

Supplementary Table 1. Most likely genomic locations and effects of multiple-trait QTLs for body weights at different ages

Chr	Multiple-trait QTL location ^a in cM (CI)	Chromosome-wide 5% LR threshold	LR ^b 1 vs 0 multiple-trait QTLs	Single traits underlying multiple-trait QTLs	LR for single trait contributing to multi-trait effect	Additive effect of single QTL underlying multitrait effect		Dominance effect of single QTL underlying multitrait effect		Single-trait QTL loci (cM)	Chromosome-wide 5% LR threshold	LR 1 vs 0 single-trait QTL	Additive effect of single-trait QTL		Dominance effect of single-trait QTL		% F ₂ -variance ^c explained by single-trait QTL
						a	SE	d	SE				a	SE	d	SE	
1	43 (36;50)	24.8	42.0	bw2	2.7	0.11	0.08	-0.12	0.12	9	9.8	3.4	0.15	0.08	0.04	0.12	0.62
				bw3	8.7	0.45	0.15	-0.02	0.21	46	9.9	8.9	0.47	0.16	-0.02	0.23	2.94
				bw4	22.2	1.18	0.25	-0.01	0.35	46	10.3	22.9	1.23	0.25	0.01	0.38	8.66
				bw5	20.9	1.21	0.26	-0.13	0.37	46	10.3	21.3	1.26	0.27	-0.19	0.40	8.01
				bw6	14.1	1.04	0.27	-0.33	0.39	68	10.2	19.1	1.15	0.29	-0.95	0.45	7.13
2	54 (45;80)	23.2	32.2	bw2	11.8	-0.11	0.09	0.48	0.15	109	9.9	12.2	-0.12	0.08	-0.39	0.12	4.29
				bw3	12.3	-0.08	0.17	0.94	0.26	55	9.7	12.3	-0.09	0.17	0.92	0.26	4.33
				bw4	10.7	0.27	0.28	1.35	0.43	50	9.1	11.2	0.34	0.29	1.43	0.45	3.87
				bw5	12.3	0.55	0.29	1.34	0.45	51	9.1	12.7	0.60	0.30	1.40	0.47	4.50
				bw6	8.7	0.59	0.31	1.03	0.47	47	9.2	10.0	0.67	0.31	1.14	0.48	3.36
3	70.5 (44.5;83.5)	23.0	24.3	bw2	9.4	-0.26	0.10	0.28	0.17	75.5	8.9	9.9	-0.29	0.10	0.20	0.16	3.38
				bw3	8.2	-0.48	0.18	0.36	0.32	68.5	9.0	8.3	-0.46	0.18	0.42	0.31	2.68
				bw4	2.9	-0.51	0.30	-0.06	0.52	83.5	8.7	8.1	-0.66	0.25	-0.33	0.36	2.61
				bw5	2.7	-0.36	0.31	0.65	0.55	83.5	8.9	4.7	-0.57	0.26	0.10	0.38	1.16
				bw6	3.8	-0.46	0.33	0.78	0.57	83.5	8.6	5.9	-0.59	0.27	0.49	0.40	1.66
7	29.5 (17.5;35.5)	23.5	33.0	bw2	23.8	0.43	0.09	0.19	0.14	21.5	9.3	24.9	0.44	0.09	0.07	0.13	9.42
				bw3	14.8	0.54	0.17	0.54	0.26	27.5	9.6	14.9	0.55	0.16	0.48	0.26	5.45
				bw4	15.5	1.06	0.27	0.34	0.43	27.5	9.5	15.7	1.05	0.27	0.29	0.42	5.76
				bw5	18.6	1.24	0.28	0.21	0.45	29.5	9.1	18.6	1.24	0.28	0.21	0.45	6.95
				bw6	11.5	1.02	0.30	0.06	0.47	10.5	9.0	15.1	1.10	0.29	-0.48	0.44	5.54
12	53 (46;55)	22.1	24.7	bw2	4.1	-0.11	0.08	0.20	0.13	55	8.7	4.6	-0.10	0.08	0.21	0.12	1.14
				bw3	5.1	0.08	0.15	0.54	0.25	55	8.8	5.8	0.08	0.14	0.51	0.22	1.65
				bw4	3.8	0.26	0.25	0.68	0.40	25	8.7	7.8	0.21	0.25	0.99	0.37	2.50
				bw5	5.8	0.24	0.26	0.95	0.42	55	8.7	7.2	0.22	0.25	0.95	0.37	2.22
				bw6	3.9	-0.10	0.27	0.84	0.44	55	8.9	4.7	-0.08	0.26	0.84	0.39	1.15
13	56 (49;73)	22.8	28.8	bw2	1.3	-0.10	0.09	0.01	0.14	33	8.9	3.2	-0.20	0.11	-0.05	0.21	0.53
				bw3	7.5	-0.36	0.16	0.34	0.25	51	8.8	8.2	-0.40	0.16	0.28	0.25	2.67
				bw4	1.8	-0.14	0.26	0.48	0.41	47	8.1	2.6	-0.35	0.25	0.24	0.35	0.27
				bw5	1.6	-0.22	0.27	0.40	0.43	75	8.1	2.5	0.07	0.25	0.59	0.37	0.23
				bw6	3.7	0.24	0.29	0.82	0.45	75	8.6	7.6	0.48	0.26	0.87	0.39	2.38

