Supplemental Materials

Supplemental Figures

Figure S1. Pedigree of the MYK x SM/J cross.

Figure S2. Parent-of-origin effect on weight gain.

Figure S3. Pairwise correlation in LOD profile between different SM/J

mapping panels.

Supplemental Tables

Table S1. Sampling locations

Table S2. Phenotyping scheme

Table S3. Correlation matrix between traits

Table S4. Datasets used in the SM/J meta-analysis

Table S5. Adaptors used for RADseq
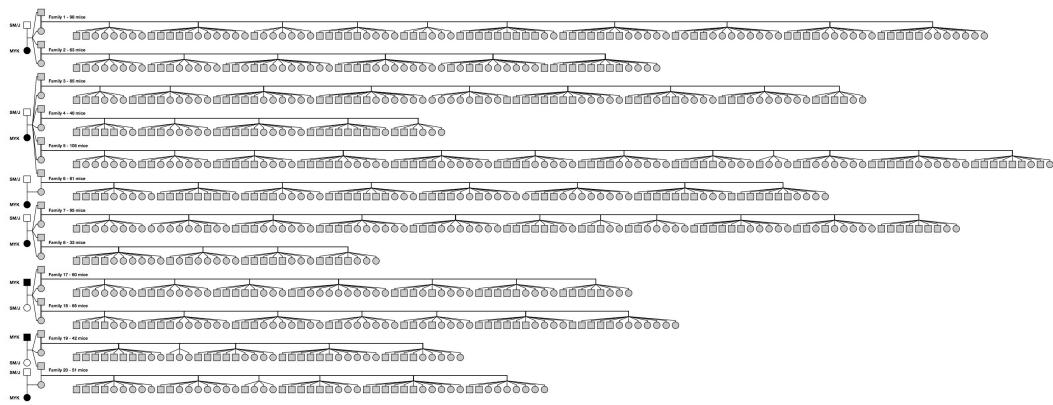
Figure S1. Pedigree of the MYK x SM/J cross. Shown are the pedigree relationship between the animals in the current study (males: squares; females: circles; MYK: black; SM/J: white), with the F2 families rotated to fit onto the page. Each horizontal row represent the offspring from an F2 family, with litters indicated by groups.
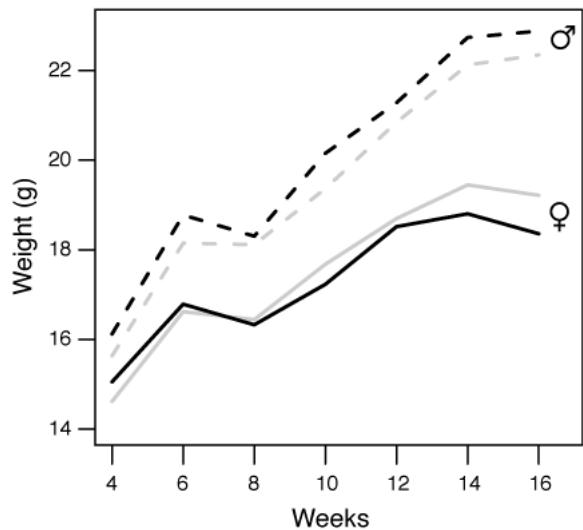
Figure S2. Parent-of-origin effect on weight gain. Shown here are the mean growth curve of the F2 mice, split by cross direction. The main difference in cross direction can be best shown by tracking the X chromosome: F2 females all carry an X chromosome from the paternal grandmother due to