT	GG	TT	TT
		chr13:108444440	G	T	missense_variant	MODERATE	LOC498308	ENSRNOT00000048200.1	6	c.555C>A	p.Asn185Lys	TT	GG	GG	GG	GG	TT	GG	GG
		chr13:108681633	A	G	missense_variant	MODERATE	Smyd2	ENSRNOT00000004783.6	9	c.851A>G	p.Asn284Ser	GG	AA	AA	AA	AA	GG	GG	AA
		chr13:110372281	C	G	missense_variant	MODERATE	RGD15601	ENSRNOT00000049634.2	1	c.118C>G	p.Pro40Ala	GG	CC	CC	CC	CC	GG	CC	CC
		chr13:55284064	C	T	missense_variant	MODERATE	Atp6v1g3	ENSRNOT00000029679.4	194	c.166C>T	p.Arg56Cys	CC	CC	CC	TT	CC	CC	TT	CC
RetroFat	chr13:55021887	chr13:56262414	C	T	missense_variant	MODERATE	AABR0702	ENSRNOT00000032908.2	209	c.209C>T	p.Pro70Leu	TT	CC	TT	CC	TT	TT	CC	CC
		chr13:56262920	G	A	missense_variant	MODERATE	AABR0702	ENSRNOT00000032908.2	692	c.692G>A	p.Arg231His	GG	GG	GG	AA	GG	GG	AA	GG
		chr13:56262923	C	T	missense_variant	MODERATE	AABR0702	ENSRNOT00000032908.2	695	c.695C>T	p.Pro232Leu	CC	CC	CC	TT	CC	CC	TT	CC
		chr13:56263171	T	A	missense_variant	MODERATE	AABR0702	ENSRNOT00000032908.2	929	c.929T>A	p.Val310Glu	TT	TT	TT	AA	TT	TT	AA	TT
		chr14:85271424	G	A	missense_variant	MODERATE	Ap1b1	ENSRNOT00000057407.4	1850	c.1822G>A	p.Ala608Thr	GG	GG	GG	GG	GG	GG	GG	AA
Fasting Glucose	chr14:86029588	chr14:85271424	G	A	missense_variant	MODERATE	Ap1b1	ENSRNOT00000089866.1	1987	c.1822G>A	p.Ala608Thr	GG	GG	GG	GG	GG	GG	GG	AA
		chr14:85756355	A	G	missense_variant	MODERATE	Xbp1	ENSRNOT00000014044.6	397	c.397A>G	p.Asn133Asp	AA	AA	AA	AA	AA	AA	AA	GG
		chr14:85833986	A	G	missense_variant	MODERATE	Ankrd36	ENSRNOT00000083756.1	1066	c.857A>G	p.Glu286Gly	AA	AA	AA	AA	AA	AA	AA	GG
		chr14:86071569	T	C	missense_variant	MODERATE	Polm	ENSRNOT00000018319.6	1163	c.916A>G	p.Met306Val	TT	TT	TT	TT	TT	TT	TT	CC
		chr14:86071595	G	A	missense_variant	MODERATE	Polm	ENSRNOT00000018319.6	1137	c.890C>T	p.Ala297Val	GG	GG	GG	GG	GG	GG	GG	AA
		chr14:86077302	C	T	missense_variant	MODERATE	Polm	ENSRNOT00000018319.6	606	c.359G>A	p.Arg120Gln	CC	CC	CC	CC	CC	CC	CC	TT
		chr14:86077440	T	C	missense_variant	MODERATE	Polm	ENSRNOT00000018319.6	468	c.221A>G	p.Glu74Gly	TT	TT	TT	TT	TT	TT	TT	CC
		chr14:86116112	G	A	missense_variant	MODERATE	Pold2	ENSRNOT00000019288.4	263	c.187C>T	p.Pro63Ser	GG	GG	GG	GG	GG	GG	GG	AA
		chr14:86116112	G	A	missense_variant	MODERATE	Pold2	ENSRNOT00000084633.1	252	c.187C>T	p.Pro63Ser	GG	GG	GG	GG	GG	GG	GG	AA
		chr14:86387400	G	T	missense_variant	MODERATE	Ddx56	ENSRNOT00000089384.1	37	c.17C>A	p.Ala6Glu	GG	GG	GG	GG	GG	GG	GG	TT
Body Length_NoTail	chr16:64014119	chr16:64052952	A	G	missense_variant	MODERATE	Nrg1	ENSRNOT00000014147.6	1422	c.1078A>G	p.Ile360Val	GG	AA	GG	GG	GG	AA	GG	GG
		chr16:64052952	A	G	missense_variant	MODERATE	Nrg1	ENSRNOT00000013991.8	1876	c.1255A>G	p.Ile419Val	GG	AA	GG	GG	GG	AA	GG	GG
		chr16:64052952	A	G	missense_variant	MODERATE	Nrg1	ENSRNOT00000014268.8	1500	c.1156A>G	p.Ile386Val	GG	AA	GG	GG	GG	AA	GG	GG
		chr16:64052952	A	G	missense_variant	MODERATE	Nrg1	ENSRNOT00000081522.1	1891	c.1270A>G	p.Ile424Val	GG	AA	GG	GG	GG	AA	GG	GG
		chr16:64052952	A	G	missense_variant	MODERATE	Nrg1	ENSRNOT00000082355.1	1876	c.1255A>G	p.Ile419Val	GG	AA	GG	GG	GG	AA	GG	GG
		chr16:64052952	A	G	missense_variant	MODERATE	Nrg1	ENSRNOT00000058727.4	1446	c.1102A>G	p.Ile368Val	GG	AA	GG	GG	GG	AA	GG	GG
		chr16:64052952	A	G	missense_variant	MODERATE	Nrg1	ENSRNOT00000038549.7	1320	c.976A>G	p.Ile326Val	GG	AA	GG	GG	GG	AA	GG	GG
RetroFat	chr1:160530456	chr1:162354117	G	A	missense_variant	MODERATE	Alg8	ENSRNOT00000016478.6	891	c.869G>A	p.Ser290Asn	AA	GG	GG	GG	GG	GG	AA	AA
		chr1:162361693	G	A	missense_variant	MODERATE	Alg8	ENSRNOT00000016478.6	1548	c.1526G>A	p.Arg509Lys	GG	GG	GG	GG	GG	GG	AA	GG
BMI_Tail	chr1:282049439	chr1:281755911	C	T	start_lost	HIGH	Prlhr	ENSRNOT00000013170.4	23	c.3G>A	p.Met1?	CC	CC	TT	CC	CC	CC	CC	TT
Body Weight	chr1:281756885	chr1:281755911	C	T	start_lost	HIGH	Prlhr	ENSRNOT00000013170.4	23	c.3G>A	p.Met1?	CC	CC	TT	CC	CC	CC	CC	TT
ParaFat	chr1:280924549	chr1:281755911	C	T	start_lost	HIGH	Prlhr	ENSRNOT00000013170.4	23	c.3G>A	p.Met1?	CC	CC	TT	CC	CC	CC	CC	TT
RetroFat	chr1:281777218	chr1:281755911	C	T	start_lost	HIGH	Prlhr	ENSRNOT00000013170.4	23	c.3G>A	p.Met1?	CC	CC	TT	CC	CC	CC	CC	TT
EpiFat	chr1:281802657	chr1:281755911	C	T	start_lost	HIGH	Prlhr	ENSRNOT00000013170.4	23	c.3G>A	p.Met1?	CC	CC	TT	CC	CC	CC	CC	TT
Body Weight	chr2:65816485	chr2:62875814	C	G	missense_variant	MODERATE	RGD13065	ENSRNOT00000039234.3	1109	c.1004G>C	p.Ser335Thr	TT	CC	TT	TT	TT	TT	TT	TT

Trait	Locus	Position	Ref	Alt	Effect	Impact	Gene	Transcript	Pos	cDNA	Protein	S1	S2	S3	S4	S5	S6	S7	S8
Body Weight	chr2:65810485	chr2:62875821	G	C	missense_variant	MODERATE	RGD13065	ENSRNOT00000039234.3	1102	c.997C>G	p.Leu333Val	AA	GG	AA	AA	AA	AA	AA	AA
RetroFat	chr3:137537161	chr3:136742468	T	G	missense_variant	MODERATE	Kif16b	ENSRNOT00000036273.4	2319	c.2263A>C	p.Lys755Gln	GG	TT	TT	TT	GG	GG	TT	TT
		chr3:136742468	T	G	missense_variant	MODERATE	Kif16b	ENSRNOT00000083061.1	2474	c.2260A>C	p.Lys754Gln	GG	TT	TT	TT	GG	GG	TT	TT
		chr3:138610633	G	A	missense_variant	MODERATE	Zfp133	ENSRNOT00000031623.3	375	c.242G>A	p.Arg81Gln	GG	GG	GG	GG	GG	GG	GG	AA
		chr3:138615104	T	A	missense_variant	MODERATE	Zfp133	ENSRNOT00000031623.3	1253	c.1120T>A	p.Phe374Ile	TT	TT	TT	TT	TT	TT	TT	AA
RetroFat	chr3:95389621	chr3:92494088	A	C	missense_variant	MODERATE	Pamr1	ENSRNOT00000064282.2	1026	c.905A>C	p.Glu302Ala	CC	AA	CC	CC	AA	CC	AA	AA
		chr3:92501374	A	G	missense_variant	MODERATE	Pamr1	ENSRNOT00000064282.2	2096	c.1975A>G	p.Asn659Asp	AA	AA	AA	AA	AA	AA	AA	AA
		chr3:92910764	A	G	missense_variant	MODERATE	Pdhx	ENSRNOT00000009552.5	1196	c.1156T>C	p.Tyr386His	AA	AA	AA	AA	GG	AA	GG	AA
		chr3:92924011	G	C	missense_variant	MODERATE	Pdhx	ENSRNOT00000088242.1	842	c.748C>G	p.Pro250Ala	GG	GG	GG	GG	CC	GG	CC	GG
		chr3:92924011	G	C	missense_variant	MODERATE	Pdhx	ENSRNOT00000009552.5	746	c.706C>G	p.Pro236Ala	GG	GG	GG	GG	CC	GG	CC	GG
		chr3:92947902	C	T	missense_variant	MODERATE	Pdhx	ENSRNOT00000088242.1	300	c.206G>A	p.Arg69Gln	CC	CC	CC	CC	TT	CC	TT	CC
		chr3:94018570	G	A	missense_variant	MODERATE	Cd59	ENSRNOT00000067085.3	102	c.11G>A	p.Arg4Gln	GG	GG	GG	GG	AA	GG	AA	GG
		chr3:94353600	C	A	missense_variant	MODERATE	Hipk3	ENSRNOT00000089554.1	3343	c.3210G>T	p.Leu1070Phe	CC	CC	CC	CC	AA	CC	AA	CC
		chr3:94353600	C	A	missense_variant	MODERATE	Hipk3	ENSRNOT00000015775.3	3614	c.3144G>T	p.Leu1048Phe	CC	CC	CC	CC	AA	CC	AA	CC
		chr3:94982464	C	T	missense_variant	MODERATE	Ccdc73	ENSRNOT00000041362.5	2435	c.2219C>T	p.Pro740Leu	CC	CC	CC	CC	TT	CC	TT	CC
		chr3:97349458	G	A	missense_variant	MODERATE	Dcdc5	ENSRNOT00000041494.4	359	c.359G>A	p.Arg120His	GG	GG	GG	GG	GG	GG	GG	AA
		chr3:97396118	G	A	missense_variant	MODERATE	Dcdc5	ENSRNOT00000041494.4	1307	c.1307G>A	p.Ser436Asn	GG	GG	GG	GG	GG	GG	AA	GG
		chr3:97396118	G	A	missense_variant	MODERATE	Dcdc5	ENSRNOT00000089524.1	1174	c.1043G>A	p.Ser348Asn	GG	GG	GG	GG	GG	GG	AA	GG
		chr3:97398578	A	C	missense_variant	MODERATE	Dcdc5	ENSRNOT00000041494.4	1500	c.1500A>C	p.Glu500Asp	AA	AA	AA	AA	AA	AA	CC	AA
		chr3:97398578	A	C	missense_variant	MODERATE	Dcdc5	ENSRNOT00000089524.1	1367	c.1236A>C	p.Glu412Asp	AA	AA	AA	AA	AA	AA	CC	AA
Body Weight	chr5:50933779	chr5:50066002	G	A	missense_variant	MODERATE	Orc3	ENSRNOT00000011085.4	250	c.250C>T	p.Leu84Phe	AA	GG	GG	AA	GG	AA	GG	GG
Body Length_Tail	chr6:137745191	chr6:137323809	G	A	missense_variant	MODERATE	Pld4	ENSRNOT00000029017.3	97	c.77G>A	p.Arg26Lys	AA	GG	GG	GG	GG	AA	GG	AA
		chr6:137326285	T	C	missense_variant	MODERATE	Pld4	ENSRNOT00000029017.3	331	c.311T>C	p.Phe104Ser	CC	TT	TT	TT	TT	CC	TT	CC
		chr6:137337270	G	A	missense_variant	MODERATE	Ahnak2	ENSRNOT00000039631.4	15980	c.15785C>T	p.Pro5262Leu	AA	GG	GG	GG	GG	AA	GG	AA
		chr6:137339352	A	G	missense_variant	MODERATE	Ahnak2	ENSRNOT00000039631.4	13898	c.13703T>C	p.Val4568Ala	GG	AA	AA	AA	AA	GG	AA	GG
		chr6:137347877	A	T	missense_variant	MODERATE	Ahnak2	ENSRNOT00000039631.4	5373	c.5178T>A	p.His1726Gln	TT	AA	AA	AA	AA	TT	AA	TT
		chr6:137347903	G	A	missense_variant	MODERATE	Ahnak2	ENSRNOT00000039631.4	5347	c.5152C>T	p.Pro1718Ser	AA	GG	GG	GG	GG	AA	GG	AA
		chr6:137348049	A	G	missense_variant	MODERATE	Ahnak2	ENSRNOT00000039631.4	5201	c.5006T>C	p.Val1669Ala	GG	AA	AA	AA	AA	GG	AA	GG
		chr6:137348399	C	T	missense_variant	MODERATE	Ahnak2	ENSRNOT00000039631.4	4851	c.4656G>A	p.Met1552Ile	TT	CC	CC	CC	CC	TT	CC	TT
		chr6:137348644	T	C	missense_variant	MODERATE	Ahnak2	ENSRNOT00000039631.4	4606	c.4411A>G	p.Asn1471Asp	CC	TT	TT	TT	TT	CC	TT	CC
		chr6:137348665	A	G	missense_variant	MODERATE	Ahnak2	ENSRNOT00000039631.4	4585	c.4390T>C	p.Trp1464Arg	AA	GG	GG	GG	GG	AA	GG	AA
		chr6:137876105	T	C	missense_variant	MODERATE	Pacs2	ENSRNOT00000056880.5	1111	c.1067T>C	p.Met356Thr	CC	TT	TT	TT	TT	TT	TT	TT
		chr6:137885119	T	C	missense_variant	MODERATE	Pacs2	ENSRNOT00000056880.5	2278	c.2234T>C	p.Val745Ala	CC	TT	TT	TT	TT	CC	TT	TT
