

Table S3: QTLs for metabolic syndrome phenotypes in studies of C57BL/6J and A/J mice fed a High-Fat, High-Caloric Diet

Chr	Trait	LOD	SNP	Position (Mb)	Interval (Mb)	# Genes
1	insulin	4.11	mCV24145570	195	182.1 - 195.0	86
4	wt gain	6.15	rs3663950	135.7	128.2 - 154.4	431
7	insulin	4.29	rs4226520	29.8	24.9 - 40.2	297
10	<i>glucose</i>	<i>3.17</i>	rs13480569	30.7	28.3 - 31.0	15
11	<i>insulin</i>	<i>3.21</i>	rs13480968	36.5	30.4 - 40.3	47
13	wt gain	6.64	rs13481871	71.3	57.3 - 80.2	188
13	<i>glucose</i>	<i>3.36</i>	rs13481983	103.4	97.3 - 112.0	79
14	<i>insulin</i>	<i>3.23</i>	rs6169105	117.3	106.3 - 122.1	40
15	<i>glucose</i>	<i>2.75</i>	rs13482673	82.2	72.2 - 101.6	490

Wt gain is body weight gain over 8 weeks. Glucose and insulin represent serum levels. # Genes = the number of genes and predicted genes within the interval. . Genes and physical positions were obtained from the Mouse Genome Informatics Database. QTLs in bold meet the 5% genome-wide significance threshold generated in R/qtI (Broman et al. 2003). QTLs in *italics* meet the less stringent 5% thresholds generated using the method of Li and Ji (Li and Ji 2005; Chen and Storey 2006).