

Table S1: Genes in RetroFat chromosome 6 QTL interval.

Gene Symbol	Gene Name	Start Location	Non-synonymous variants in WKY founder†	Polyphen prediction
Alk	ALK receptor tyrosine kinase	22696415		
LOC108351180	uncharacterized	22988727		
LOC108351181	uncharacterized	23205628		
Clip4	CAP-GLY domain containing linker protein family, member 4	23222020		
LOC103692578	basic proline-rich protein-like	23298261		
RGD1304963	similar to hypothetical protein MGC38716	23337507		
Togaram2	TOG array regulator of axonemal microtubules 2	23358762		
Wdr43*	WD repeat domain 43	23433532		
Trnac-gca30	transfer RNA cysteine (anticodon GCA) 30	23487063		
LOC102551341	tRNA (adenine(58)-N(1))-methyltransferase, mitochondrial-like	23487545		
Spdya	speedy/RINGO cell cycle regulator family member A	23493686	23495595	unknown
LOC102548558	protein tyrosine phosphatase type IVA 1-like	23493704		
Ppp1cb*	protein phosphatase 1 catalytic subunit beta	23548507		
LOC108351182	ALK tyrosine kinase receptor-like	23725713		
LOC298795	similar to 14-3-3 protein sigma	23757225		
LOC108351183	uncharacterized	23771355		
LOC103692567	uncharacterized	23885316		
LOC108351327	glyceraldehyde-3-phosphate dehydrogenase pseudogene	23936327		
LOC103692568	uncharacterized	23986197		
LOC102553396	uncharacterized	24064737		
Ypel5	yippee-like 5	24069351		
Lbh	limb bud and heart development	24154207		
LOC108351184	uncharacterized	24192828		
LOC108351185	uncharacterized	24256909		
LOC102547591	uncharacterized	24336223		
LOC100912066	uncharacterized	24342924		
Lclat1	lysocardiolipin acyltransferase 1	24377398		
LOC102547438	uncharacterized	24527464		
LOC685881	hypothetical protein	24562761		
Capn13	calpain 13	24579590		
LOC102554046	uncharacterized	24623564		
LOC102553955	uncharacterized	24657682		
Galnt14	polypeptide N-acetylgalactosaminyltransferase 14	24770308		
Ehd3	EH-domain containing 3	25076012		
LOC102554201	uncharacterized	25101552		
Xdh	xanthine dehydrogenase	25149570		
LOC100363233	splicing factor 3b, subunit 4-like	25226245		
Srd5a2	steroid 5 alpha-reductase 2	25279635		

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Plb1	phospholipase B1	25375699		
LOC683819	hypothetical protein	25565221		
Fosl2	FOS like 2, AP-1 transcription factor subunit	25598936		
Babam2	BRISC and BRCA1 A complex member 2	25666654		
LOC103692569	uncharacterized	25885973		
Rbks	ribokinase	26051568	26072561 T to A	benign
Mrpl33	mitochondrial ribosomal protein L33	26130278		
LOC102548914	uncharacterized	26201017		
Slc4a1ap	solute carrier family 4 member 1 adaptor protein	26214083		
Supt7l	SPT7-like STAGA complex gamma subunit	26241672		
Gpn1*	GPN-loop GTPase 1	26255081		
RGD1560110	similar to RIKEN cDNA 4930548H24	26278440		
Zfp512	zinc finger protein 512	26284749		
LOC102556504	titin-like	26322470		
Gckr	glucokinase regulator	26355296		
LOC100910821	uncharacterized	26387284		
Ift172	intraflagellar transport 172	26390686		
LOC108351187	uncharacterized	26407404		
LOC108351186	60S ribosomal protein L37 pseudogene	26415619		
LOC103692570	dihydropyrimidinase-related protein 5-like	26423841		
Krtcap3*	keratinocyte associated protein 3	26485126		
Nrbp1	nuclear receptor binding protein 1	26486823		
Ppm1g	protein phosphatase, Mg2+/Mn2+ dependent, 1G	26517840		
Zfp513	zinc finger protein 513	26537707		
Snx17	sorting nexin 17	26541137		
Eif2b4	eukaryotic translation initiation factor 2B subunit delta	26546917		
Gtf3c2	general transcription factor IIIC subunit 2	26560601	26581578 T to C	unknown
Mpv17	MpV17 mitochondrial inner membrane protein	26585713		
Ucn	urocortin	26602144		
Trim54	tripartite motif-containing 54	26603364		
Dnajc5g	DnaJ heat shock protein family (Hsp40) member C5 gamma	26625526		
Slc30a3*	solute carrier family 30 member 3	26629752		
Cad	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	26657507		
Atraid*	all-trans retinoic acid-induced differentiation factor	26680628		
Slc5a6	solute carrier family 5 member 6	26685823		
Tcf23	transcription factor 23	26763159		
Prr30	proline rich 30	26780352		