		chr6:137970275	G	C	missense_variant	MODERATE	LOC690422	ENSRNOT00000029223.6	574	c.379G>C	p.Val127Leu	CC	GG	GG	GG	GG	CC	GG	GG
		chr6:138068384	T	C	missense_variant	MODERATE	Ighm	ENSRNOT00000081908.1	265	c.220A>G	p.Ile74Val	CC	TT	TT	TT	TT	CC	TT	TT
EpiFat	chr6:26266960	chr6:23340330	A	T	missense_variant	MODERATE	RGD13049	ENSRNOT00000011832.7	2760	c.2520A>T	p.Glu840Asp	TT	AA	AA	AA	AA	AA	AA	TT
		chr6:23341333	A	G	missense_variant	MODERATE	RGD13049	ENSRNOT00000011832.7	3763	c.3523A>G	p.Thr1175Ala	GG	AA	AA	AA	AA	AA	AA	GG
		chr6:26099033	G	A	missense_variant	MODERATE	Rbks	ENSRNOT00000006452.6	1039	c.787G>A	p.Val263Met	AA	GG	GG	GG	GG	GG	GG	AA
		chr6:26135860	A	G	missense_variant	MODERATE	Mrpl33	ENSRNOT00000034712.4	94	c.94T>C	p.Tyr32His	GG	AA	AA	AA	AA	AA	AA	GG
		chr6:26382623	G	A	missense_variant	MODERATE	Gckr	ENSRNOT00000073228.2	622	c.445C>T	p.Arg149Cys	GG	GG	GG	GG	GG	GG	GG	AA
		chr6:26382623	G	A	missense_variant	MODERATE	Gckr	ENSRNOT00000073228.2	622	c.445C>T	p.Arg149Cys	GG	GG	GG	GG	GG	GG	GG	AA
		chr6:26786379	A	G	missense_variant	MODERATE	Preb	ENSRNOT00000009565.6	1051	c.881A>G	p.Gln294Arg	AA	AA	AA	AA	AA	AA	AA	GG
		chr6:26786379	A	G	missense_variant	MODERATE	Preb	ENSRNOT00000009565.6	1051	c.881A>G	p.Gln294Arg	AA	AA	AA	AA	AA	AA	AA	GG
		chr6:27428501	G	A	missense_variant	MODERATE	Drc1	ENSRNOT00000036815.5	1856	c.1811C>T	p.Thr604Ile	GG	GG	GG	GG	GG	GG	GG	AA
		chr6:27428501	G	A	missense_variant	MODERATE	Drc1	ENSRNOT00000036815.5	1856	c.1811C>T	p.Thr604Ile	GG	GG	GG	GG	GG	GG	GG	AA
RetroFat	chr6:28148338	chr6:28004664	A	G	missense_variant	MODERATE	Dtnb	ENSRNOT00000077830.1	421	c.308A>G	p.Asn103Ser	AA	AA	AA	AA	AA	AA	AA	GG
		chr6:28004664	A	G	missense_variant	MODERATE	Dtnb	ENSRNOT00000060810.2	594	c.308A>G	p.Asn103Ser	AA	AA	AA	AA	AA	AA	AA	GG
		chr6:28004664	A	G	missense_variant	MODERATE	Dtnb	ENSRNOT00000077830.1	421	c.308A>G	p.Asn103Ser	AA	AA	AA	AA	AA	AA	AA	GG
		chr6:28004664	A	G	missense_variant	MODERATE	Dtnb	ENSRNOT00000060810.2	594	c.308A>G	p.Asn103Ser	AA	AA	AA	AA	AA	AA	AA	GG
		chr6:28572363	T	C	missense_variant	MODERATE	Adcy3	ENSRNOT00000005389.6	585	c.362T>C	p.Leu121Pro	TT	TT	TT	TT	TT	TT	TT	CC
Body Weight	chr7:36497588	chr7:34310284	T	G	missense_variant	MODERATE	Lta4h	ENSRNOT00000005930.4	1407	c.1314T>G	p.Asp438Glu	TT	TT	GG	TT	TT	TT	TT	TT
Body Length_NoTail	chr7:36517726	chr7:34310284	T	G	missense_variant	MODERATE	Lta4h	ENSRNOT00000005930.4	1407	c.1314T>G	p.Asp438Glu	TT	TT	GG	TT	TT	TT	TT	TT
Body Length_Tail	chr7:36517726	chr7:34310284	T	G	missense_variant	MODERATE	Lta4h	ENSRNOT00000005930.4	1407	c.1314T>G	p.Asp438Glu	TT	TT	GG	TT	TT	TT	TT	TT
		chr7:34889309	T	C	missense_variant	MODERATE	Vezt	ENSRNOT00000030015.4	2061	c.2002A>G	p.Met668Val	TT	TT	CC	TT	CC	CC	CC	TT
		chr7:34889309	T	C	missense_variant	MODERATE	Vezt	ENSRNOT00000030015.4	2061	c.2002A>G	p.Met668Val	TT	TT	CC	TT	CC	CC	CC	TT
		chr8:116614891	G	C	missense_variant	MODERATE	Rbm6	ENSRNOT00000024939.5	1333	c.1093C>G	p.Gln365Glu	CC	GG	GG	GG	GG	GG	GG	GG
		chr8:117289662	C	A	missense_variant	MODERATE	Usp19	ENSRNOT00000085038.1	4102	c.3803C>A	p.Ala1268Asp	CC	CC	CC	AA	CC	CC	CC	CC
		chr8:117289662	C	A	missense_variant	MODERATE	Usp19	ENSRNOT00000074772.2	3797	c.3797C>A	p.Ala1266Asp	CC	CC	CC	AA	CC	CC	CC	CC
		chr8:117661846	C	T	missense_variant	MODERATE	Tmem89	ENSRNOT00000049240.5	496	c.470C>T	p.Ala157Val	CC	CC	CC	TT	CC	TT	TT	TT

Trait	QTL	Position	Ref	Alt	Effect	Impact	Gene	Transcript	Pos	c.	p.	S1	S2	S3	S4	S5	S6	S7	S8
Body Length_Tail	chr8:118711320	chr8:117706643	A	G	missense_variant	MODERATE	Col7a1	ENSRNOT00000027994.6	4258	c.4258A>G	p.Ser1420Gly	GG	AA	AA	AA	AA	AA	AA	AA
		chr8:117714681	G	A	missense_variant	MODERATE	Col7a1	ENSRNOT00000027994.6	6034	c.6034G>A	p.Gly2012Ser	GG	GG	GG	AA	GG	AA	AA	AA
		chr8:117796955	G	A	missense_variant	MODERATE	Trex1	ENSRNOT00000033719.5	192	c.167C>T	p.Pro56Leu	AA	GG	GG	GG	GG	GG	GG	GG
		chr8:117931377	T	C	missense_variant	MODERATE	Camp	ENSRNOT00000028130.7	496	c.344A>G	p.Gln115Arg	CC	TT	CC	TT	CC	TT	TT	TT
		chr8:118119545	G	A	missense_variant	MODERATE	Map4	ENSRNOT00000056161.4	2882	c.2864G>A	p.Arg955Gln	GG	GG	GG	AA	GG	AA	AA	AA
		chr8:118121377	A	G	missense_variant	MODERATE	Map4	ENSRNOT00000056161.4	4714	c.4696A>G	p.Asn1566Asp	AA	AA	AA	GG	AA	GG	GG	GG
		chr8:118378322	C	T	missense_variant	MODERATE	RGD15637	ENSRNOT00000047247.4	139	c.139G>A	p.Ala47Thr	TT	CC	CC	CC	CC	CC	CC	CC
		chr8:118664419	C	T	stop_gained	HIGH	Ngp	ENSRNOT00000029755.2	329	c.316C>T	p.Gln106*	TT	CC	CC	CC	CC	CC	CC	CC
		chr8:118664420	A	C	missense_variant	MODERATE	Ngp	ENSRNOT00000029755.2	330	c.317A>C	p.Gln106Pro	CC	AA	AA	AA	AA	AA	AA	AA
		chr8:118822162	T	C	missense_variant	MODERATE	Setd2	ENSRNOT00000087154.1	716	c.485T>C	p.Val162Ala	TT	TT	TT	CC	TT	CC	CC	CC
		chr8:118822165	C	T	missense_variant	MODERATE	Setd2	ENSRNOT00000087154.1	719	c.488C>T	p.Ala163Val	CC	CC	CC	TT	CC	TT	TT	TT
		chr8:118822336	C	T	missense_variant	MODERATE	Setd2	ENSRNOT00000087154.1	890	c.659C>T	p.Ala220Val	CC	CC	CC	TT	CC	TT	TT	TT
		chr8:118824592	A	G	missense_variant	MODERATE	Setd2	ENSRNOT00000028409.6	2656	c.2228A>G	p.Glu743Gly	GG	AA	AA	AA	AA	AA	AA	AA
		chr8:118824592	A	G	missense_variant	MODERATE	Setd2	ENSRNOT00000087154.1	3146	c.2915A>G	p.Glu972Gly	GG	AA	AA	AA	AA	AA	AA	AA
		chr8:118825098	G	C	missense_variant	MODERATE	Setd2	ENSRNOT00000028409.6	3162	c.2734G>C	p.Val912Leu	GG	GG	GG	CC	GG	CC	CC	CC
		chr8:118825098	G	C	missense_variant	MODERATE	Setd2	ENSRNOT00000087154.1	3652	c.3421G>C	p.Val1141Leu	GG	GG	GG	CC	GG	CC	CC	CC
		chr8:118825125	A	G	missense_variant	MODERATE	Setd2	ENSRNOT00000028409.6	3189	c.2761A>G	p.Ile921Val	AA	AA	AA	GG	AA	GG	GG	GG
		chr8:118825125	A	G	missense_variant	MODERATE	Setd2	ENSRNOT00000087154.1	3679	c.3448A>G	p.Ile1150Val	AA	AA	AA	GG	AA	GG	GG	GG
		chr8:118825138	T	C	missense_variant	MODERATE	Setd2	ENSRNOT00000028409.6	3202	c.2774T>C	p.Met925Thr	TT	TT	TT	CC	TT	CC	CC	CC
		chr8:118825138	T	C	missense_variant	MODERATE	Setd2	ENSRNOT00000087154.1	3692	c.3461T>C	p.Met1154Thr	TT	TT	TT	CC	TT	CC	CC	CC
		chr8:118890799	T	C	missense_variant	MODERATE	Nradd	ENSRNOT00000028416.4	801	c.476A>G	p.Gln159Arg	TT	TT	TT	CC	TT	CC	CC	CC
		chr8:118897582	C	T	missense_variant	MODERATE	Nbeal2	ENSRNOT00000056130.5	6917	c.6719G>A	p.Arg2240Gln	TT	CC	TT	CC	TT	CC	CC	CC
		chr8:118901536	T	C	missense_variant	MODERATE	Nbeal2	ENSRNOT00000056130.5	5161	c.4963A>G	p.Met1655Val	CC	TT	CC	TT	CC	TT	TT	TT
		chr8:118903111	G	A	missense_variant	MODERATE	Nbeal2	ENSRNOT00000056130.5	4181	c.3983C>T	p.Pro1328Leu	AA	GG	AA	GG	AA	GG	GG	GG
		chr8:119084015	G	A	missense_variant	MODERATE	Prss44	ENSRNOT00000051947.5	116	c.82G>A	p.Val28Ile	AA	GG	AA	GG	AA	GG	GG	GG
		chr8:119084015	G	A	missense_variant	MODERATE	Prss44	ENSRNOT00000048655.5	95	c.82G>A	p.Val28Ile	AA	GG	AA	GG	AA	GG	GG	GG
		chr8:119115774	G	A	missense_variant	MODERATE	Prss45	ENSRNOT00000043249.2	221	c.173G>A	p.Arg58His	AA	GG	GG	GG	GG	GG	GG	GG
		chr8:119139251	A	G	missense_variant	MODERATE	Prss50	ENSRNOT00000056114.3	676	c.676A>G	p.Lys226Glu	GG	AA	AA	AA	AA	AA	AA	AA
		chr8:119160764	C	A	missense_variant	MODERATE	Als2cl	ENSRNOT00000046745.4	34	c.34C>A	p.Leu12Met	AA	CC	CC	CC	CC	CC	CC	CC
		chr8:119236824	T	A	missense_variant	MODERATE	Lrrc2	ENSRNOT00000043737.5	317	c.251T>A	p.Val84Glu	TT	TT	AA	AA	AA	AA	AA	AA
		chr8:119236824	T	A	missense_variant	MODERATE	Lrrc2	ENSRNOT00000078439.1	435	c.251T>A	p.Val84Glu	TT	TT	AA	AA	AA	AA	AA	AA
		chr8:119236869	A	G	missense_variant	MODERATE	Lrrc2	ENSRNOT00000043737.5	362	c.296A>G	p.Asn99Ser	AA	AA	GG	GG	GG	GG	GG	GG
		chr8:119236869	A	G	missense_variant	MODERATE	Lrrc2	ENSRNOT00000078439.1	480	c.296A>G	p.Asn99Ser	AA	AA	GG	GG	GG	GG	GG	GG
		chr8:119640095	A	G	missense_variant	MODERATE	Trank1	ENSRNOT00000028633.5	5963	c.5963A>G	p.Lys1988Arg	GG	AA	AA	AA	AA	GG	GG	AA
		chr8:119640688	C	G	missense_variant	MODERATE	Trank1	ENSRNOT00000028633.5	6556	c.6556C>G	p.Leu2186Val	GG	CC	CC	CC	CC	GG	GG	CC
		chr8:119691654	G	A	missense_variant&sp	MODERATE	Dclk3	ENSRNOT00000044742.5	267	c.88G>A	p.Gly30Ser	AA	GG	GG	GG	GG	AA	AA	GG
Body Length_Tail	chr9:65078205	chr9:64913080	A	G	missense_variant	MODERATE	Sgo2	ENSRNOT00000029526.6	1024	c.785A>G	p.Lys262Arg	GG	AA	GG	AA	GG	GG	GG	GG
		chr9:64953533	G	A	missense_variant	MODERATE	Aox1	ENSRNOT00000068633.4	376	c.328G>A	p.Gly110Ser	GG	GG	GG	AA	GG	GG	GG	GG
		chr9:65026169	G	A	missense_variant	MODERATE	Aox3	ENSRNOT00000081146.1	535	c.458G>A	p.Arg153His	GG	GG	GG	AA	GG	GG	GG	GG
		chr9:65063124	G	A	missense_variant	MODERATE	Aox3	ENSRNOT00000092906.1	2430	c.1688G>A	p.Gly563Asp	GG	GG	GG	AA	GG	GG	GG	GG
		chr9:65063124	G	A	missense_variant	MODERATE	Aox3	ENSRNOT00000081146.1	2428	c.2351G>A	p.Gly784Asp	GG	GG	GG	AA	GG	GG	GG	GG

Supplementary Figure S1

Genetic and phenotypic correlation between adiposity traits, fasting glucose and tail length. Phenotypic correlations are depicted in the upper part, genetic – in the lower part of the matrix. Number inside squares show p-value > 0.05.
