Supplemental Table 1. mRNA Expression Analysis. For each gene tested, the average C_t value is given for LG/J and SM/J samples, as well as the associated standard error (SE). The significance of the difference between strains (listed under "Prob.") and the associated R^2 value are given for each sample. Bold values indicate significance at the $p < 0.05$ level.

Gene	Av C_t LG/J	Av C_t SM/J	SE	Prob.	R^2
Comp	23.13	22.85	0.14	**0.001**	13.5%
Igf1	28.57	28.91	0.16	**0.022**	3.8%
Ihh	26.32	26.58	0.18	**0.001**	7.7%
Pthlh	30.84	31.24	0.15	**0.010**	4.7%
Runx2	26.95	27.11	0.15	0.107	1.9%
Smad1	28.77	29.09	0.14	**3.3E-5**	17.2%
Male	29.15	29.72	0.17	**1.1E-5**	25.9%
Female	28.35	28.42	0.19	0.189	2.5%
Sox5	29.17	29.35	0.15	**0.031**	3.4%
Sox9	24.57	25.26	0.13	**1.1E-6**	36.7%
Tgfb1	25.89	26.01	0.12	0.100	1.9%
Vegfa	28.81	29.03	0.14	**0.033**	3.2%

Supplemental Table 2. QTL Positional Candidate Coding Region Polymorphisms. QTL positional candidate genes tested for coding region polymorphisms are listed by chromosome, pleiotropic QTL name, gene name, and mRNA RefSeq number. The position of each SNP (in bp) in the gene and the strand (+ or -) are indicated; a * denotes that two SNPs comprise a single polymorphism. The nucleotide at each polymorphism is given for the reference strain C57BL/6J (C57), LG/J (LG), and SM/J (SM). The change in amino acid residue is noted, followed by whether the amino acid change caused a change in chemical property (denoted with an X) as defined previously (see Results and (23)). The classification groups examined were polarity and volume (Pol/Vol), charge and aromaticity (Ch/Ar), or charge and polarity (Ch/Pol). Finally, using the cSNP tool of the PANTHER program (see Materials and Methods and (16-18)), the probability of the amino acid change being deleterious (P_{del}) were calculated for each SNP (see (16-18)). The higher P_{del} is, the more likely that a change is deleterious. This information was only available for some SNPs.

Chr	QTL	Gene	RefSeq	SNP (bp)	Strand	C57	LG	SM	AA Change	Pol/Vol	Ch/Ar	Ch/Pol	P_{del}
1	*Lbn1.1a*	*Atg9a*	NM_001003917	75179497	-	C	C	G	G780A				0.17
		Chpf	NM_001001565	75472392	-	C	C	T	R331Q	X	X	X	0.82
		Rufy4	NM_001170641	74176306	+	G	G	C	A141P				0.13
				74187522	+	T	C	T	V454A	X			0.16
	Lbn1.1b	*Trip12*	NM_133975	84790700	-	A	G	A	F101L	X	X		
2	*Lbn2.1a*	*Kif18a*	NM_139303	109173671	+	A	A	T	Q736L	X		X	0.86
	Lbn2.1b	*Arhgap11a*	NM_181416	113673494	-	A	A	T	L867H	X	X	X	0.21
				113673926	-	C	C	A	G723V	X			0.05
				113683481	-	C	C	T	A74T			X	0.14
		Zfp770	NM_175466	114022899	-	A	A	G	W142R	X	X	X	
				114023279	-	A	A	C	L15R	X	X	X	
		Aven	NM_028844	112470054	+	T	T	C	L245F	X	X		
		Fmn1	NM_010230	113365405	+	G	G	A	G776E	X	X	X	0.69
				113365676	+	T	T	G	H866Q	X	X	X	0.92
	Lbn2.1c	*Dnajc17*	NM_139139	118998396	-	A	A	T	F273Y			X	0.7
				119005108	-	C	C	T	G258S			X	0.62
				119006271	-	C	C	A	E184D				0.7
				119006702	-	C	C	T	R161E	X	X	X	0.77
				119009358	-	T	T	C	Q152R	X	X	X	0.67
		Mapkbp1	NM_011941	119847031	+	G	G	C	G900A				