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Preb	prolactin regulatory element binding	26784088	26786379 A to G	benign
Abhd1	abhydrolase domain containing 1	26787807		
Cgrefl	cell growth regulator with EF hand domain 1	26797126		
Khk	ketoheokinase	26810577		
Emilin1	elastin microfibril interfacier 1	26821249		
LOC103692571	uncharacterized	26833107		
Ost4	oligosaccharyltransferase complex subunit 4, non-catalytic	26836216		
Agbl5	ATP/GTP binding protein-like 5	26837299		
Trnaa-agc6	transfer RNA alanine (anticodon AGC) 6	26856068		
Trnay-gua	transfer RNA tyrosine (anticodon GUA)	26856459		
Trnay-gua3	transfer RNA tyrosine (anticodon GUA) 3	26856459		
Tmem214	transmembrane protein 214	26867638		
Mapre3	microtubule-associated protein, RP/EB family, member 3	26878738		
LOC108351190	uncharacterized	26890051		
LOC108351189	uncharacterized	26918219		
LOC108351188	60S ribosomal protein L37 pseudogene	26931127		
Dpysl5	dihydropyrimidinase-like 5	26939696		
LOC103692572	uncharacterized	27069013		
Cenpa	centromere protein A	27072259		
Slc35f6	solute carrier family 35, member F6	27095144		
LOC103692573	uncharacterized	27139210		
Kcnk3	potassium two pore domain channel subfamily K member 3	27154274		
Cib4	calcium and integrin binding family member 4	27241804		
RGD1559683	similar to RIKEN cDNA 1700001C02	27305402		
Otof	otoferlin	27328343		
Drc1	dynein regulatory complex subunit 1	27425237	27428501 G to A	benign
Selenoi	selenoprotein I	27473748		
Adgrf3	adhesion G protein-coupled receptor F3	27534525		
Hadhb	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), beta subunit	27555408		
Hadha	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit	27589840		
Garem2	GRB2 associated regulator of MAPK1 subtype 2	27631364		
LOC503104	similar to retinoblastoma binding protein 4	27651115		
Rab10	RAB10, member RAS oncogene family	27668387		
Kif3c	kinesin family member 3C	27768943		

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Asxl2	additional sex combs like 2, transcriptional regulator	27835346		
LOC108351319	28S ribosomal protein S21, mitochondrial pseudogene	27856408		
LOC103692577	RNA pseudouridylate synthase domain-containing protein 4 pseudogene	27875868		
Dtnb	dystrobrevin, beta	27975302	28004664 A to G	benign
LOC102556400	transcription factor BTF3-like	28022498		
LOC103692574	uncharacterized	28034953		
Dnmt3a	DNA methyltransferase 3 alpha	28205375		
LOC108351191	60S ribosomal protein L37 pseudogene	28284681		
LOC100911610	dihydropyrimidinase-related protein 5-like	28293250		
RGD1565766	hypothetical gene supported by BC088468; NM_001009712	28367389		
Pomc	proopiomelanocortin	28382937		
Efr3b	EFR3 homolog B	28390541		
Dnajc27	DnaJ heat shock protein family (Hsp40) member C27	28515054		
LOC108351192	cytochrome c oxidase subunit 7B, mitochondrial pseudogene	28539158		
LOC103692575	cytochrome c oxidase subunit 7B, mitochondrial pseudogene	28539172		
LOC689056	similar to general transcription factor IIH, polypeptide 5	28556618		
Adcy3	adenylate cyclase 3	28570941	28572363 A to C	damaging
Cenpo	centromere protein O	28648804		
Pthrhl	peptidyl-tRNA hydrolase domain containing 1	28663602		
Ncoal	nuclear receptor coactivator 1	28677563		
LOC103692576	uncharacterized	28812571		

Genes in bold are found within the most likely region of the QTL based on multi-SNP fine-mapping analysis.

*Full or partial mediators of RetroFat called by mediation analysis.

†RetroFat chromosome 6 haplotype effects: WKY has decreased fat pad weight (Figure 3D).