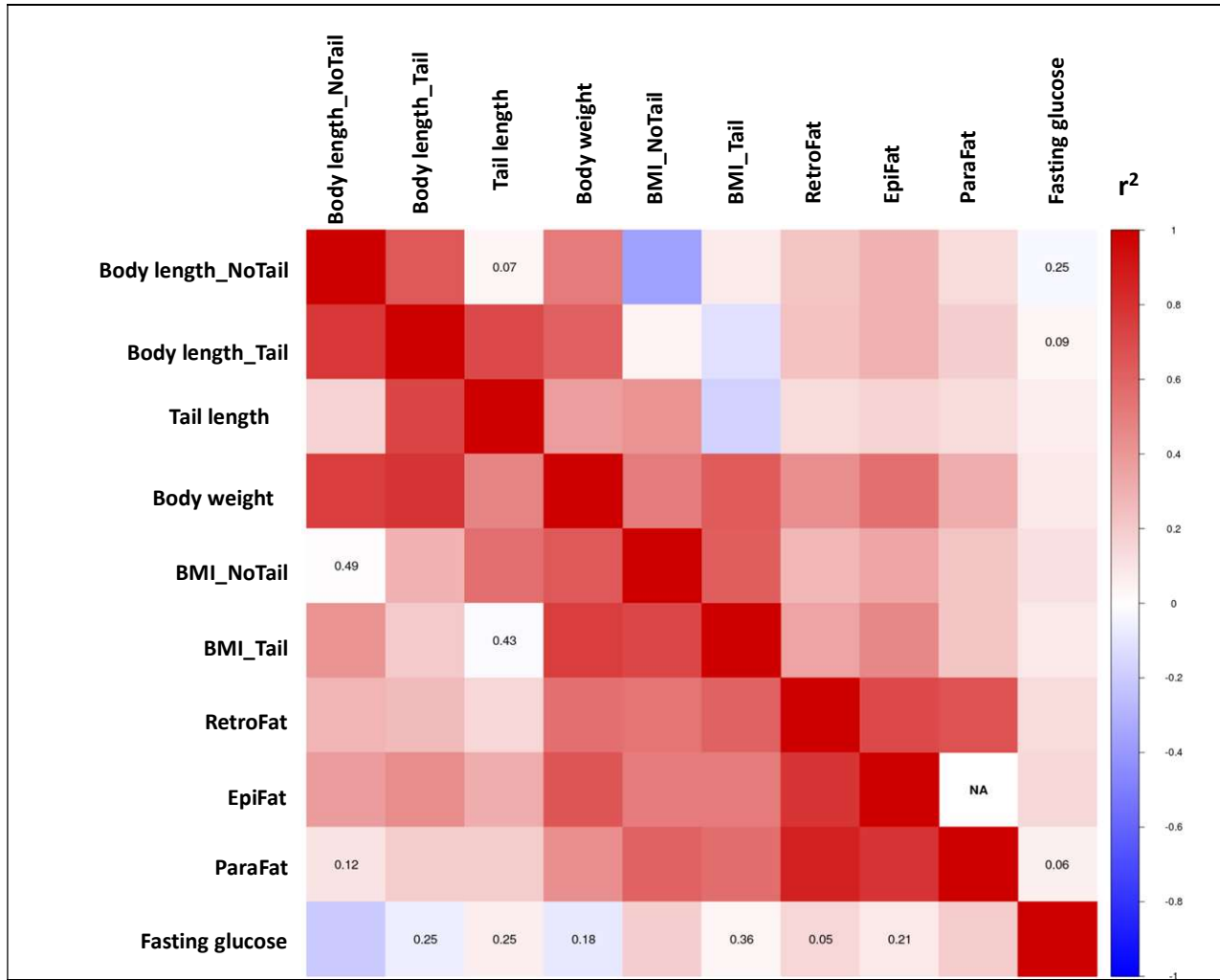
Supplementary Figure S2

Manhattan plots. Genome-wide association results from the GWA analysis for 9 adiposity traits. The chromosomal distribution of all the P-values (-log$_{10}$P values) is shown

Retroperitoneal fat weight
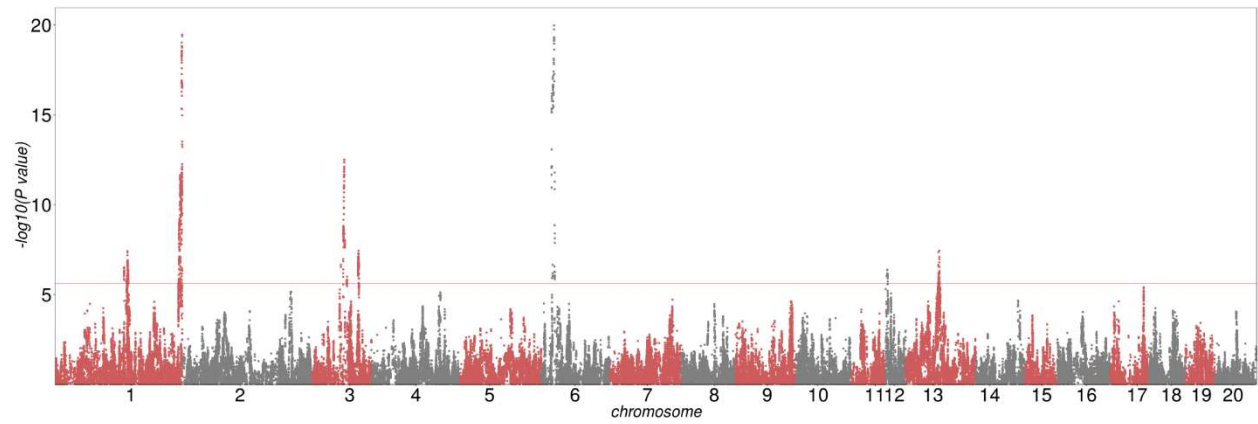
Body weight
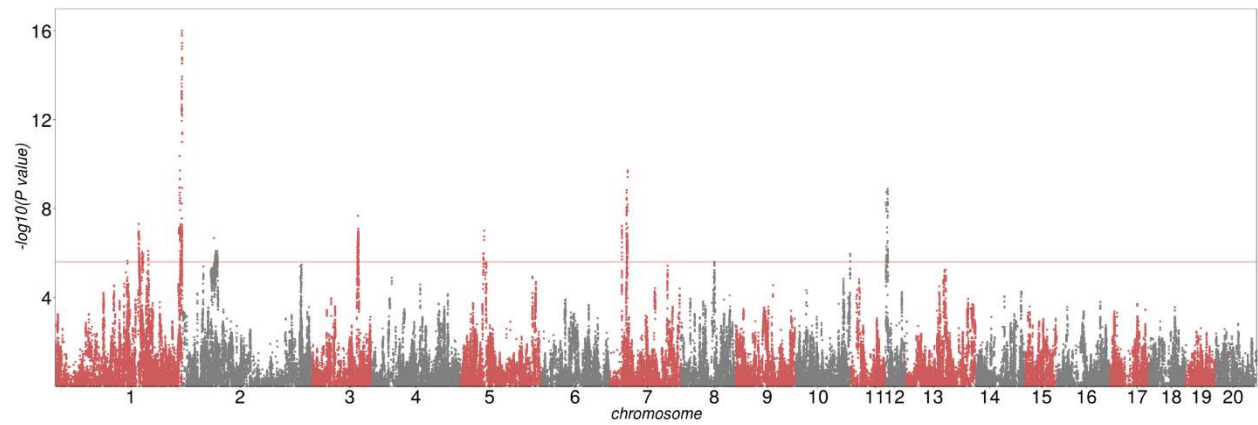
Body length with tail
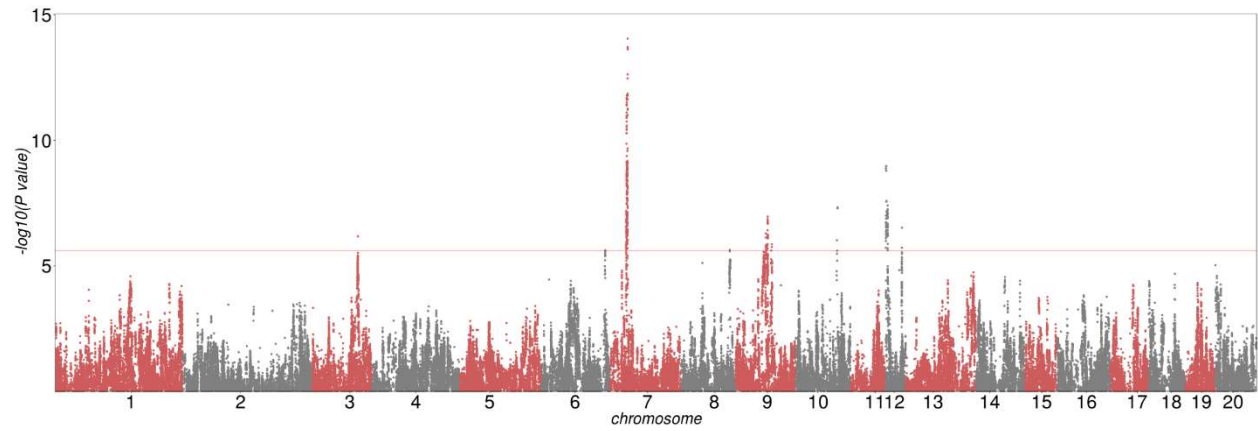
Body length without tail
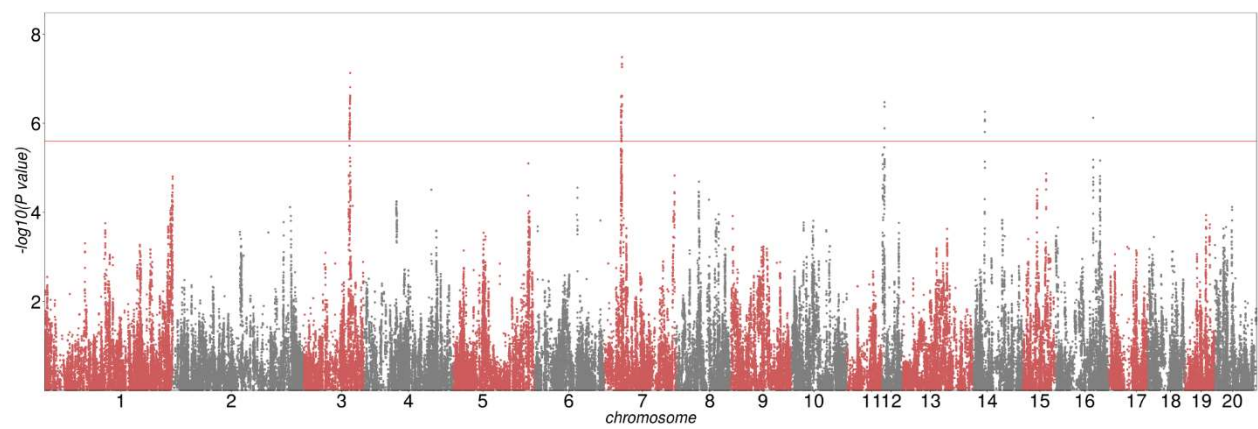
BMI – body length with tail
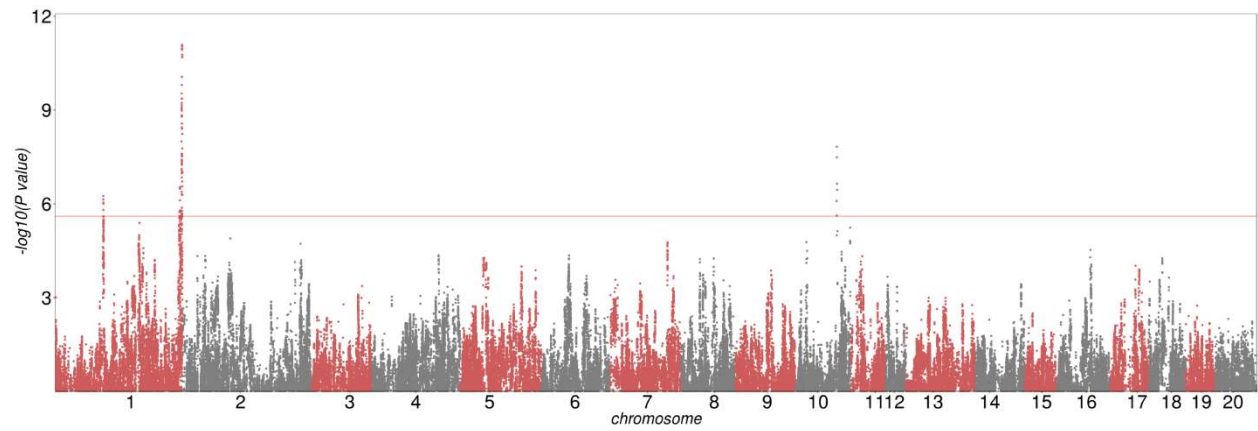
BMI – body length without tail
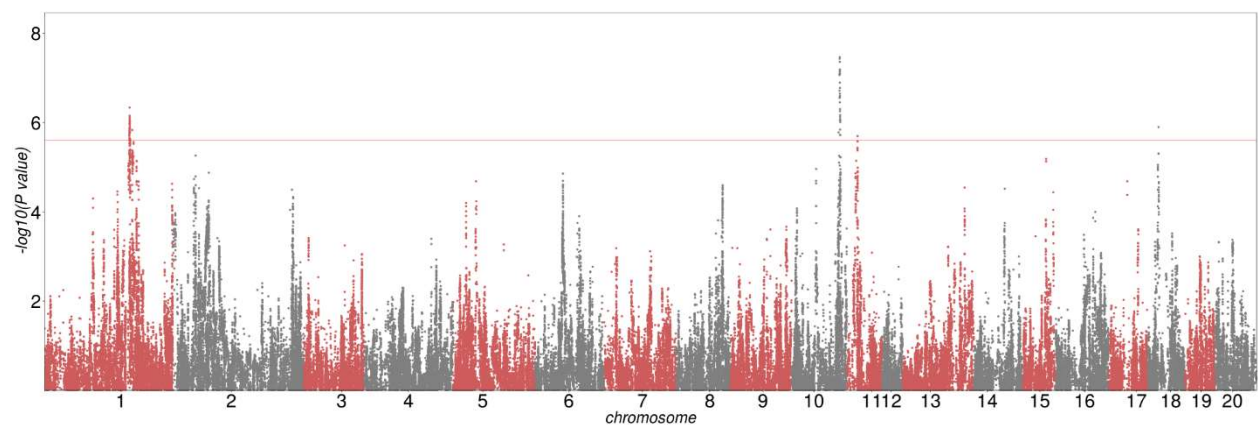
Epididymis fat weight
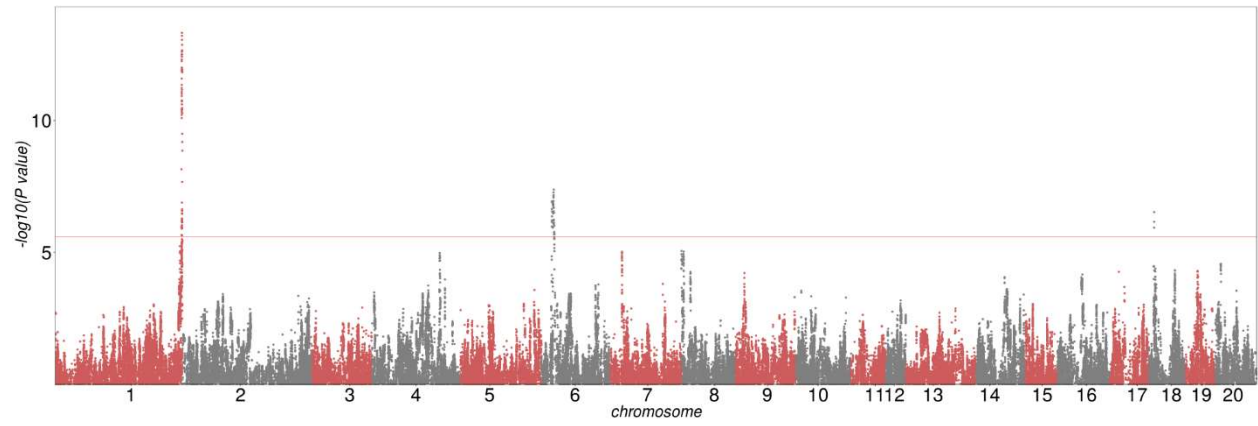
Parametrial fat weight
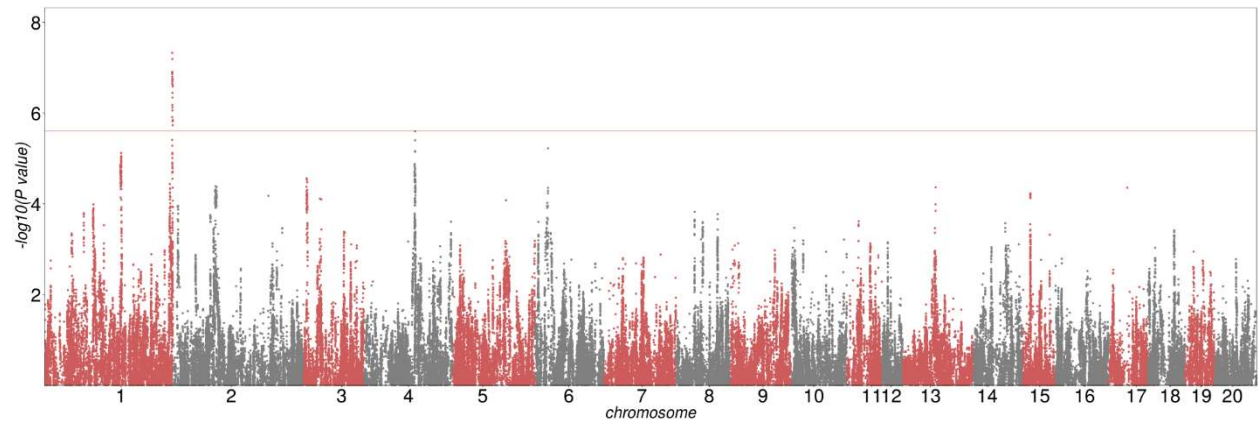
