

Table S1 Descriptive statistics for four traits (body weight, standard length, body depth and body thickness)^{a)}

Population	Trait	Average (SD)	Max	Min	Skewness	Kurtosis	<i>P</i>
A	W	284.7(50.1)	431.3	167.5	0.084	−0.612	0.594
	SL	19.7(1.6)	22.9	16.3	−0.065	0.030	0.987
	H	8.4(0.8)	10.1	7.0	0.205	−0.701	0.328
	BT	4.2(0.5)	5.1	3.3	0.113	−0.939	0.169
B	W	280.2(55.3)	457.0	162.4	−0.009	−0.205	0.699
	SL	19.8(1.7)	23.4	17.0	−0.181	0.166	0.697
	H	8.2(0.8)	9.8	6.6	−0.065	−0.044	0.934
	BT	4.1(0.6)	5.2	3.1	0.402	−0.187	0.628
C	W	291.2(60.7)	394.5	141.7	0.281	0.952	0.118
	SL	19.3(1.6)	22.0	15.1	−0.253	0.173	0.322
	H	8.6(0.7)	9.9	6.7	−0.358	0.968	0.107
	BT	4.3(0.5)	5.3	3.0	−0.119	0.948	0.153
D	W	240.3(37.7)	346.4	141.2	0.151	0.608	0.734
	SL	18.7(1.0)	20.6	16.2	−0.174	0.442	0.728
	H	8.2(0.5)	9.2	7.1	0.093	−0.025	0.414
	BT	4.2(0.3)	5.0	3.8	0.489	0.654	0.202

a) Body weight (W, g), standard length (SL, cm), body depth (H, cm), body thickness (BT, cm).

Table S2 QTL results for all populations^{a)}

Panel	Trait	QTL name	LG ^a	Position	LG ^b	Position	CI ^c	Flanking markers	Nearest marker	LOD	LOD threshold		PVE ^d (%)
											Genome-wide	Linkage-wide	
A	W	<i>Wa-12-1</i>	H30	69.3	12	12.5	0-20	HLJE747-SNP0686	HLJ1097	2.7	4.5	2.3	21.8
		<i>Wa-32-2</i>	H13	98.9	32	5	0-5	SNP1207-SNP0780	SNP1207	2.0	4.5	2	12.1
		<i>Wa-43-3</i>	H8	20.8	43	2	0-2	HLJ541-SNP0881	SNP0881	2.6	4.5	2	24.3
	SL	<i>SLa-4-1</i>	H19	62.9	4	32	17-32	SNP0348-SNP0631	SNP0631	2.6	4.3	2.5	19.9
		<i>SLa-32-2</i>	H13	98.9	32	5	0-5	SNP1207-SNP0780	SNP1207	4.6 ^e	4.3	2	25.1
		<i>SLa-41-3</i>	H32	0	41	4.3	0-4.3	HLJ2538-SNP1158	SNP1158	2.0	4.3	1.9	12.1
	H	<i>Ha-8-1</i>	H30	19.1	8	12	4-12	SNP0726-koi12	koi12	2.5	4.5	2.5	13.7
		<i>Ha-12-2</i>	H30	69.3	12	12.5	0-20	HLJE747-SNP0686	SNP0686	2.6	4.5	2.4	15.5
		<i>Ha-32-3</i>	H13	98.9	32	5	0-5	SNP1207-SNP0780	SNP1207	2.0	4.5	1.9	15.8
	BT	<i>BTa-5-1</i>	H25	8.1	5	24.7	20-33	HLJ2310-HLJ668	SNP0167	2.5	4.8	2.5	13.9
		<i>BTa-6-2</i>	H17	35.8	6	10.9	0-28	SNP0249-HLJ357	SNP1120	3.7	4.8	2.6	24.2
		<i>BTa-8-3</i>	H30	35.5	8	4	1-12	HLJ2236-koi12	HLJ2491	3.6	4.8	2.5	22.1
		<i>BTa-26-4</i>	H9	0	26	19	1-22	HLJ1148-SNP0617	HLJ1148	2.6	4.8	2.5	20.9
	B	<i>BTa-43-5</i>	H8	20.8	43	2.4	0-2.4	HLJ541-SNP0881	SNP0881	2.9	4.8	1.9	16.6
		<i>Wb-4-1</i>	H1	3	4	28.9	13-33.5	SNP1481-HLJ030	HLJ035	2.5	4.3	2.5	18.9
		<i>Wb-7-2</i>	H4	54	7	9.6	0-26	HLJ091-SNP1091	SNP0786	2.7	4.3	2.6	17.2
B	W	<i>Wb-12-3</i>	H18	99.2	12	20	0-36	SNP0145-SNP0898	HLJ407	2.8	4.3	2.6	21.3
		<i>Wb-15-4</i>	H9	29.2	15	5.5	0-22	HLJ1148-HLJE387	HLJE265	2.6	4.3	2.5	13.5
		<i>Wb-25-5</i>	H34	18.1	25	17	2-34	HLJE399-SNP1465	SNP1080	2.9	4.3	2.5	29
		<i>Wb-36-6</i>	H28	84.3	36	13.8	0-13.8	HLJ688-HLJE6	HLJE6	2.5	4.3	2.2	24.3
	SL	<i>SLb-4-1</i>	H1	3	4	29	17-33	SNP1482-HLJ030	HLJ035	2.7	4.4	2.5	21.5
		<i>SLb-7-2</i>	H4	54	7	9.6	0-33	HLJ091-SNP0146	SNP0786	3.1	4.4	2.5	23.1

