

Table S1: Genes in RetroFat chromosome 6 QTL interval (continued).

Gene Symbol	Gene Name	Start Location	Non-synonymous variants in WKY founder†	Polyphen prediction
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		

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Prr30	proline rich 30	26780352		
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		

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Gene Symbol	Gene Name	Start Location	Non-synonymous variants in WKY founder†	Polyphen prediction
Kif3c	kinesin family member 3C	27768943		
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		
Ptrhd1	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).