Fasting glucose
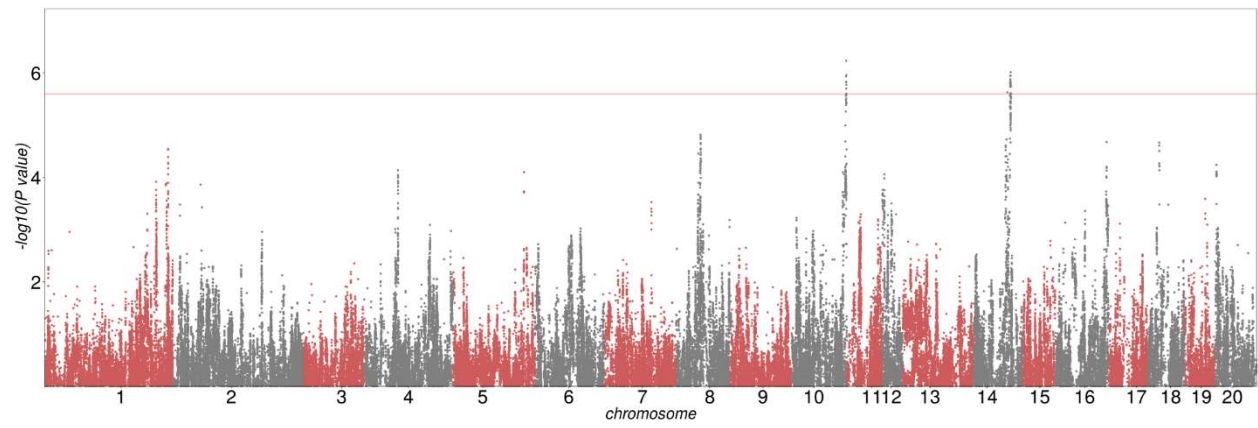
Tail length
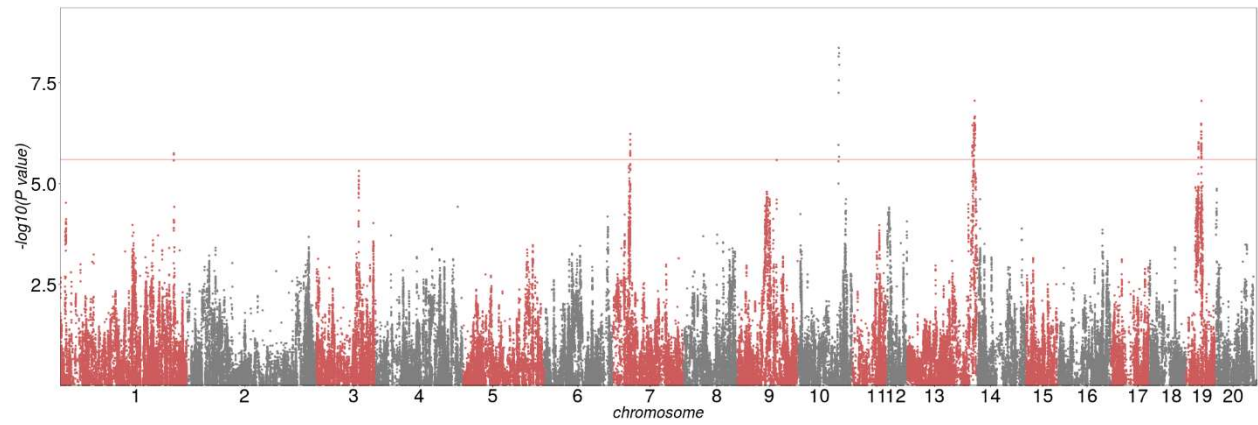
Supplementary Figure S3. 46 QTLs for 10 traits. Regional association plots show the vicinity of the top SNPs for each QTL. The SNPs with the lowest p-value ("top SNP) is shown in purple. Correlation of each SNP with the top SNP is shown in color. Credible set track shows the smallest set of SNPs accounting for 99% of the posterior probability ("credible set"). Genes in the region were annotated using Refseq annotation. The chromosome regions were chosen to optimally show LD structure of the region
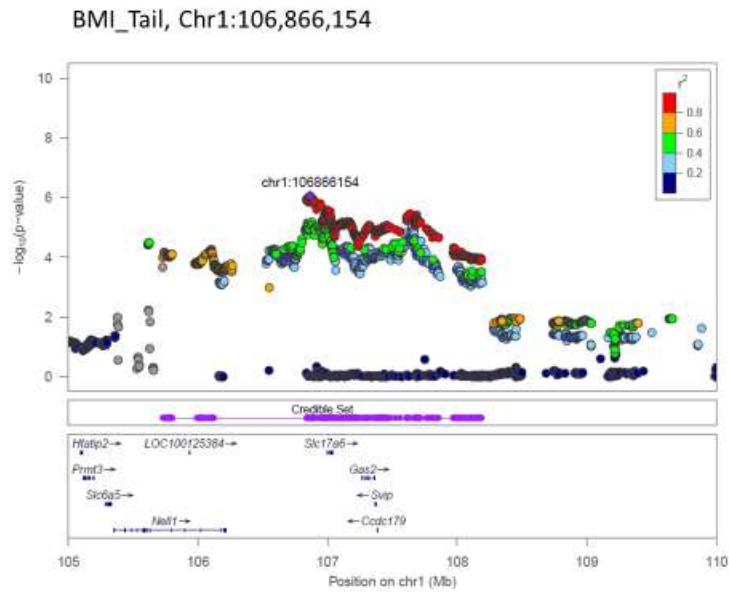
RetroFat, Chr1:160,530,456
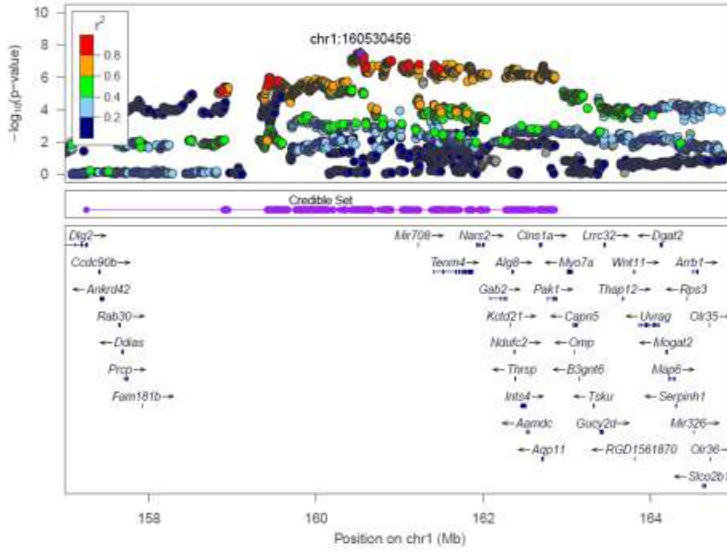
Body weight, Chr1:185,730,317
