Supplemental table 1 QTLs for liver weight in (A/J × SM.A-*T2dm2sa*)F2 mice after 11 weeks feeding of a high-fat diet.

Phenotype	Nearest Marker	Position (Mb)	LOD[a]	QTL	%[b]	Phenotype based on genotype[c]		
						SM/SM	SM/A	A/A
Liver	D11Mit242	63.2	**8.7****	*Livq3sa*	15	**4.63 ± 0.71 (69)**	4.24 ± 0.59 (129)	3.92 ± 0.53 (57)
(g/100g bw)	D13Mit53	113.1	2.1		4	4.24 ± 0.71 (57)	4.18 ± 0.62 (128)	**4.48 ± 0.66 (70)**
	D15Mit52	22.4	**6.3****	*Livq4sa*	6	4.09 ± 0.56 (72)	4.17 ± 0.61 (112)	**4.62 ± 0.71 (71)**
	D17Mit68	47.7	3.5		6	4.01 ± 0.61 (68)	4.40 ± 0.69 (120)	**4.31 ± 0.60 (67)**

** Highly significant level; the other LOD scores without asterisks denote suggestive level linkage.

[a] The maximum LOD scores, exceeding suggestive threshold level. Suggestive, significant, or highly significant thresholds derived from free model permutation for each trait were as follows: for liver weight (2.1, 3.6, 5.1).

[b] Percentage of phenotypic variance explained by the QTL.

[c] Phenotype based on genotype at the nearest marker. Data are expressed means ± SD for genotypes. The number of mice of each genotype is indicated in parentheses. The higher mean of SM/SM or A/A were written by bold-faced letter.