

Table S4: Genes in RetroFat chromosome 6 QTL interval that support $X \rightarrow M$ relationship.

Gene Symbol	Gene Name	Start location	q-value
RGD1304963	similar to hypothetical protein MGC38716	23337507	4.79E-05
Wdr43	WD repeat domain 43	23433532	7.82E-02
Ppp1cb	protein phosphatase 1 catalytic subunit beta	23548507	7.46E-03
Galnt14	polypeptide N-acetylgalactosaminyltransferase 14	24770308	3.09E-02
Rbks	ribokinase	26051568	3.13E-11
Gpn1	GPN-loop GTPase 1	26255081	3.38E-04
Krtcap3	keratinocyte associated protein 3	26485126	3.30E-41
Slc30a3	solute carrier family 30 member 3	26629752	1.19E-07
Atraid	all-trans retinoic acid-induced differentiation factor	26680628	7.46E-03
Dpysl5	dihydropyrimidinase-like 5	26939696	9.66E-14
Hadha	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit	27589840	3.96E-03

Gene Symbol	Gene Name	Start location	q-value
Asxl2	additional sex combs like 2, transcriptional regulator	27835346	7.39E-02
Dtnb	dystrobrevin, beta	27975302	6.12E-02
Adcy3	adenylate cyclase 3	28570941	5.05E-05

Gene positions overlayed with SNP associations in Figure 3C.