the pedigree structure. Here, we observed a significant interaction with cross direction in females (solid lines; repeated measures ANOVA, $P < 0.0003$; but $P < 0.89$ in males, dashed lines). F2 females carrying an MYK X chromosome were born with lower weaning weight at 4 weeks of age, but gained greater weight by week 16 There was no discernible effect among males.
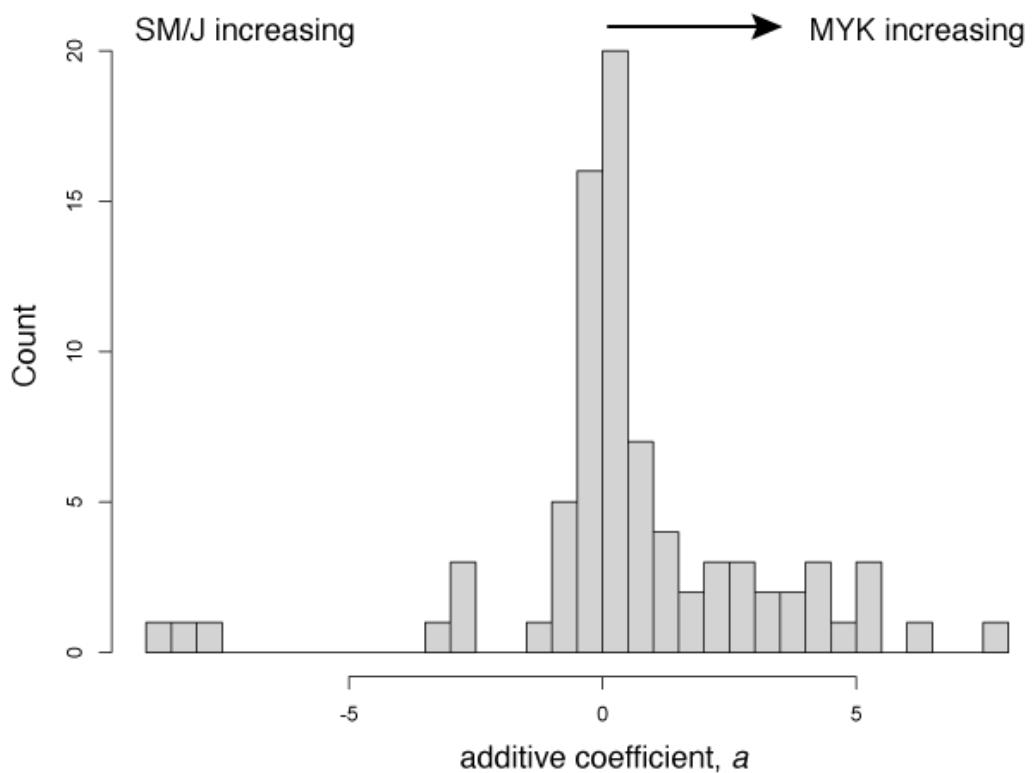
Fig. S3. Distribution of effect size. The additive coefficient*, a*, here is the normalized and standardized effect size per allele and not in raw measurement units. These include all weight, length and plasma protein level measurements (directionality assigned according to the function of each hormone on growth) but not PCA scores.
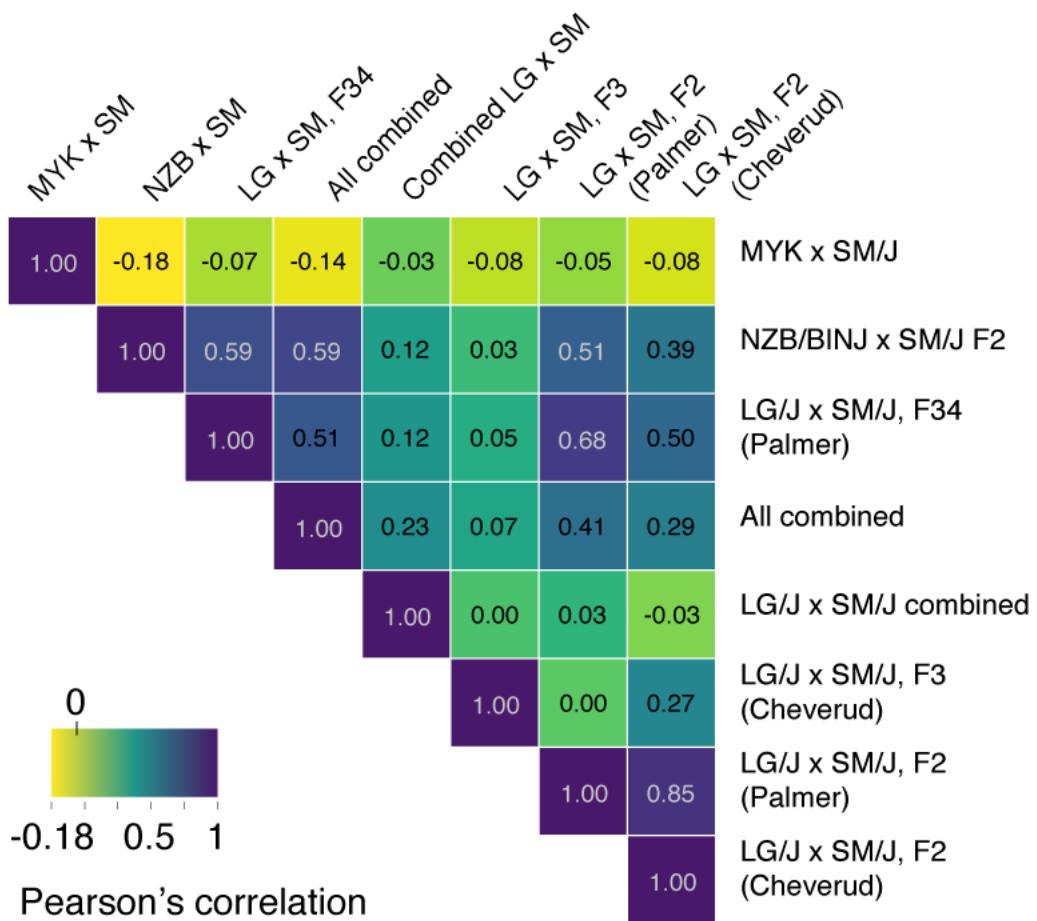
Figure S4. Pairwise correlation in LOD profile between different SM/J mapping panels. Joint QTL mapping was performed for 16-week body weight in various mapping panels involving the SM/J strain and their combinations. The Pearson's correlation of the LOD profiles in each configuration is shown here as a pairwise heatmap (and labelled with the numerical values).