				119848202	+	A	A	G	H1056R				
				119848468	+	A	A	G	Q1090R	X	X	X	
				119848950	+	A	A	G	H1167R				
				119849312	+	A	A	G	Q1212R	X	X	X	
				119849477	+	T	T	C	V1267A	X			
				119850850	+	A	A	G	T1432C	X			
	Lbn2.3a	*Esf1*	NM_001081090	139946462	-	G	G	C	D808E				0.12
				139993648	-	T	T	G	K168T	X	X	X	
				139993713	-	C	C	A	Q146H	X		X	
				139993882	-	C	C	T	S90N	X			0.29
		Sptlc3	NM_175467	139392329	+	G	G	T	K209N	X	X	X	0.72
				139407348	+	G	G	A	V309I				0.42
		2310003L22Rik	NM_027093	139996639	+	C	C	G	D64E				0.13
		Sel1l2	NM_001033296	140069695	-	A	A	T	L534M				0.50
		Macrod2	NM_001013802	142122308	+	G	G	A	V364M				
	Lbn2.3b	*Rya3*	NM_194357	153754480	+	A	G	A	T354A			X	0.65
				153755094	+	A	A	G	I397V				0.56
				153757199	+	G	G	A	M434I				0.46
4	*Lbn4.1*	*Leprot*	NM_175036	101328896	+	A	G	A	D92G	X	X	X	0.28
		Lepr	NM_010704	101437552	+	A	G	A	I359V				
		Insl5	NM_011831	102699132	-	A	C	A	S56A			X	
	Lbn4.2	*Gmeb1*	NM_020273	131782224	-	C	C	T	S382K	X	X	X	
				131786982	-	C	T	C	V263I				
		Map3k6	NM_016693	132797022	+	G	A	G	G7R	X	X	X	
				132802856	+	G	A	G	V550M				
				132802862	+	A	G	A	T552A			X	
				132802885	+	C	G	C	D559E				
				132803155	+	C	T	C	A593V	X			
		Rcan3	NM_022980	134981213	-	T	A	T	E37D				0.18
	Lbn4.3	*Tnfsf15*	NM_026281	63406030	-	C	C	T	G30E	X	X	X	

	Lbn4.4	*Cdc20*	NM_023223	118109621	-	T	G	T	T36P			X	
	Lbn4.5	*Snip1*	NM_175246	124745402	+	A	G	A	Q90R	X	X	X	
6	*Lbn6.2*	*Itpr2*	NM_019923	146128853	-	A	G	A	V2265A	X			0.65
				146188951	-	T	G	T	K1738T	X	X	X	0.29
				146188979	-	T	C	T	S1729G			X	0.32
				146189713	-	T	C	T	I1710V				
				146331335	-	C	G	C	E528D				
		4933424B01Rik	NM_138757	146506127	-	T	T	C	S303G			X	0.12
		Fgfr1op2	NM_026218	146538484	+	A	A	G	M108V				0.29
		Tm7sf3	NM_026281	146554677	-	C	C	A	V470F	X	X		
				146559465	-	T	T	C	I318V				
				146561954	-	C	C	A	V296F	X	X		
				146567061	-	A	A	G	F283S	X	X	X	
				146568529	-	T	T	C	T170A			X	
		Arntl2	NM_172309	146767353	+	A	A	G	I164M				0.33
				146769073	+	T	T	C	Y207H	X	X	X	0.85
				146769091	+	A	A	G	M213V				0.41
				146778231	+	C	C	T	P504L	X			0.43
		1700023A16Rik	NM_027059	146801158	+	G	G	T	R13L	X	X	X	
				146801212	+	C	C	T	S31L	X		X	
				146804656	+	T	T	C	M62T	X		X	
				146807462	+	T	T	C	V98A	X			
				146819832	+	T	T	G	L337V				
		1700034J05Rik	NM_028509	146901480	-	T	T	G	Q195H	X	X	X	
				146901916	-	G	G	C	S50C	X			
		Ppfibp1	NM_026221	146954499	+	T	T	C	L360P	X			0.57
		2210417D09Rik	NM_025620	146981493	+	C	C	G	Q103E		X	X	
				146981793	+	A	A	G	I203V				
		Mrps35	NM_145573	146991348	+	C	C	G	T11S				
				147009968	+	G	G	A	C216Y	X	X		0.28
				147019259	+	A	A	G	I293V				0.12

		EG545893	uc009est.1	147023650	-	C	C	T	R330H				
				147023681	-	T	T	C	M320V				
				147023698	-	C	C	T	R314Q	X	X	X	
				147023750	-	T	T	C	I297V				
				147023813	-	A	A	G	W276R	X		X	
				147023862	-	T	T	G	K259N	X	X	X	
				147023999	-	T	T	C	M214L				
				147024025	-	T	T	G	N205T	X			
				147024044	-	A	A	T	L199I				
				147024112	-	G	G	A	T176I	X		X	
				147024119	-	C	C	G	A174P				
				147024134	-	G	G	A	P169S			X	
				147024181	-	C	C	G	S153T				
				147024232	-	C	C	G	S137T				
		Pthlh	NM_008970	147205487	-	G	G	T	P166T			X	0.20
7	*Lbn7.1*	*Hapln3*	NM_178255	86262746	-	G	G	A	A262V	X			0.50
	Lbn7.4	*Sox6*	NM_011445	122944979	-	C	T	C	M47I				
8	*Lbn8.1a*	*Cilp2*	NM_026818	72405878	-	C	C	A	A790S			X	0.19
				72406790	-	C	C	T	G486R	X	X	X	0.67
		Gdf1	NM_008107	72854735	+	A	T	A	S145C	X			0.94
		*Gdf15**	NM_011819	73153835	-	C	T	C	T173A				
		*Insl3**	NM_013564	74214158	+	T	G	T	L88R	X	X	X	0.10
	Lbn8.1b	*Hhip*	NM_020259	82581329	-	T	C	T	N29S	X			0.25
9	*Lbn9.3*	*Pcolce2*	NM_029620	95578805	+	A	T	A	T163S				0.88
10	*Lbn10.2*	*Os9*	NM_001171026	126535465	-	T	C	T	N453D		X	X	0.56
				126535602	-	T	C	T	D407G	X	X	X	0.43
		Rdh7	NM_017473	127321810	-	G	G	T	Q250K	X	X	X	
		Hsd17b6	NM_013786	127428363	-	C	C	T	A299T			X	
				127430808	-	C	C	T	V194I				0.90
		Stat2	NM_019963	127721007	+	C	C	T	A532V	X			0.71
				127727644	+	C	C	G	H727Q	X	X	X	0.56