Supplementary Table 1. (cont.)

Chr	Multiple-trait QTL location ^a in cM (CI)	Chromosome-wide 5% LR threshold	LR ^b 1 vs 0 multiple-trait QTLs	Single traits underlying multiple-trait QTLs	LR for single trait contributing to multi-trait effect	Additive effect of single QTL underlying multitrait effect		Dominance effect of single QTL underlying multitrait effect		Single-trait QTL loci (cM)	Chromosome-wide 5% LR threshold	LR 1 vs 0 single-trait QTL	Additive effect of single-trait QTL		Dominance effect of single-trait QTL		% F ₂ -variance ^c explained by single-trait QTL
						a	SE	d	SE				a	SE	d	SE	
14	23 (19;27)	23.9	57.5	bw2	24.9	-0.30	0.09	0.55	0.13	25	9.7	25.4	-0.30	0.09	0.53	0.13	9.62
				bw3	31.8	-0.56	0.17	1.21	0.24	25	9.7	32.4	-0.57	0.17	1.18	0.24	12.33
				bw4	37.1	-1.02	0.28	2.12	0.40	22	9.2	37.2	-1.01	0.27	2.12	0.40	14.13
				bw5	39.5	-1.10	0.29	2.30	0.42	22	9.1	39.8	-1.10	0.29	2.30	0.42	15.11
				bw6	17.2	-0.40	0.30	1.78	0.44	21	8.8	17.6	-0.39	0.30	1.79	0.44	6.54
				bw6	17.2	-0.40	0.30	1.78	0.44	21	8.8	17.6	-0.39	0.30	1.79	0.44	6.54
15	40.4 (27.4;53.4)	22.6	25.1	bw2	14.2	0.36	0.09	0.02	0.15	38.4	9.2	14.3	0.37	0.10	0.04	0.15	5.19
				bw3	8.7	0.49	0.17	0.30	0.27	36.4	9.0	9.0	0.50	0.18	0.36	0.28	3.00
				bw4	11.7	0.98	0.28	0.21	0.44	38.4	9.2	11.7	0.99	0.29	0.28	0.45	4.12
				bw5	10.5	0.96	0.30	0.21	0.46	53.4	9.3	13.1	1.02	0.28	-0.15	0.43	4.67
				bw6	2.4	0.47	0.31	0.17	0.49	57.4	9.2	5.3	0.64	0.28	-0.13	0.39	1.43
				bw6	2.4	0.47	0.31	0.17	0.49	57.4	9.2	5.3	0.64	0.28	-0.13	0.39	1.43

Trait abbreviations as in Table 1.

CI, confidence interval (1 LOD drop); LR, likelihood ratio (defined as 2 log (LR)).

^a The most likely genomic locations are given as distances from the centromere. The 1 LOD drop confidence intervals are given in parentheses.

^b The chromosome-wide 1% and 5% likelihood ratio thresholds were estimated via permutation analyses. The genome-wide 1% and 5% likelihood ratio thresholds are 34.8 and 31.5, respectively. Highly significant likelihood ratios at the genome-wide level are given in **bold** type and significant likelihood ratios in **bold italic**.

^c The multiple-trait QTL effects are given as the reduction of the residual sum of squares fitting the 1 versus 0 single QTL for each trait separately.