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Panel	Trait	QTL name	LG ^a	Position	LG ^b	Position	CI ^c	Flanking markers	Nearest marker	LOD	LOD threshold		PVE ^d (%)	
											Genome-wide	Linkage-wide		
C	H	<i>SLb-12-3</i>	H18	99.2	12	20	0-36	SNP0145-SNP0898	HLJ407	2.7	4.4	2.7	17.3	
		<i>SLb-15-4</i>	H9	29.2	15	5.5	0-22	HLJ1148-HLJE387	HLJE265	2.6	4.4	2.5	13.5	
		<i>SLb-25-5</i>	H34	18.1	25	17	0-42	HLJE399-SNP1465	SNP1080	2.9	4.4	2.3	24.1	
		<i>Hb-12-1</i>	H18	99.2	12	20	0-38	SNP0145-SNP0898	HLJ407	2.8	4.2	2.7	25	
		<i>Hb-15-2</i>	H9	29.2	15	5.5	0-22	HLJ1148-HLJE387	HLJE265	2.6	4.2	2.5	15.1	
		<i>Hb-25-3</i>	H34	18.1	25	17	2-32	HLJE399-SNP1465	SNP1080	4.5*	4.2	2.5	34.1	
		<i>Hb-36-4</i>	H28	84.3	36	13.8	0-13.8	HLJ688-HLJE6	HLJE6	2.5	4.2	2.2	14.5	
	BT	<i>BTb-4-1</i>	H1	9.4	4	33	10-33	HLJ301-HLJ030	HLJ030	2.6	4.5	2.6	25.4	
		<i>BTb-8-2</i>	H16	12	8	22.9	0-40	HLJ2591-HLJ643	SNP0818	4.6*	4.5	2.8	25.9	
		<i>BTb-17-3</i>	H30	16.7	17	0	0-56	SNP1130-HLJE418	HLJE418	2.9	4.5	2.7	35.1	
		<i>BTb-22-4</i>	H17	32.7	22	6	0-14	HLJ2347-SNP0042	SNP0662	1.3	4.5	1.1	13.4	
		<i>BTb-25-5</i>	H34	18.1	25	17	0-35	HLJE399-SNP1465	SNP1080	2.8	4.5	2.7	43.1	
		<i>BTb-36-6</i>	H28	84.3	36	13.8	0-13.8	HLJ688-HLJE6	HLJE6	2.2	4.5	2.2	11.7	
	W	<i>Wc-12-1</i>	H30	67.1	12	38.4	0-47.4	HLJ2386-HLJE69	SNP0686	2.3	4.5	2.1	22	
		<i>Wc-12-2</i>	H30	19.1	12	81	68-100	HLJ2182-HLJ428	koi12	2.9	4.5	2.9	17.8	
		<i>Wc-40-3</i>	H8	20.8	40	4	0-4.2	HLJ541-SNP0881	SNP0881	2.6	4.5	2.5	21.8	
		<i>Wc-42-4</i>	H19	77.9	42	4	0-72	SNP0162-HLJ2394	SNP0244	3.1	4.5	2.9	12.8	
	SL	<i>SLc-15-1</i>	H39	0	15	1	0-6.5	HLJ2309-HLJ352	HLJ517	2.3	4.4	1.9	14.6	
		<i>SLc-20-2</i>	H29	33.1	20	15.6	13-28.4	HLJ763-HLJ1290	HLJ1563	2.8	4.4	2.6	16.4	
		<i>SLc-32-3</i>	H9	79.4	32	6	0-6	SNP0846-SNP1486	SNP1486	2.0	4.4	2.0	11.8	
	H	<i>Hc-12-1</i>	H30	19.1	12	81	69-100	HLJ2182-HLJ428	koi12	3.0	4.5	3.0	18.5	