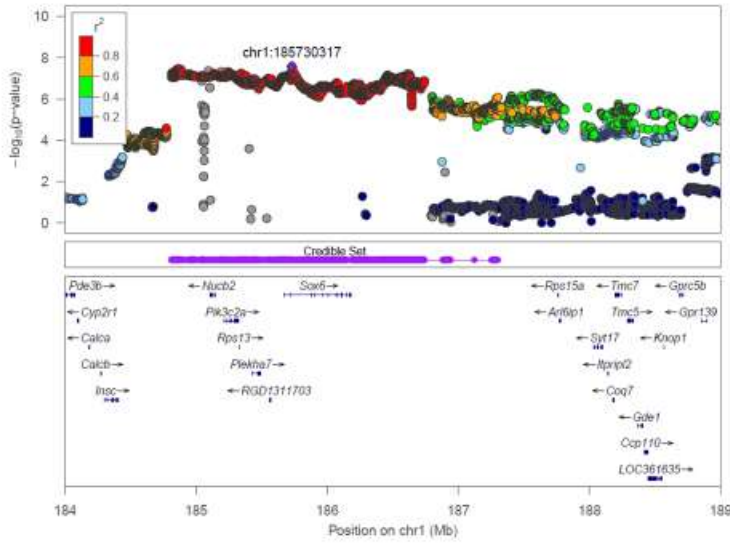
BMI_NoTail, Chr1:187,300,775
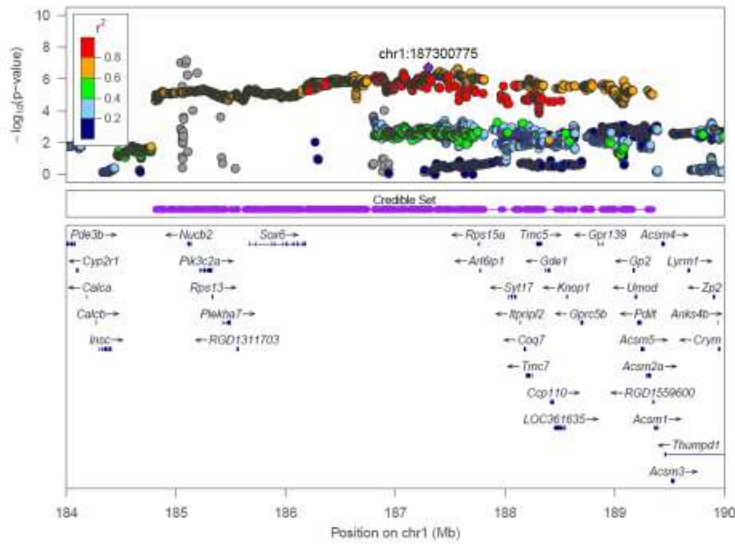
TL, Chr1:253,524,003
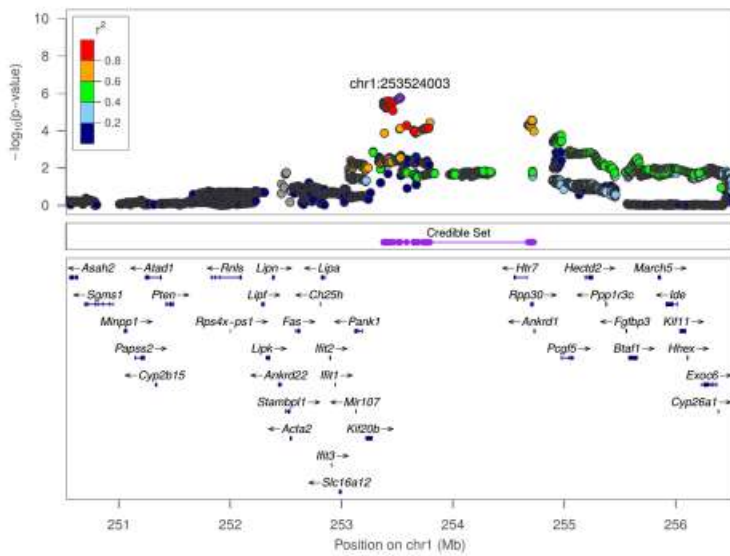
ParaFat, Chr1:280,924,549
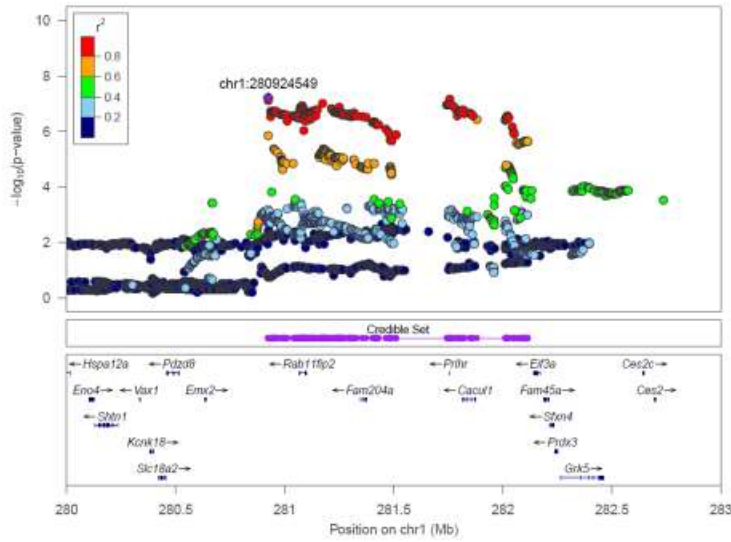
Body weight, Chr1:281,756,885
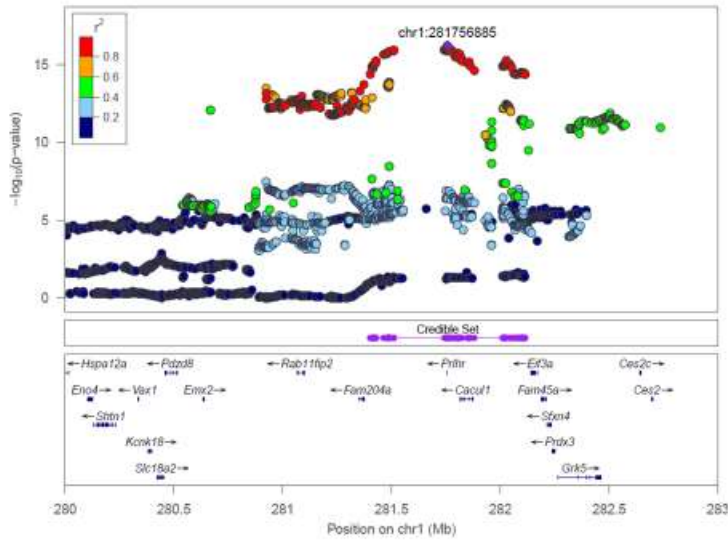
RetroFat, Chr1:281,777,218
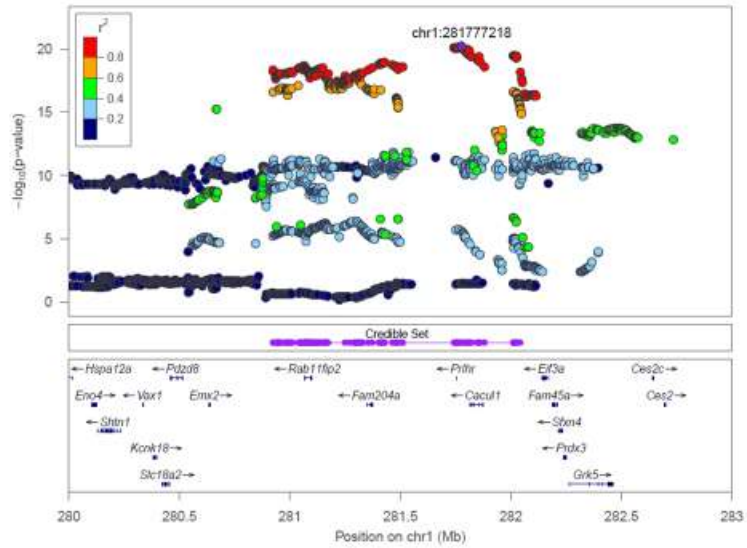
EpiFat, Chr1:281,802,657
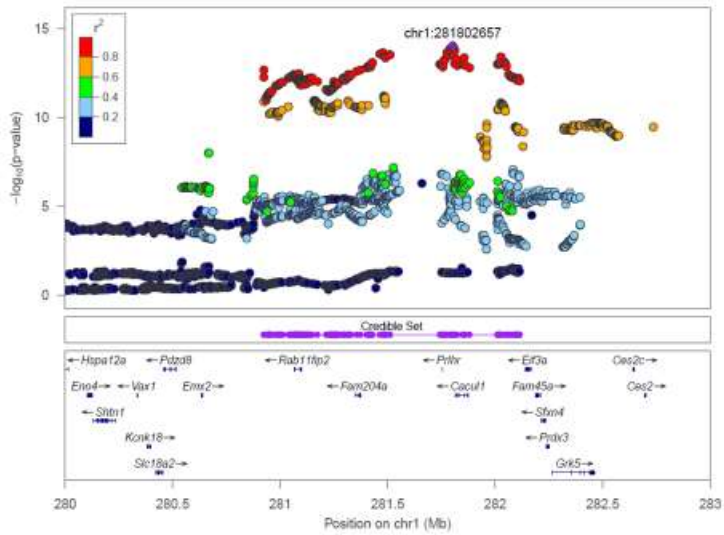
BMI_Tail, Chr1:282,049,439
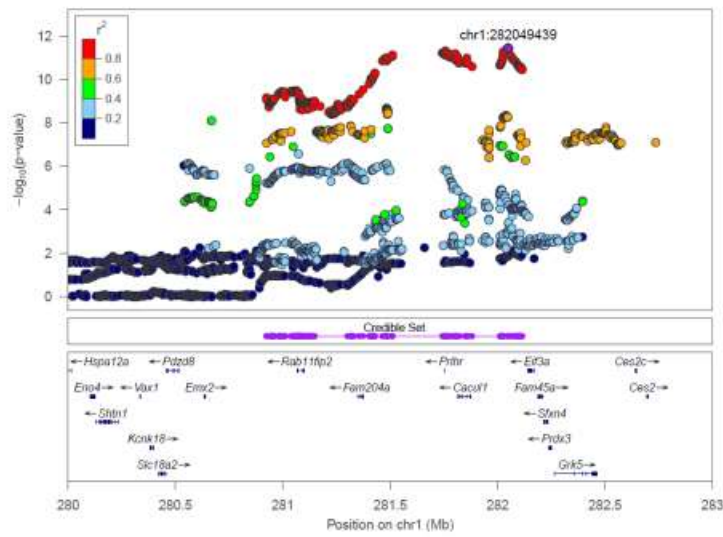
Body weight, Chr2:65,816,485
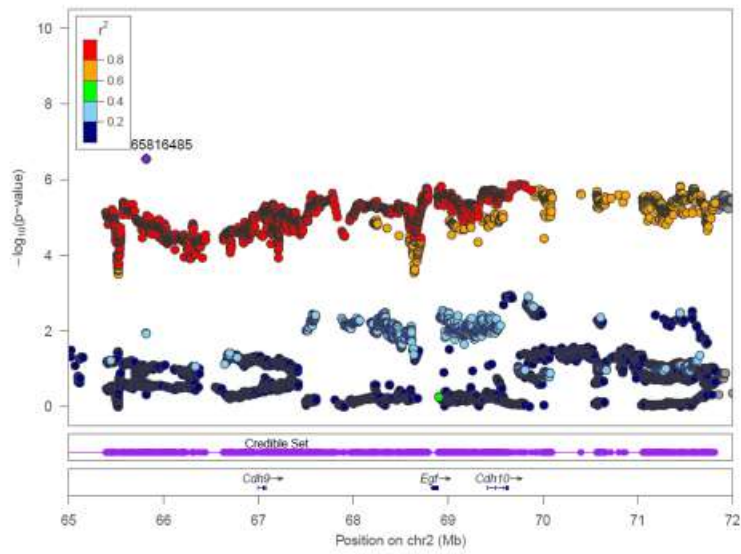
RetroFat, Chr3:95,389,621
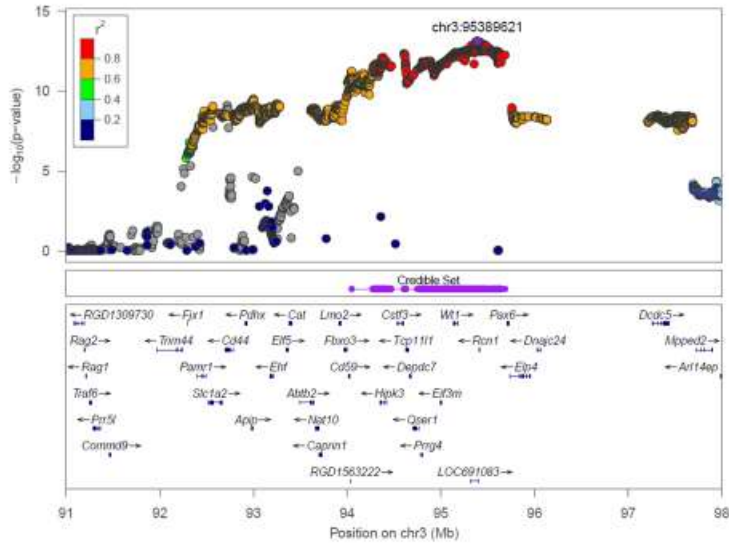
Body weight, Chr3:136,021,511
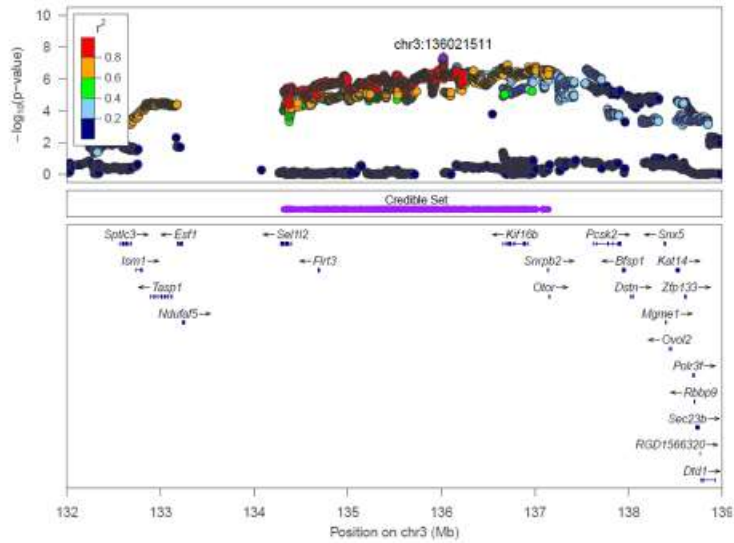
Body Length_Tail, Chr3:136,021,511