				127727937	+	T	T	C	L825P	X			0.58
				127728080	+	C	C	A	L873M				
		Mmp19	NM_021412	128231644	+	G	A	G	R80H				0.44
				128231929	+	C	T	C	L120F	X	X		
				128233564	+	G	G	A	V297M				0.64
				128235989	+	T	T	C	S473P			X	
		Rdh5	NM_134006	128350946	-	T	T	G	E260D				0.82
				128351226	-	A	A	G	I233T	X		X	
		Itga7	NM_008398	128380017	+	G	A	G	R315H				0.71
				128382560	+	A	A	C	T613P			X	0.40
11	*Lbn11.2*	*Flt4*	NM_008029	49438950	+	C	T	C	A126V	X			
		Col23a1	NM_153393	51381401	+	G	C	G	A288P				0.57
		Gdf9	NM_008110	53250607	+	T	C	T	I296T	X		X	
		Kif3a	NM_008443	53400418	+	A	G	A	K404R				0.72
				53412324	+	T	C	T	M683T	X		X	0.71
12	*Lbn12.1*	*Nkx2-9*	NM_008701	57712825	-	C	T	C	R197H				
	Lbn12.4	*Rdh12*	NM_030017	80319824	+	C	A	C	L274I				0.83
13	*Lbn13.1*	*Adamts6*	NM_001081020	105102839	+	T	T	A	S226T				0.41
14	*Lbn14.1*	*Diap3*	NM_019670	87056221	-	T	T	C	K1142R				0.32
				87228885	-	T	T	C	I960V				0.55
				87366380	-	C	C	A	G550C	X		X	0.87
				87385469	-	C	C	T	S380N	X			0.50
				87490835	-	G	G	T	P93T			X	0.58
		Tdrd3	NM_172605	87905647	+	C	C	G	T408S				
				87905830	+	A	A	G	K469R				
				87905889	+	C	C	T	L489F	X	X		0.17
				87906099	+	G	G	T	V559F	X	X		0.20
				87906152	+	G	G	T	R576S	X	X	X	0.15
		Pcdh20	NM_178685	88866853	-	C	C	G	L939F	X	X		
				88870769	-	A	A	G	L10S	X		X	

15	*Lbn15.2*	*Kif21a*	NM_001109041	90797721	-	A	A	C	I975S	X		X	
				90816305	-	T	T	C	M376V				0.93
	Lbn15.3	*Col14a1*	NM_181277	55280294	+	G	T	G	K1229N	X	X	X	
				55351491	+	C	T	C	S1770F	X	X	X	
19	*Lbn19.1*	*Fosl1*	NM_010235	5454995	+	C	C	T	P170L	X			0.78
		Ltbp3	NM_008520	5751413	+	A	A	G	T662A			X	0.85
		Map4k2	NM_009006	6341786	+	G	G	C	R66P	X	X	X	0.99

Supplemental Table 3. Known skeletal growth gene polymorphism summary. The number of polymorphisms in each region of the gene (+10K, 10 Kbp upstream; 5' UTR; Introns; Exons; and 3' UTR; -10K, 10 Kbp downstream) is given for each gene, as well as the total number of polymorphisms in all regions combined (Total). Bold numbers denote the presence of polymorphisms with PhastCon scores greater than 0.5; italicized number indicate the presence of polymorphisms with PhastCon scores greater than 0.95

Gene	+10K	5' UTR	Introns	Exons	3' UTR	-10K	Total
COMP	1					***4***	5
Igf1			***5***	***1***[a]			6
Ihh	***33***		5			2	40
Pthlh	***73***	2	***46***			**57**	178
Runx2	1		***578***		**3**	**28**	610
Smad1	7		24				31
Sox5	***74***[a]	***1***	***3175***[ab]		***1***	***61***	3312
Sox9			1		3		4
Tgfb1	9		12			**2**	23
Vegfa	1		**5**		***1***	8	15

[a] indicates the presence of a polymorphism in a *Foxa2* regulatory region
[b] indicates the presence of a polymorphism in an *Esr1* regulatory region