		<i>Hc-19-2</i>	H10	33.5	19	5	0-18.7	SNP0922-HLJ534	HLJ534	2.2	4.5	2.2	16.2	
		<i>Hc-23-3</i>	H5	27.1	23	27	2-39	HLJE697-HLJ870	HLJ551	2.5	4.5	2.5	17.7	
		<i>Hc-26-4</i>	H9	172.8	26	27	10-43	SNP0705-HLJ456	SNP0238	2.6	4.5	2.6	24.1	
		<i>Hc-42-5</i>	H19	77.9	42	3	0-22	SNP0162-SNP0003	SNP0244	2.9	4.5	2.9	20.8	
		<i>Hc-45-6</i>	H38	39.3	45	6.3	0-20	SNP1221-HLJ726	SNP0470	2.5	4.5	2.4	20.7	
	BT	<i>BTc-12-1</i>	H30	19.1	12	81	70-100	HLJ2182-HLJ428	koi12	2.6	4.1	2.5	26.3	
		<i>BTc-20-2</i>	H29	11.9	20	30	5-30	SNP1452-HLJ1290	HLJ1290	2.8	4.1	2.5	17.3	
		<i>BTc-26-3</i>	H9	148.8	26	12	0-15	HLJ119-SNP0329	HLJ2463	2.5	4.1	2.5	14.2	
		<i>BTc-45-4</i>	H38	45.6	45	0	0-38	HLJ2541-SNP1190	SNP1221	2.4	4.1	2.1	21.2	
	D	W	<i>Wd-8-1</i>	H10	26.7	8	45.5	31-50	SNP0922-HLJ534	SNP0815	4.7*	4.4	2.7	37.6
			<i>Wd-42-2</i>	H5	0	42	8.4	0-8.4	HLJ1190-SNP0703	SNP0703	2.0	4.4	2	14.3
			<i>Wd-54-3</i>	H22	62.8	54	23.5	2-23.5	SNP0225-HLJ416	HLJ416	2.7	4.4	2.2	26.3
			<i>SLd-11-1</i>	H13	23.3	11	7	0-35	SNP0123-SNP0858	SNP1116	2.1	4.5	2.1	15.5
		SL	<i>SLd-36-2</i>	H30	83.7	36	2.5	0-15	HLJE325-HLJ1098	HLJE747	2.2	4.5	2.2	16.4
			<i>SLd-38-3</i>	H32	8.4	38	8.3	0-8.3	SNP1158-SNP0099	SNP0099	2.6	4.5	2	31
			<i>SLd-42-4</i>	H5	0	42	8.4	0-8.4	HLJ1190-SNP0703	SNP0703	1.9	4.5	1.9	14.9
			<i>SLd-54-5</i>	H22	62.8	54	23.5	0-23.5	SNP0225-HLJ416	HLJ416	2.9	4.5	2.2	34.3
		H	<i>Hd-3-1</i>	H6	0	3	0	0-32	HLJ925-SNP0392	HLJ925	2.6	4.5	2.5	21.2
			<i>Hd-8-2</i>	H10	13.3	8	30	30-50	SNP0922-HLJ534	SNP0922	3.0	4.5	2.7	34.6
			<i>Hd-36-3</i>	H30	81.6	36	0	0-10	HLJE325-SNP0686	HLJE325	2.1	4.5	2.1	14.8
	BT	<i>BTd-6-1</i>	H8	49.5	6	50	48-55	HLJ1093-HLJ476	SNP1231	3.0	4.7	2.9	42.7	
		<i>BTd-27-2</i>	H23	5	27	17.7	16-23	SNP0138-HLJ697	SNP0902	3.5	4.7	2.9	47	
		<i>BTd-54-3</i>	H22	62.8	54	23.5	0-23.5	SNP0225-HLJ416	HLJ416	2.2	4.7	2.3	13.1	
		<i>BTd-56-4</i>	H38	12.9	56	11	0-27	HLJ1207-HLJ527	HLJ1207	2.1	4.7	2.1	13	