Table. S1. Sampling locations.

Site name	Longitude	Latitude	n	# lab progeny/ matings	Remarks
MYK01	62.1042562	-7.6427027	0		Basement
MYK02	62.1034092	-7.6451416	4	0/1	Basement, guest house
MYK03	62.1033446	-7.6447564	4	13/1	Store room
MYK04	62.1034391	-7.6437744	1		
MYK05	62.1026023	-7.6450156	3	27/1	Helicopter terminal; used for QTL cross
MYK06	62.1033887	-7.6448121	0		
MYK07	62.1017152	-7.6431949	5	27;23/2	Sheep barn
MYK08	62.1023514	-7.6491337	2	0/1	Harbour supplies stores
MYK09	62.1064193	-7.6335588	2	15/1	Outpost
MYK10	62.1035093	-7.6432685	1		

Mating pairs were set up between mice from the same sampling site, further reducing the number of variants segregating within a parent. MYK07 was the alternate for the QTL cross, but eventually was not used for this study. The number of progenies here include mice born after the QTL cross was initiated.

Table. S2. Phenotyping scheme.

	Birth		Early growth				Puberty	Late growth		Full adulthood	Remarks
Weeks	**0**	**2**	**4**	**6**	**8**		**10**	**12**	**14**	**16***	
					Single housing						
Weight			X	X	X		X	X	X	X	Only around ~200 data points collected for Week 4
Length					X					X	Body and tail length separately measured. Summed to give "Total length"
Growth hormone										X	*igf1*, i*gfbp2* and *igfbp3 using ELISA*
Organ weight										X	liver, weighed immediately following dissection

* Animals were sacrificed at this time-point

This table schematically represents the phenotyping time-course of each F2 mouse in the mapping experiment.

