Table S3 (A) SNPs which exist in the region of *Ap3m2* fit the distribution pattern of C57BL/6J=I/LnJ=iWSP-2 and AKR=129=DBA2=iWSR-1 and are the likely underlying causative nucleotides involved in the altered regulation of *Ap3m2* and the phenotypic differences mapped in the two QTL studies due to their identification as being within a regulatory feature. (B) Summary of the reported experimental evidence for each of the Ensembl regulatory features identified in A.

(A)

RefSnpID	Build 37 SNP location	Build 38 SNP location	SNP Genotypes		Ensembl Regulatory Feature ID	Transfac regulatory features (BIOBASE ID)
			C57BL/6J; I/LnJ (+)	129P3/J;AKR/J; DBA/2J (-)		
rs33255299	23605138	22494666	C	T		Pax-3 (M00327)
rs45867690	23604110	22493638	C	T		POU1F1 (M00744)
rs33346701	23601865	22491393	A	T		VDR, CAR, PXR (M00096)
rs51987012	23597278	*22486806*	*A*	*G*	*ENSMUSR00000225022*	*VDR, CAR, PXR (M00096)*
rs45944337	23597260	*22486788*	*A*	*T*	*ENSMUSR00000225022*	*C - GR (M00205)*
rs49759176	23594851	22484379	T	C		SMAD3 (M00701)
rs32743569	23589809	22479337	C	T		myogenin / NF-1 (M00056)
rs32650954	23589790	22479318	T	C		myogenin / NF-1 (M00056)
rs32926479	23587531	***22477059***	***C***	***T***	***ENSMUSR00000299557***	
rs259599964	23587232	***22476760***	***C***	***G***	***ENSMUSR00000299557***	***GABP (M00341)***
rs52251207	23587140	***22476668***	***T***	***C***	***ENSMUSR00000299557***	***ETF (M00695)***
rs32882991	23587093	***22476621***	***T***	***C***	***ENSMUSR00000299557***	
rs33346694	23583851	22473379	C	A		Kid3 (M01160);myogenin / NF-1 (M0056)
rs33468918	23259740	22149268	G	A		CdxA (M00101)
rs32693908	23259552	22149080	A	T		myogenin / NF-1 (M00056)
rs33391608	23259407	22148935	C	T		myogenin / NF-1 (M00056)
rs48407506	23257246	22146774	A	G		FAC1 (M00456)
rs49292343	23257245	22146773	T	A		FAC1 (M00456)
rs51735649	23257094	22146622	C	T		Muscle initiator sequences-19 (M00323)
rs33612810	23256679	22146207	A	G	ENSMUSR00000397963	
rs33559386	23256427	22145955	G	C	ENSMUSR00000397963	
rs33189424	23256368	22145896	A	G	ENSMUSR00000397963	
rs49087640	23256134	22145662	C	T		Tst-1 (M00133)

rs33450716	23242568	22132096	C	T		PPARgamma:RXRalpha (M00512), LEF1, TCF1 (M00978), PPAR, HNF-4, COUP, RAR (M00762), HNF-4 (M01031), PPAR direct repeat 1 (M00763), HNF4alpha (M00638), COUP direct repeat 1 (M00765)
rs49767895	23242250	22131778	G	T		Oct-1 (M00136)
rs13474140	23238914	22128442	T	C		Ets-1 p54 (M01078), v-Myb (M00227), BRCA1:USF2 (M01082)
rs32641536	23236602	22126130	A	G		FOXJ2 (M00423), PLZF (M01075), C/EBP/gamma (M00622)
rs51839162	23235528	22125056	G	A	ENSMUSR00000397962	
rs48010023	23235514	22125042	C	T	ENSMUSR00000397962	
rs33210112	23228975	22118503	C	T		Tst-1 (M00133)
rs45645647	23154126	22043654	G	A		STAT (M00777)
rs33155370	23085975	21975503	C	T		VDR, CAR, PXR (M00966)
rs50493771	23057769	21947297	T	G		HNF3alpha (M00724)

(B)

Ensembl Regulatory Feature ID	Sensitivity to DNase1	Transcription Factor Binding									Histone Methylation				Histone Acetylation	Polymerase Binding
		CTCF	Esrrb	C/Nmyc	E2F1	Esrrb	Max	NELFe	Zfx	H3K36me3	H3K4me1	H3K4me3	H3K4me2	H3K9ac	PolII
ENSMUSR00000225022	3	3	1							3	1				
ENSMUSR00000299557	***5***			***7***	***1***	***2***	***4***	***1***	***3***	***1***		***10***	***1***	***2***	***4***
ENSMUSR00000397963	1														
ENSMUSR00000397962	2	1										1	1		

Cell values indicate the number of experimental sources providing evidence for each transcription regulatory relation to a given feature.