a) *, Significant genome-wide; a, in the consensus maps; b, in the individual linkage maps; c, confidence interval; d, phenotypic variation explained; LG (linkage group); LOD (logarithm of odds).

Table S3 Blast results of peak QTL loci

Locus	Gene symbol	Accession No.	Position	E-value	Identify (%)	Gene description/function
SNP1158	<i>rpl10</i>	NW_001878407.3	20001078	0	87.0	structural constituent of ribosome
SNP0786	<i>pvalb4</i>	NW_001878827.3	61785183	4e-86	89.2	calcium ion binding
HLJ407	<i>LOC565649</i>	NW_003336050	40269211	3e-06	100.0	FYVE and coiled-coil domain-containing protein 1-like
HLJE418	<i>ccdc147</i>	NW_003334061.1	49099469	3e-53	95.5	coiled-coil domain containing 147
SNP0662	<i>mbp</i>	NW_003040590.2	22298441	3e-102	91.2	myelin basic protein, structural constituent of myelin sheath
SNP0244	<i>lgals2b</i>	NW_003334444.1	23853427	5e-144	97.4	galactoside binding, sugar binding
HLJ1563	<i>ccdc147</i>	NW_003334061.1	48343076	3e-90	90.2	coiled-coil domain containing 147
SNP0815	<i>pnp5a</i>	NW_003039658.2	873080	8e-68	91.8	catalytic activity, purine-nucleoside phosphorylase activity, transferase activity, transferring pentosyl groups
SNP1116	<i>atp5c1</i>	NW_001878908.3	24265513	3e-71	89.4	hydrogen ion transporting ATP synthase activity, rotational mechanism, proton-transporting ATPase activity, rotational mechanism
SNP0099	<i>ppdpfb</i>	NW_001878407.3	17599747	2e-83	87.5	pancreatic progenitor cell differentiation and proliferation factor b, cell differentiation
SNP0922	<i>tpma</i>	NW_003039680.2	31291766	2e-68	96.9	alpha-tropomyosin, actin binding
SNP1231	<i>dio2</i>	NW_003040454.2	16714520	0	91.4	oxidoreductase activity, thyroxine 5'-deiodinase activity
SNP0686	<i>krt18</i>	NW_001878402.3	46386876	1e-157	88.6	structural molecule activity, Filament; Intermediate filament protein
SNP0902	<i>cep152</i>	NW_001878606.3	33289220	1e-125	86.3	centrosomal protein 152 kD, protein binding, protein kinase binding