Supplementary Table 2. *Most likely genomic locations and effects of multiple-trait QTLs for body composition, organ weights and body weight at 6 weeks*

Chr	Multiple-trait QTL location ^a in cM (CI)	Chromosome-wide 5% LR threshold	LR ^b 1 vs 0 multiple-trait QTL	Single-trait underlying multiple-trait QTL	LR for single trait contributing to multitrait effect	Additive effect of single QTL underlying multitrait effect		Dominance effect of single QTL underlying multitrait effect		Single-trait QTL loci in cM	Chromosome-wide 5% LR threshold	LR 1 vs 0 single-trait QTL	Additive effect of single-trait QTL		Dominance effect of single-trait QTL		% F ₂ -variance ^c explained by single-trait QTL
						a	SE	d	SE				a	SE	d	SE	
1	71 (60;80)	30.6	45.8	bw6	21.2	1.17	0.28	-1.12	0.45	65	10.3	22.1	1.15	0.26	-0.86	0.39	8.25
				afw	3.9	0.02	0.01	-0.02	0.02	9	9.8	7.5	0.03	0.01	0.01	0.02	2.33
				afp	0.5	0.03	0.04	-0.02	0.06	9	9.8	6.9	0.07	0.03	0.06	0.05	2.10
				mw	18.2	0.01	0.003	-0.01	0.01	63	10.9	21.5	0.01	0.003	-0.01	0.004	8.02
				liv	6.8	0.06	0.02	-0.04	0.04	45	10.0	12.6	0.08	0.02	-0.01	0.03	4.43
				kid	30.7	0.03	0.01	-0.02	0.01	69	11.0	30.9	0.03	0.01	-0.02	0.01	11.68
				spl	15.4	0.01	0.003	-0.01	0.004	74	9.7	15.6	0.01	0.003	-0.01	0.004	5.65
2	45 (29;53)	29.2	47.5	bw6	9.6	0.76	0.29	0.74	0.44	97	9.9	11.2	0.98	0.31	-0.80	0.58	3.85
				afw	17.6	0.05	0.01	0.03	0.02	45	9.6	17.6	0.05	0.01	0.03	0.02	6.49
				afp	17.1	0.14	0.04	0.09	0.06	43	9.9	17.2	0.14	0.04	0.08	0.05	6.32
				mw	0.8	0.002	0.004	0.004	0.01	9	9.3	6.6	-0.003	0.003	0.01	0.01	1.99
				liv	18.3	0.09	0.02	0.08	0.04	49	9.5	19.0	0.09	0.03	0.08	0.04	7.04
				kid	21.8	0.02	0.01	0.01	0.01	33	9.1	22.4	0.02	0.01	0.01	0.01	8.40
				spl	0.7	0.002	0.003	0.001	0.004	100	9.0	9.4	0.01	0.003	0.0003	0.01	3.07
3	39.5 (29.5;45.5)	28.5	28.6	bw6	2.7	0.42	0.26	0.12	0.36	83.5	8.8	3.6	-0.38	0.26	0.45	0.37	0.67
				afw	0.6	0.01	0.01	0.01	0.02	65.5	8.9	4.3	0.004	0.01	0.04	0.02	0.97
				afp	0.4	-0.004	0.03	0.03	0.05	64.5	9.5	4.1	0.01	0.04	0.12	0.06	0.91
				mw	1.5	0.004	0.003	0.001	0.004	18.5	8.9	5.9	0.003	0.003	-0.01	0.004	1.65
				liv	17.3	0.08	0.02	-0.05	0.03	37.5	9.2	17.3	0.09	0.02	-0.05	0.03	6.37
				kid	2.5	0.01	0.004	-0.002	0.01	58.5	8.8	3.5	0.01	0.004	0.01	0.01	0.66
				spl	5.9	0.01	0.003	-0.002	0.003	34.5	9.0	5.9	0.01	0.003	-0.001	0.004	1.70
4	67.1 (63.1;74.1)	30.1	44.0	bw6	12.8	0.96	0.27	0.35	0.37	63.1	9.7	13.5	1.03	0.29	0.49	0.41	4.81
				afw	9.5	0.03	0.01	0.03	0.02	68.1	9.3	9.5	0.03	0.01	0.03	0.02	3.19
				afp	8.5	0.06	0.04	0.11	0.05	66.1	9.1	8.6	0.06	0.04	0.11	0.05	2.80
				mw	7.4	0.01	0.003	0.01	0.004	64.1	8.9	7.6	0.01	0.003	0.01	0.01	2.38
				liv	14.5	0.09	0.02	0.02	0.03	63.1	10.1	15.6	0.10	0.02	0.02	0.03	5.68
				kid	1.6	0.01	0.01	0.004	0.01	45.1	9.8	6.6	0.01	0.004	-0.004	0.01	1.96
				spl	17.7	0.01	0.003	0.01	0.004	66.1	9.6	18.1	0.01	0.003	0.01	0.003	6.68
5	68 (66;74)	29.8	40.2	bw6	7.3	0.57	0.28	-0.62	0.38	68	9.8	7.3	0.57	0.28	-0.62	0.38	2.25
				afw	0.3	-0.002	0.01	-0.01	0.02	39	9.5	4.8	-0.01	0.01	0.03	0.02	1.18
				afp	1.1	-0.04	0.04	0.01	0.05	42	9.4	4.0	-0.03	0.04	0.09	0.05	0.86
				mw	0.2	0.001	0.003	0.0003	0.01	8	10.0	1.3	0.003	0.003	0.001	0.01	-0.33*
				liv	1.9	0.03	0.02	-0.03	0.03	8	9.6	4.6	0.05	0.02	0.001	0.03	1.10
				kid	1.1	0.002	0.01	-0.01	0.01	39	9.5	2.7	-0.01	0.004	0.01	0.01	0.29
				spl	11.1	-0.01	0.003	-0.0002	0.004	65	9.6	11.7	-0.01	0.003	0.001	0.004	4.09