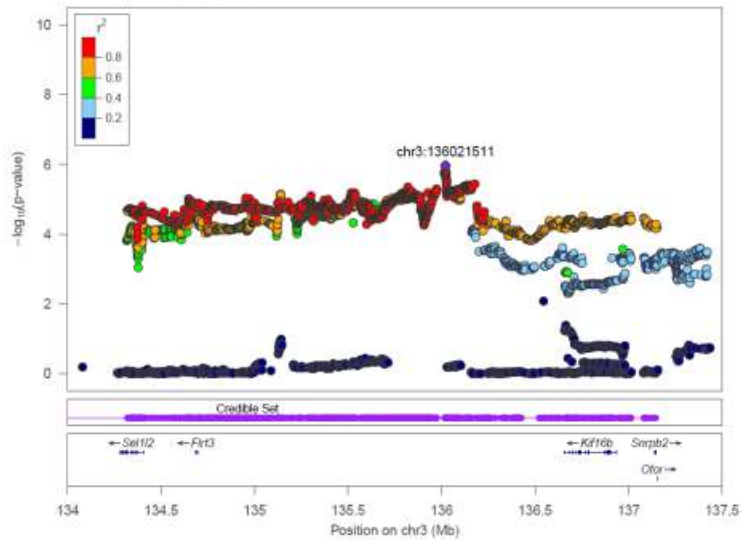
Body weight, Chr3:136,021,511
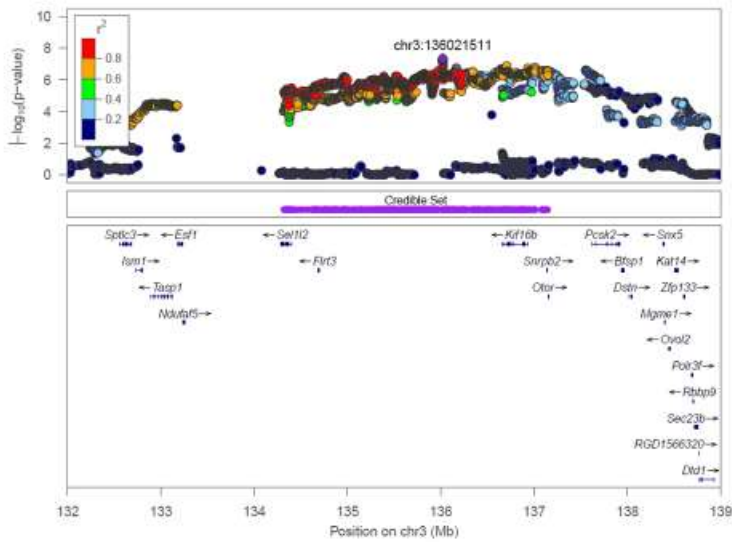
RetroFat, Chr3:137,537,161
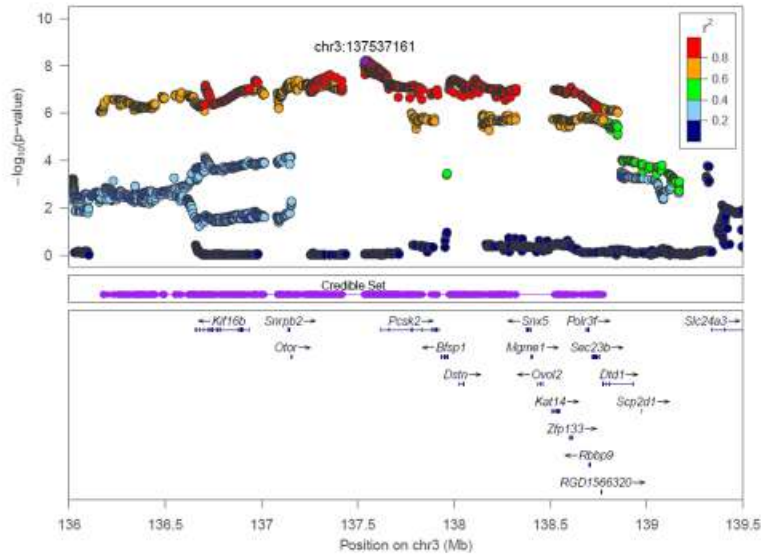
Body weight, Chr5:50,933,779
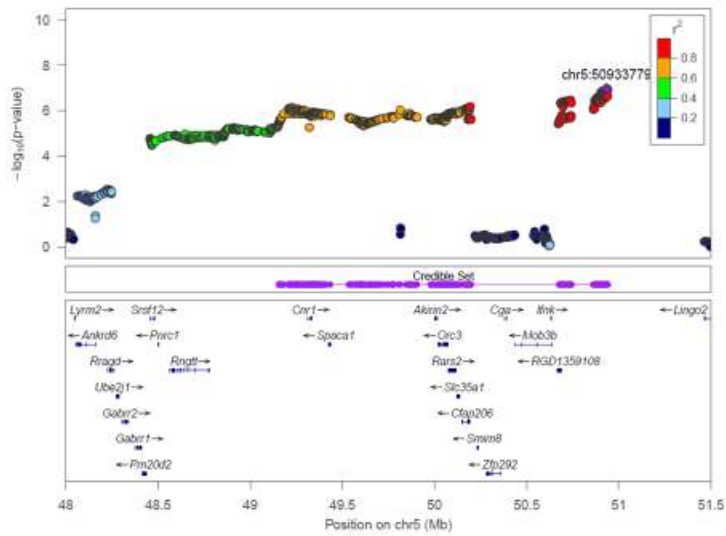
EpiFat, Chr6:26,266,960
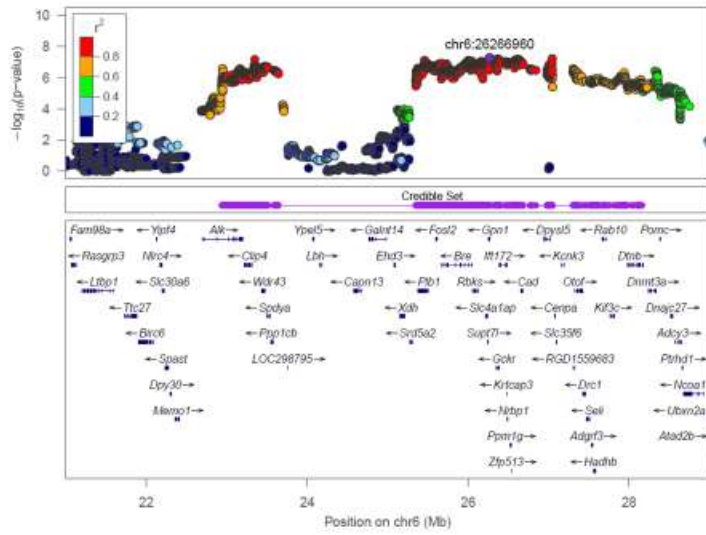
RetroFat, Chr6:28,148,338
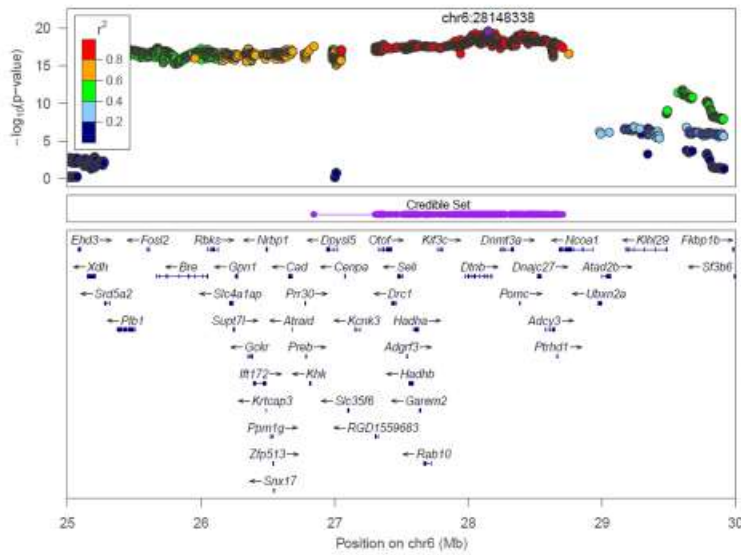
Body Length_Tail, Chr6:137,745,191
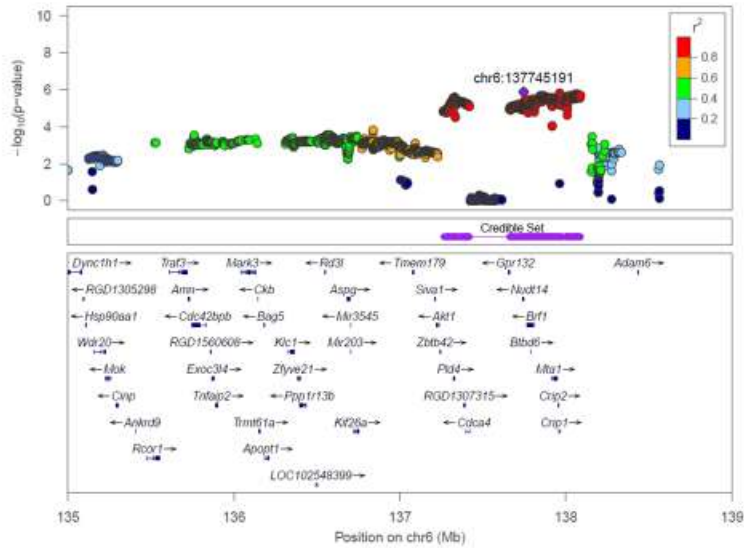
Body weight, Chr7:24,886,476
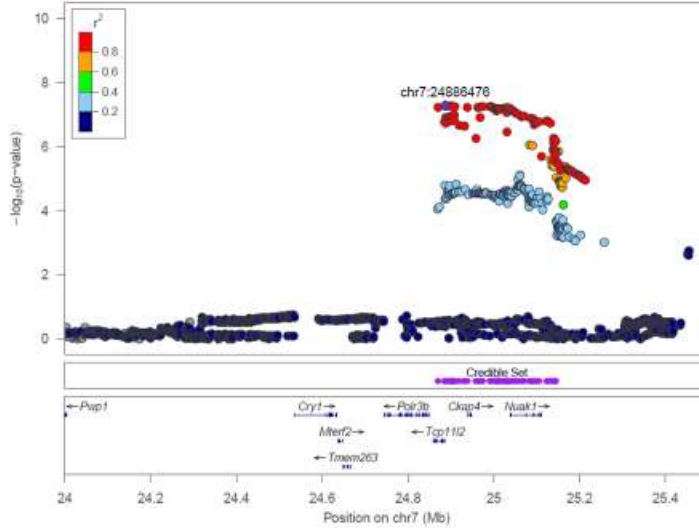
Body weight, Chr7:36,497,588
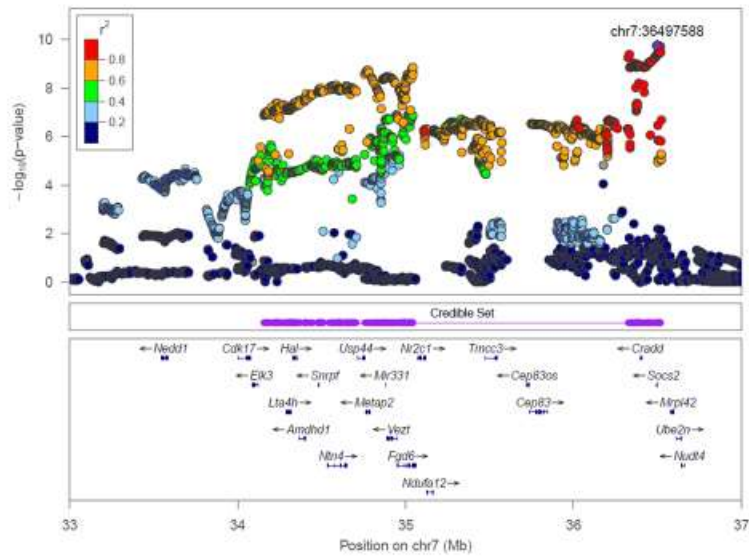
Body Length_NoTail, Chr7:36,517,726
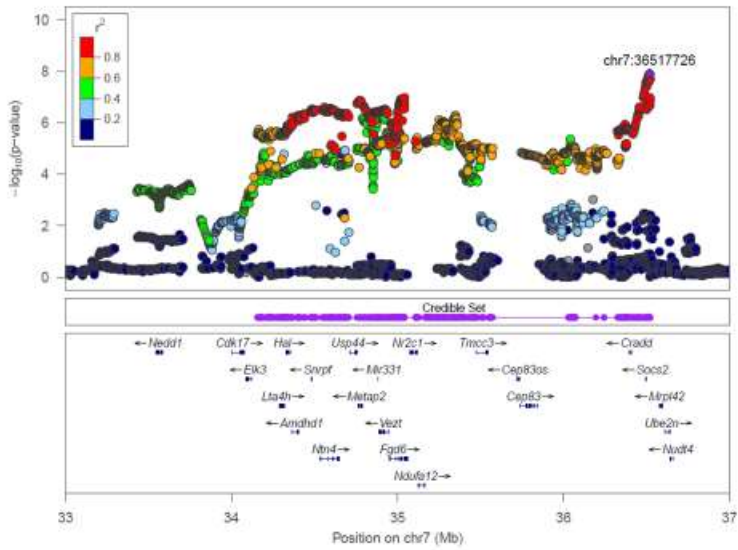
Body Length_Tail, Chr7:36,517,726
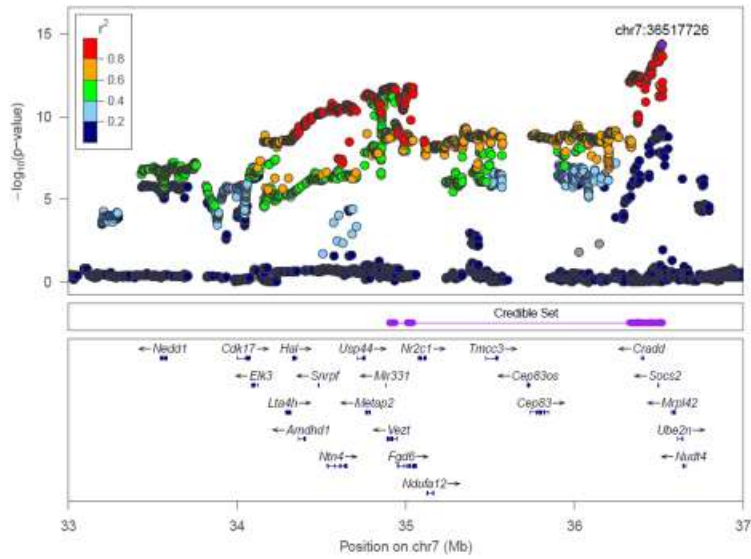