Table S3. Correlation matrix between measured traits.

	IGF1.ELISA	IGFBP2.ELISA	IGFBP3.ELISA	GrowthModel.A	GrowthModel.μ	BodyWeight.4Wk	BodyWeight.6Wk	BodyWeight.8Wk	BodyWeight.10Wk	BodyWeight.12Wk	BodyWeight.14Wk	BodyWeight.16Wk	LiverWeight.16Wk	TotalLength.8Wk	TotalLength.16Wk	TailLength.8Wk	TailLength.16Wk	BodyLength.8Wk	BodyLength.16Wk
IGF1.ELISA	1.00	0.39	0.71	0.52	0.09	0.13	0.31	0.43	0.41	0.47	0.55	0.61	0.58	0.35	0.51	0.25	0.34	0.34	0.55
IGFBP2.ELISA	0.39	1.00	0.38	0.31	0.12	-0.04	0.14	0.25	0.23	0.28	0.35	0.38	0.36	0.19	0.30	0.06	0.21	0.25	0.32
IGFBP3.ELISA	0.71	0.38	1.00	0.36	0.11	0.05	0.23	0.32	0.35	0.39	0.46	0.51	0.57	0.26	0.39	0.18	0.23	0.25	0.46
GrowthModel.A	0.52	0.31	0.36	1.00	-0.04	0.60	0.56	0.71	0.70	0.84	0.89	0.92	0.70	0.58	0.69	0.45	0.56	0.53	0.67
GrowthModel.μ	0.09	0.12	0.11	-0.04	1.00	-0.26	0.03	0.37	0.37	0.24	0.22	0.20	0.21	0.24	0.24	0.19	0.21	0.21	0.21
BodyWeight.4Wk	0.13	-0.04	0.05	0.60	-0.26	1.00	0.52	0.49	0.45	0.49	0.42	0.40	0.22	0.47	0.38	0.50	0.36	0.31	0.34
BodyWeight.6Wk	0.31	0.14	0.23	0.56	0.03	0.52	1.00	0.70	0.64	0.60	0.60	0.58	0.47	0.55	0.52	0.44	0.42	0.49	0.50
BodyWeight.8Wk	0.43	0.25	0.32	0.71	0.37	0.49	0.70	1.00	0.85	0.82	0.82	0.74	0.60	0.72	0.65	0.54	0.52	0.68	0.63
BodyWeight.10Wk	0.41	0.23	0.35	0.70	0.37	0.45	0.64	0.85	1.00	0.81	0.80	0.72	0.60	0.63	0.63	0.48	0.49	0.57	0.61
BodyWeight.12Wk	0.47	0.28	0.39	0.84	0.24	0.49	0.60	0.82	0.81	1.00	0.87	0.78	0.65	0.61	0.65	0.45	0.49	0.58	0.66
BodyWeight.14Wk	0.55	0.35	0.46	0.89	0.22	0.42	0.60	0.82	0.80	0.87	1.00	0.91	0.73	0.64	0.73	0.45	0.55	0.62	0.74
BodyWeight.16Wk	0.61	0.38	0.51	0.92	0.20	0.40	0.58	0.74	0.72	0.78	0.91	1.00	0.80	0.60	0.73	0.42	0.55	0.58	0.74
LiverWeight.16Wk	0.58	0.36	0.57	0.70	0.21	0.22	0.47	0.60	0.60	0.65	0.73	0.80	1.00	0.44	0.61	0.32	0.42	0.41	0.64
TotalLength.8Wk	0.35	0.19	0.26	0.58	0.24	0.47	0.55	0.72	0.63	0.61	0.64	0.60	0.44	1.00	0.79	0.82	0.77	0.85	0.60
TotalLength.16Wk	0.51	0.30	0.39	0.69	0.24	0.38	0.52	0.65	0.63	0.65	0.73	0.73	0.61	0.79	1.00	0.73	0.89	0.60	0.86
TailLength.8Wk	0.25	0.06	0.18	0.45	0.19	0.50	0.44	0.54	0.48	0.45	0.45	0.42	0.32	0.82	0.73	1.00	0.84	0.41	0.43
TailLength.16Wk	0.34	0.21	0.23	0.56	0.21	0.36	0.42	0.52	0.49	0.49	0.55	0.55	0.42	0.77	0.89	0.84	1.00	0.48	0.53
BodyLength.8Wk	0.34	0.25	0.25	0.53	0.21	0.31	0.49	0.68	0.57	0.58	0.62	0.58	0.41	0.85	0.60	0.41	0.48	1.00	0.57
BodyLength.16Wk	0.55	0.32	0.46	0.67	0.21	0.34	0.50	0.63	0.61	0.66	0.74	0.74	0.64	0.60	0.86	0.43	0.53	0.57	1.00