Supplementary Table 2. (cont.)

Chr	Multiple-trait QTL location ^a in cM (CI)	Chromosome-wide 5% LR threshold	LR ^b 1 vs 0 multiple-trait QTL	Single-trait underlying multiple-trait QTL	LR for single trait contributing to multitrait effect	Additive effect of single QTL underlying multitrait effect		Dominance effect of single QTL underlying multitrait effect		Single-trait QTL loci in cM	Chromosome-wide 5% LR threshold	LR 1 vs 0 single-trait QTL	Additive effect of single-trait QTL		Dominance effect of single-trait QTL		% F ₂ -variance ^c explained by single-trait QTL
						a	SE	d	SE				a	SE	d	SE	
7	6.5 (1.5;12.5)	30.3	59.0	bw6	12.9	1.02	0.28	0.04	0.43	31.5	9.9	13.8	0.91	0.28	0.76	0.45	4.92
				afw	34.4	0.07	0.01	-0.001	0.02	7.5	9.2	34.5	0.07	0.01	-0.001	0.02	13.01
				afp	41.8	0.25	0.04	0.002	0.06	7.5	8.9	42.0	0.25	0.04	0.004	0.06	15.77
				mw	17.4	0.01	0.003	-0.001	0.01	7.5	9.7	17.5	0.01	0.003	-0.001	0.01	6.44
				liv	10.8	0.07	0.02	-0.05	0.04	6.5	9.5	10.8	0.07	0.02	-0.05	0.04	3.69
				kid	2.6	0.01	0.01	-0.001	0.01	14.5	9.7	3.0	0.01	0.004	-0.001	0.01	0.41
				spl	2.7	0.004	0.003	-0.002	0.004	53.5	9.6	4.2	-0.001	0.002	-0.01	0.004	0.96
9	54 (47;54)	27.3	36.4	bw6	4.3	0.46	0.25	-0.39	0.37	30	8.7	7.9	0.74	0.27	0.32	0.39	2.48
				afw	8.4	0.03	0.01	-0.02	0.02	43	8.5	9.2	0.04	0.01	-0.01	0.02	3.04
				afp	6.4	0.08	0.03	-0.03	0.05	44	8.8	7.1	0.10	0.04	-0.02	0.06	2.16
				mw	6.7	0.01	0.003	-0.004	0.004	38	8.2	7.1	0.01	0.004	0.004	0.01	2.15
				liv	2.3	-0.01	0.02	0.05	0.03	39	8.2	3.7	0.02	0.03	0.08	0.04	0.71
				kid	0.3	-0.002	0.004	0.0003	0.01	28	8.2	7.2	0.01	0.004	0.01	0.01	2.21
				spl	0.2	0.001	0.002	0.001	0.004	7	8.0	3.5	-0.001	0.002	0.01	0.003	0.65
11	18 (15;22)	29.7	70.1	bw6	4.6	0.58	0.28	0.24	0.42	24	9.9	5.1	0.62	0.27	-0.05	0.39	1.33
				afw	3.2	0.02	0.01	-0.002	0.02	22	9.5	3.5	0.02	0.01	-0.01	0.02	0.66
				afp	2.1	0.05	0.04	-0.01	0.05	68	9.5	3.5	0.05	0.04	-0.06	0.05	0.65
				mw	23.8	0.02	0.003	0.002	0.01	16	10.0	24.3	0.02	0.003	0.003	0.01	9.11
				liv	2.2	-0.03	0.02	0.04	0.04	68	9.6	3.9	-0.03	0.02	0.05	0.03	0.83
				kid	1.5	-0.004	0.01	0.01	0.01	68	10.1	4.7	0.01	0.004	0.01	0.01	1.18
				spl	5.3	0.002	0.003	-0.01	0.004	60	9.7	6.7	0.01	0.003	-0.01	0.004	1.96
12	22 (17;40)	28.2	43.0	bw6	4.0	0.07	0.26	0.80	0.41	26	8.8	4.2	0.02	0.26	0.78	0.38	0.94
				afw	4.6	0.01	0.01	0.03	0.02	28	8.6	6.0	0.004	0.01	0.04	0.02	1.72
				afp	4.8	0.03	0.03	0.10	0.05	28	8.6	6.9	0.03	0.03	0.12	0.05	2.06
				mw	5.0	0.004	0.003	0.01	0.01	28	8.6	5.4	0.004	0.003	0.01	0.004	1.45
				liv	0.9	0.02	0.02	-0.02	0.03	55	8.6	2.6	0.003	0.02	0.05	0.03	0.25
				kid	0.4	0.003	0.004	0.001	0.01	16	8.9	0.8	0.004	0.004	0.0002	0.01	-0.52*
				spl	22.6	-0.01	0.003	-0.01	0.004	37	8.5	25.9	-0.01	0.003	-0.002	0.004	9.75
13	27 (16;39)	29.4	39.7	bw6	0.4	-0.19	0.38	0.21	0.72	75	9.1	5.2	0.30	0.25	0.74	0.36	1.36
				afw	0.5	0.01	0.02	-0.01	0.03	75	8.8	4.4	0.02	0.01	0.02	0.02	1.01
				afp	1.5	0.04	0.05	-0.06	0.09	75	9.0	3.6	0.06	0.03	0.04	0.05	0.67
				mw	13.5	-0.02	0.01	-0.003	0.01	24	9.2	13.6	-0.02	0.01	-0.002	0.01	4.87
				liv	1.1	-0.03	0.03	-0.02	0.06	47	9.2	3.3	-0.04	0.02	-0.02	0.03	0.57
				kid	0.4	0.003	0.01	0.01	0.01	6	9.2	1.0	0.003	0.01	0.01	0.01	-0.43*
				spl	0.4	0.0000	0.004	0.004	0.01	61	8.9	1.6	0.001	0.002	-0.004	0.004	-0.14*