TL, Chr7:36,526,715
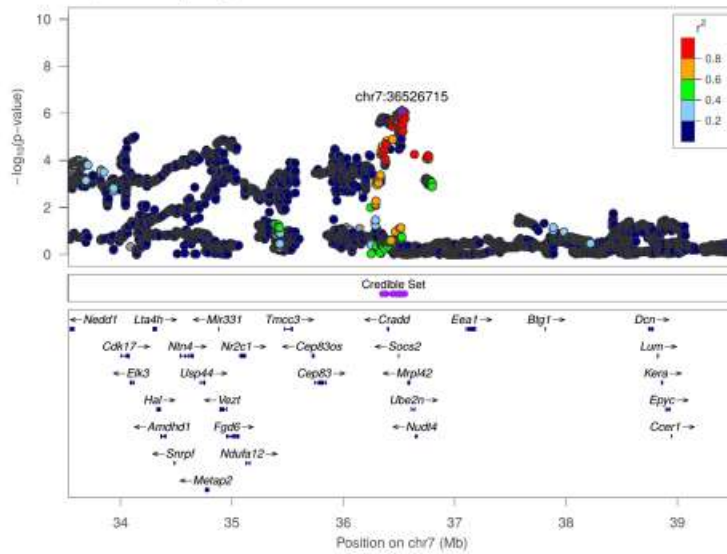
Body Length_Tail, Chr8:118,711,320
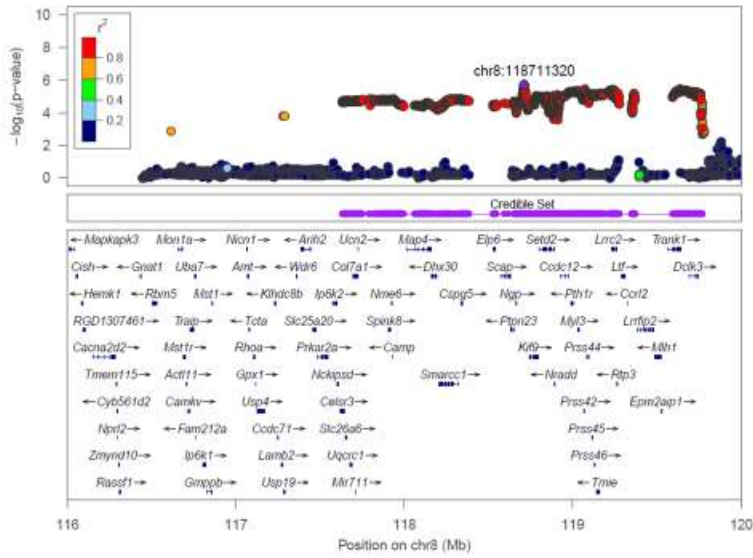
Body Length_Tail, Chr9:65,078,205
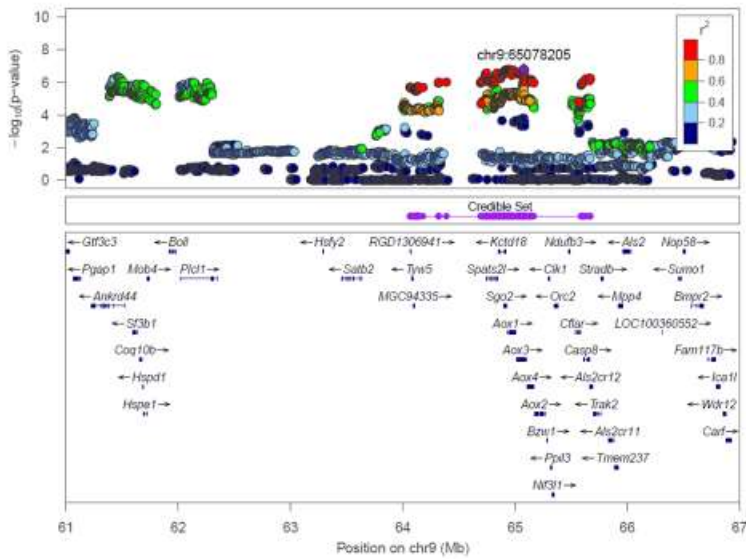
BMI_Tail, Chr10:84,080,794
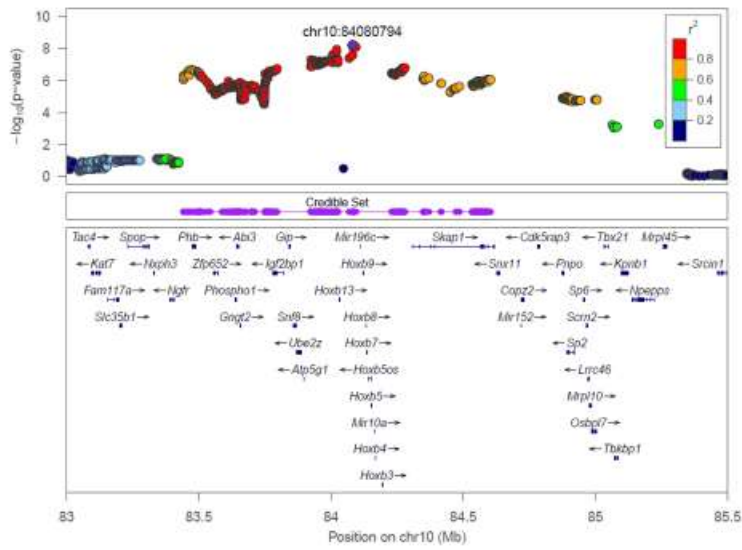
TL, Chr10:84,263,936
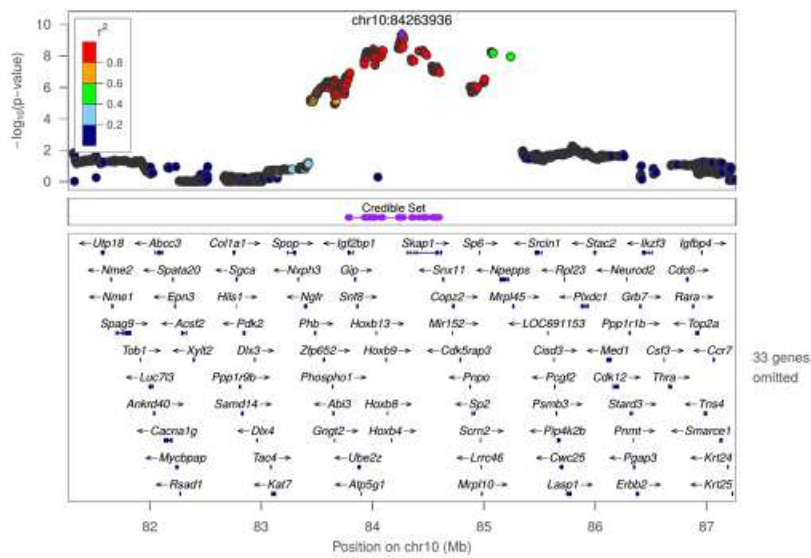
Body Length_Tail, Chr10:85,082,795
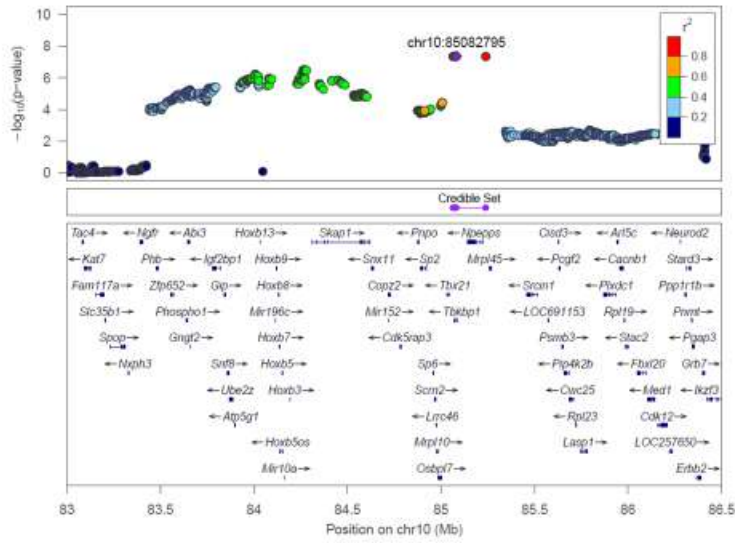
BMI_NoTail, Chr10:96,804,258
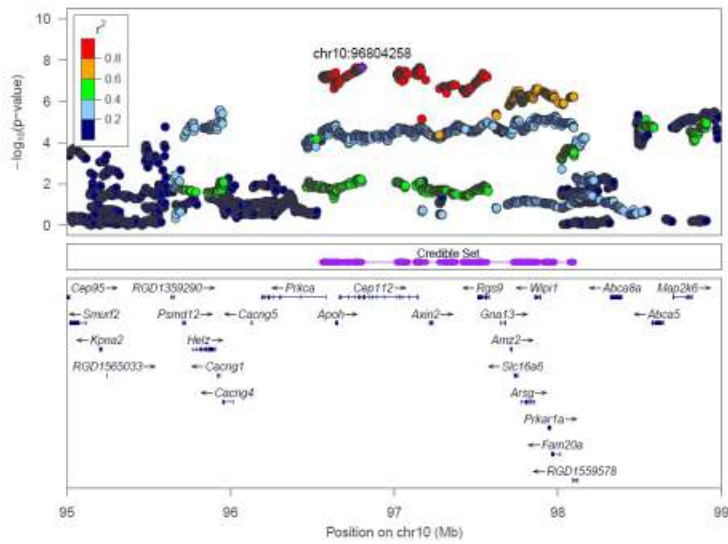
Fasting glucose, Chr10:109,944,213
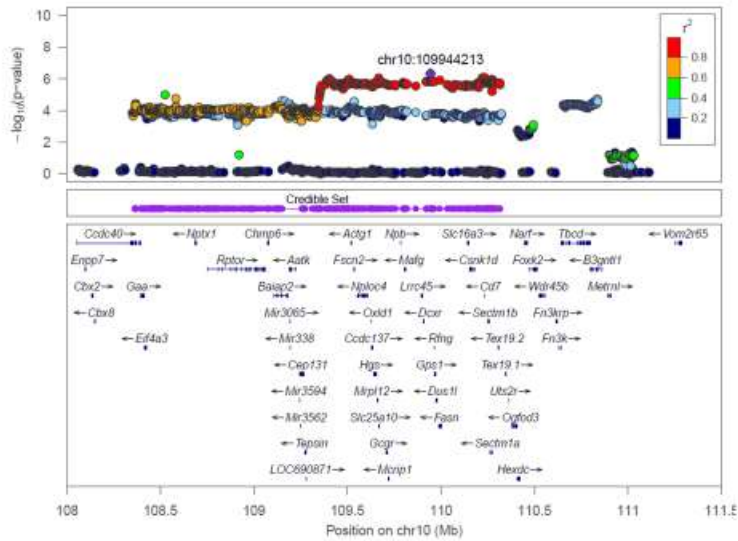
Body weight, Chr10:111,010,289
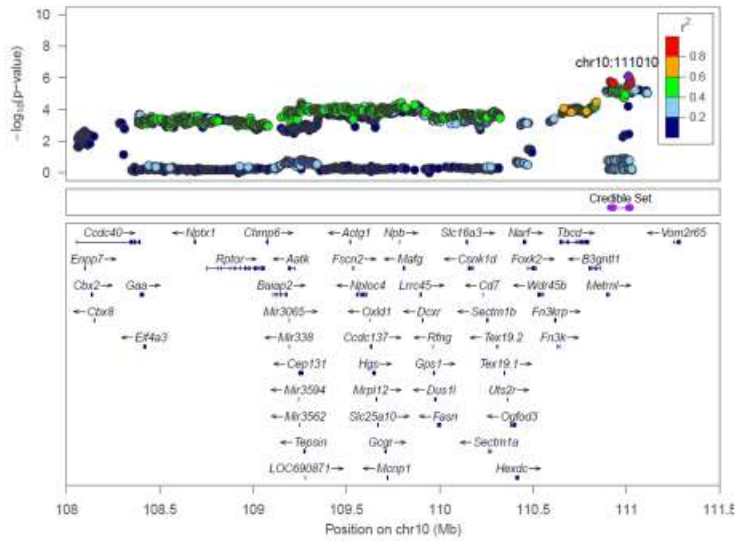
Body Length_Tail, Chr12:2,199,384
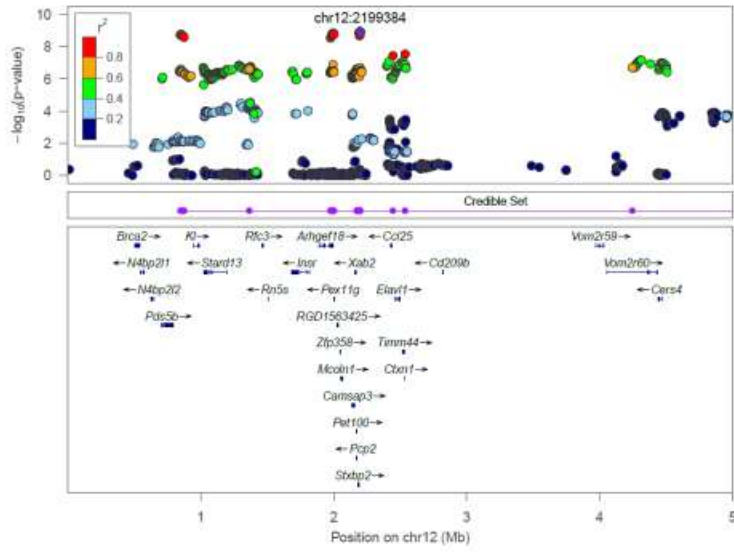
Body weight, Chr12:5,738,696
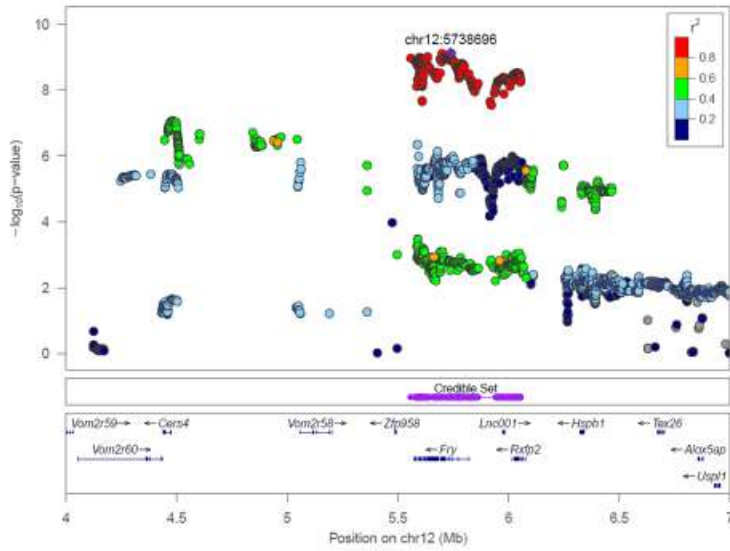