Table S4. Datasets used in the SM/J meta-analysis.

Panel	Parent 1	Parent 2	Generation	N*	Reference
Chan F2	MYK	SM/J	F2	761	This study
Cheverud F2	LG/J	SM/J	F2	505	Cheverud *et al.*, 1996
Cheverud F3	LG/J	SM/J	F3	1611	Norgard *et al.*, 2008
Palmer F2	LG/J	SM/J	F2	490	Parker *et al.*, 2011
Palmer F34	LG/J	SM/J	F34	687	Parker *et al.*, 2011
Stylianou F2	NSB/BINJ	SM/J	F2	489	Stylianou *et al.*, 2006

* retained samples with comparable phenotypes

Table S5. Adaptors used for RADseq

Read	Barcode Type	Barcode	Overhang	Sample Position
1	5prime	CAGATA	TGCAG	A01
1	5prime	GAAGTG	TGCAG	B01
1	5prime	TAGCGGAT	TGCAG	C01
1	5prime	TATTCGCAT	TGCAG	D01
1	5prime	ATAGAT	TGCAG	E01
1	5prime	CCGAACA	TGCAG	F01
1	5prime	GGAAGACAT	TGCAG	G01
1	5prime	AACGCACATT	TGCAG	H01
1	5prime	GAGCGACAT	TGCAG	A02
1	5prime	CCTTGCCATT	TGCAG	B02
1	5prime	GGTATA	TGCAG	C02
1	5prime	TCTTGG	TGCAG	D02
1	5prime	GGTGT	TGCAG	E02
1	5prime	GGATA	TGCAG	F02
1	5prime	CTAAGCA	TGCAG	G02
1	5prime	ATTAT	TGCAG	H02
1	5prime	GCGCTCA	TGCAG	A03
1	5prime	ACTGCGAT	TGCAG	B03
1	5prime	TTCGTT	TGCAG	C03
1	5prime	ATATAA	TGCAG	D03
1	5prime	TGGCAACAGA	TGCAG	E03
1	5prime	CTCGTCG	TGCAG	F03
1	5prime	GCCTACCT	TGCAG	G03
1	5prime	CACCA	TGCAG	H03
1	5prime	AATTAG	TGCAG	A04
1	5prime	GGAACGA	TGCAG	B04
1	5prime	ACTGCT	TGCAG	C04
1	5prime	TGCTT	TGCAG	D04
1	5prime	GCAAGCCAT	TGCAG	E04
1	5prime	CGCACCAATT	TGCAG	F04
1	5prime	CTCGCGG	TGCAG	G04
1	5prime	AACTGG	TGCAG	H04
1	5prime	ATGAGCAA	TGCAG	A05
1	5prime	CTTGA	TGCAG	B05
1	5prime	GCGTCCT	TGCAG	C05
1	5prime	ACCAGGA	TGCAG	D05
1	5prime	CCACTCA	TGCAG	E05
1	5prime	TCACGGAAG	TGCAG	F05
1	5prime	TATCA	TGCAG	G05
1	5prime	TAGCCAA	TGCAG	H05

1	5prime	ATATCGCCA	TGCAG	A06
1	5prime	CTCTA	TGCAG	B06
1	5prime	GGTGCACATT	TGCAG	C06
1	5prime	CTCTCGCAT	TGCAG	D06
1	5prime	CAGAGGT	TGCAG	E06
1	5prime	GCGTACAAT	TGCAG	F06
1	5prime	ACGCGCG	TGCAG	G06
1	5prime	GTCGCCT	TGCAG	H06
1	5prime	AATAACCAA	TGCAG	A07
1	5prime	AATGAACGA	TGCAG	B07
1	5prime	ATGGCAA	TGCAG	C07
1	5prime	GAAGCA	TGCAG	D07
1	5prime	AACGTGCCT	TGCAG	E07
1	5prime	CCTCG	TGCAG	F07
1	5prime	CTCAT	TGCAG	G07
1	5prime	ACGGTACT	TGCAG	H07
1	5prime	GCGCCG	TGCAG	A08
1	5prime	CAAGT	TGCAG	B08
1	5prime	GGAGTCAAG	TGCAG	C08
1	5prime	TGAAT	TGCAG	D08
1	5prime	CATAT	TGCAG	E08
1	5prime	GTGACACAT	TGCAG	F08
1	5prime	TATGT	TGCAG	G08
1	5prime	TGCAGA	TGCAG	H08
1	5prime	CATCTGCCG	TGCAG	A09
1	5prime	GGACAG	TGCAG	B09
1	5prime	ATCTGT	TGCAG	C09
1	5prime	AAGACGCT	TGCAG	D09
1	5prime	GAATGCAATA	TGCAG	E09
1	5prime	TAGCAG	TGCAG	F09
1	5prime	CTTAG	TGCAG	G09
1	5prime	TTATTACAT	TGCAG	H09
1	5prime	GCCAACAAGA	TGCAG	A10
1	5prime	TGCCGCAT	TGCAG	B10
1	5prime	CGTGTCA	TGCAG	C10
1	5prime	CAACCACACA	TGCAG	D10
1	5prime	GCTCCGA	TGCAG	E10
1	5prime	CGTTCA	TGCAG	F10
1	5prime	CATCACAAG	TGCAG	G10
1	5prime	TCCAG	TGCAG	H10
1	5prime	AACTGAAG	TGCAG	A11
1	5prime	GATTCA	TGCAG	B11
1	5prime	CAAGCCAATT	TGCAG	C11

1	5prime	TTGCGCT	TGCAG	D11
1	5prime	CGCAGACACT	TGCAG	E11
1	5prime	TGTGGA	TGCAG	F11
1	5prime	TGGATA	TGCAG	G11
1	5prime	ATAGCGT	TGCAG	H11
1	5prime	CCATAGA	TGCAG	A12
1	5prime	GGCACGCAT	TGCAG	B12
1	5prime	ATTAACAATT	TGCAG	C12
1	5prime	CAATA	TGCAG	D12
1	5prime	TAGTCCAT	TGCAG	E12
1	5prime	CGTGACCT	TGCAG	F12
1	5prime	CTTCAGA	TGCAG	G12
1	5prime	ATCTGCAACA	TGCAG	H12

Adapters

Adapter 1

Barcoded adapters ("Adapter1")

```
5' CACGACGCTCTTCCGATCTXXXXXTGCA
```

```
3' GTGCTGCGAGAAGGCTAGAXXXXX
```

Adapter 2

Adapter_2_MseI_top

```
5'–[Phos]TAAGATCGGAAGAGCGGGGACTTTAAG*C
```

Adapter_2_MseI_bottom

```
5'–[Phos]GATCGGTCTCGGCATTCCTGCTGAACCGCTCTTCCGATC*T
```

5'-[Phos] stands for phosphorylation at the 5' end.
* stands for a phosphorothioate linkage at the first 3' terminal internucleotide linkage.