RetroFat, Chr12:5,782,829
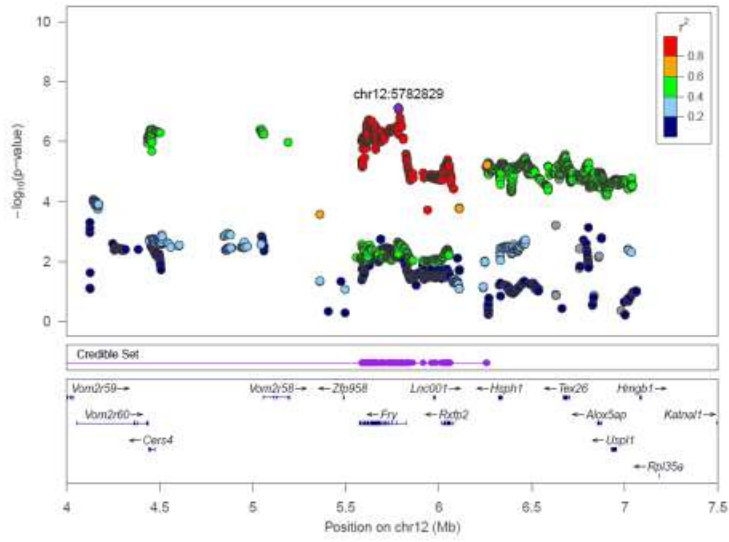
Body Length_NoTail, Chr12:6,239,515
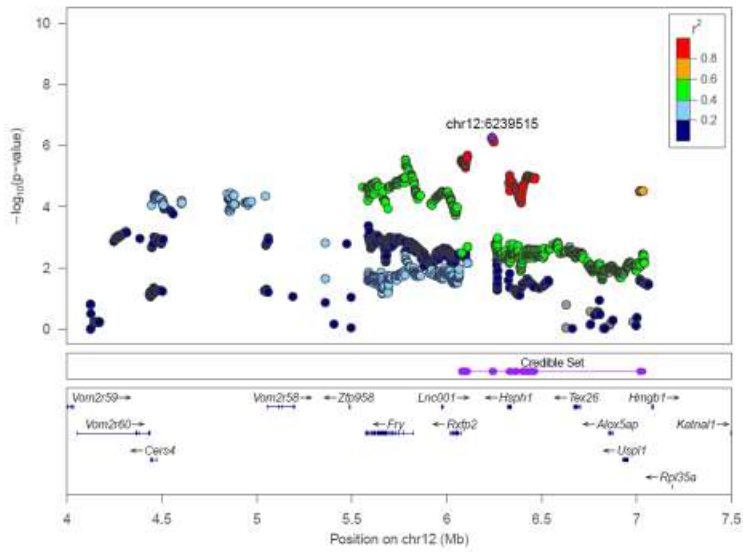
Body Length_Tail, Chr12:43,060,205
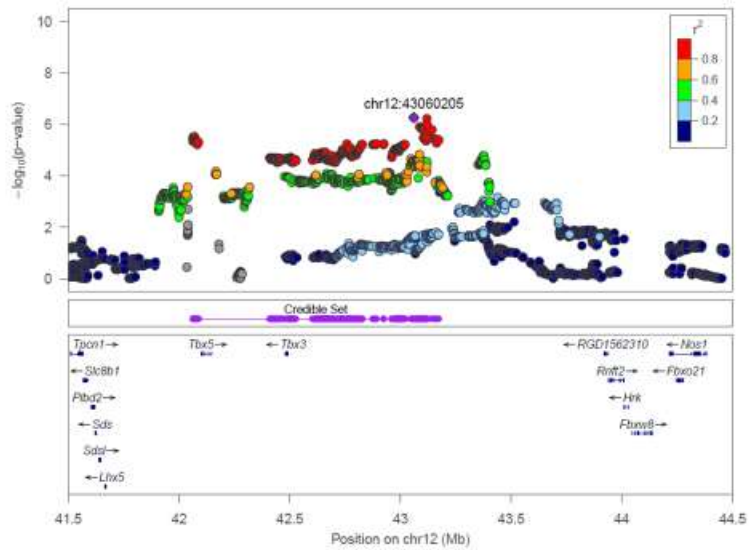
RetroFat, Chr13:55,021,887
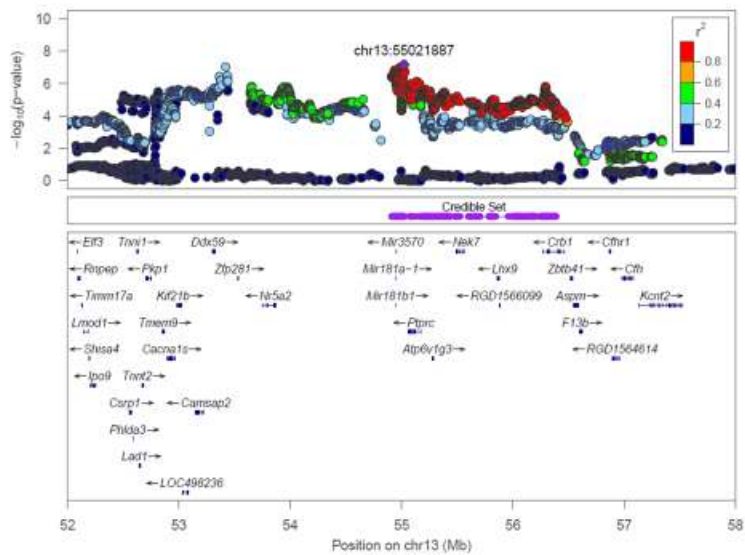
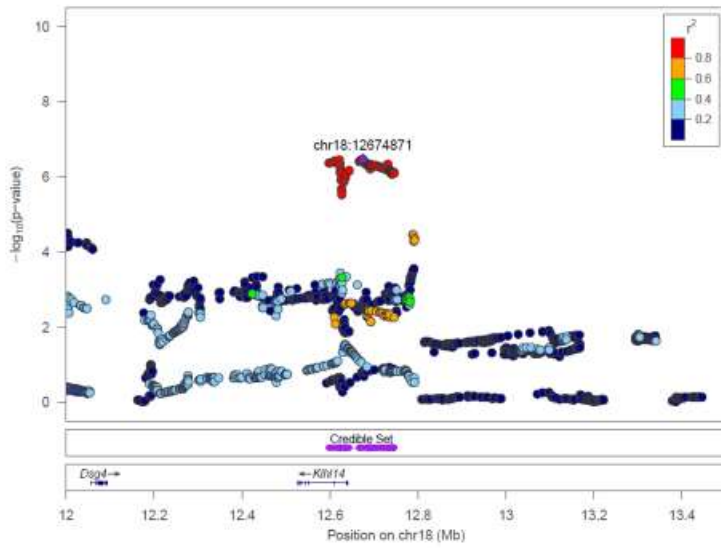## TL, Chr13:109,566,014
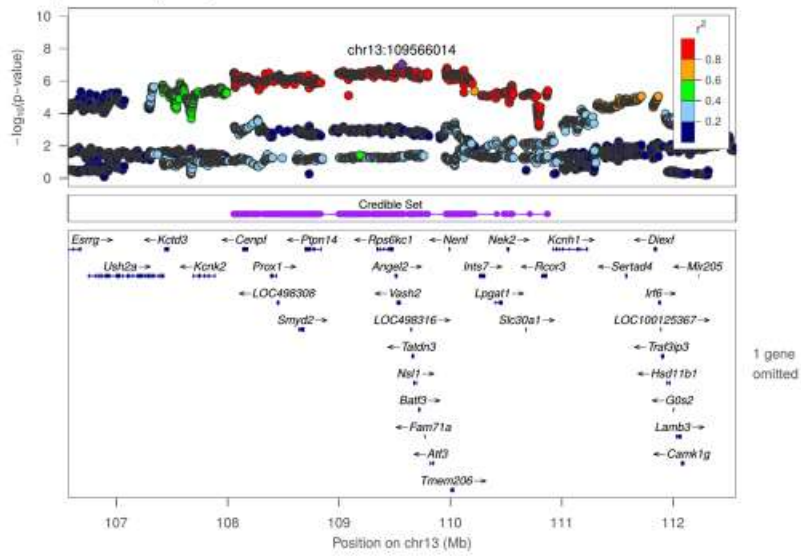
Body Length_NoTail, Chr14:26,365,986
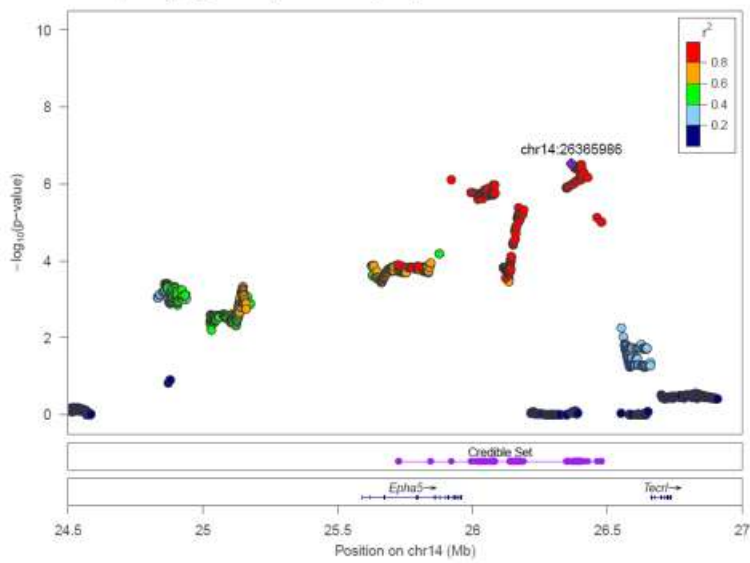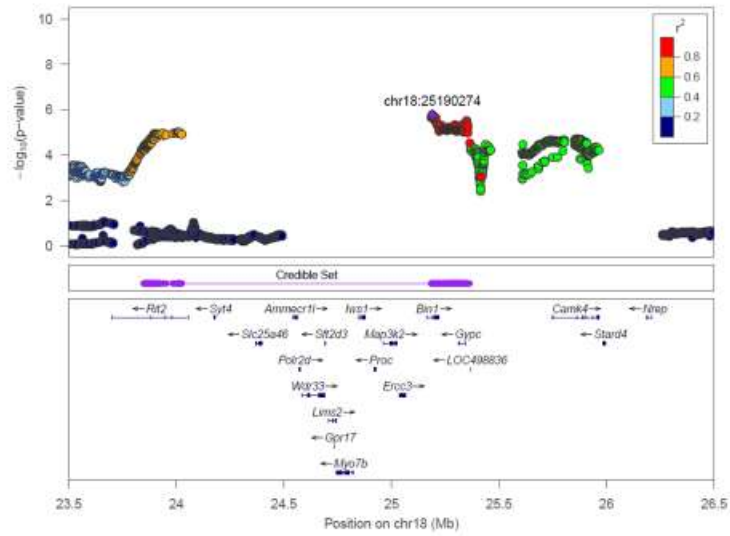
Fasting glucose, Chr14:86,029,588
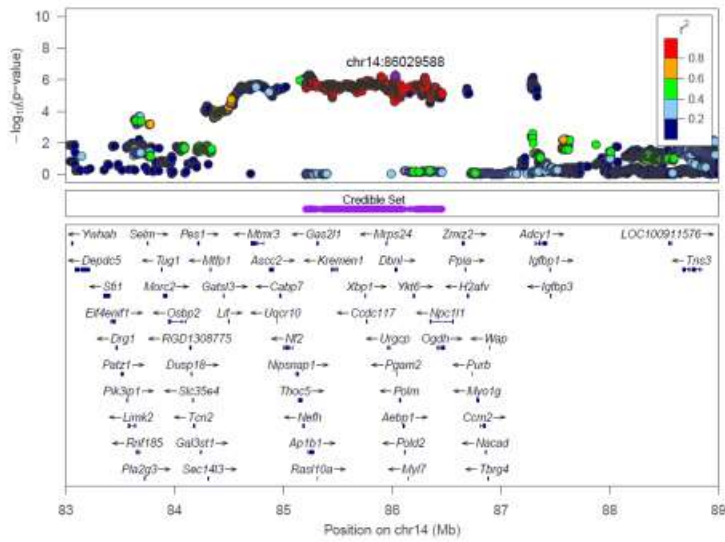
Body Length_NoTail, Chr16:64,014,119
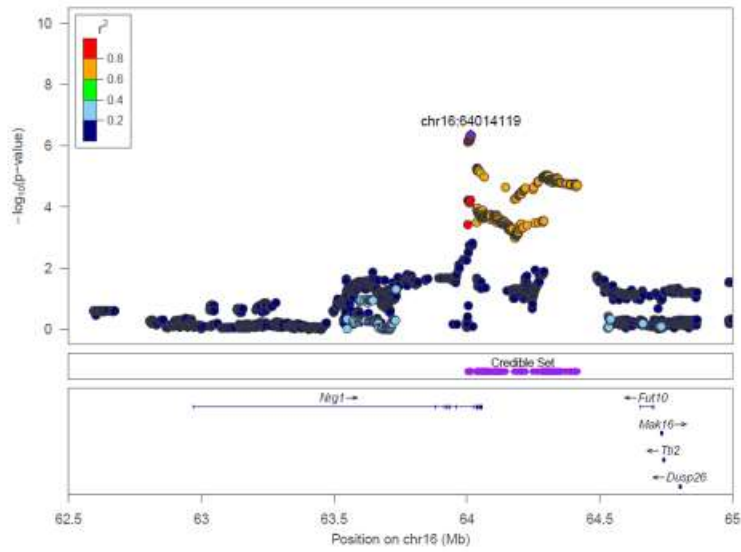
EpiFat, Chr18:12,674,871

BMI_NoTail, Chr18:25,190,274

TL, Chr19:25,190,274