Supplementary Table 2. (cont.)

Chr	Multiple-trait QTL location ^a in cM (CI)	Chromosome-wide 5% LR threshold	LR ^b 1 vs 0 multiple-trait QTL	Single-traits underlying multiple-trait QTL	LR for single trait contributing to multitrait effect	Additive effect of single QTL underlying multitrait effect		Dominance effect of single QTL underlying multitrait effect		Single-trait QTL loci in cM	Chromosome-wide 5% LR threshold	LR 1 vs 0 single-trait QTL	Additive effect of single-trait QTL		Dominance effect of single-trait QTL		% F ₂ -variance ^c explained by single-trait QTL
						a	SE	d	SE				a	SE	d	SE	
14	23 (18;30)	28.9	49.8	bw6	19.8	-0.09	0.28	1.88	0.41	23	9.2	19.8	-0.09	0.28	1.88	0.41	7.35
				afw	23.5	-0.02	0.01	0.08	0.02	24	9.5	23.5	-0.02	0.01	0.08	0.02	8.83
				afp	23.8	-0.10	0.04	0.23	0.05	22	9.3	23.8	-0.10	0.04	0.23	0.05	8.95
				mw	24.2	-0.003	0.003	0.03	0.01	21	9.1	24.8	-0.003	0.003	0.03	0.01	9.29
				liv	6.1	-0.02	0.02	0.08	0.03	28	9.2	7.2	-0.02	0.02	0.08	0.03	2.20
				kid	15.9	-0.003	0.01	0.03	0.01	15	9.2	17.2	-0.003	0.01	0.03	0.01	6.32
				spl	9.2	0.008	0.003	-0.002	0.004	41	9.3	14.2	0.01	0.003	-0.004	0.004	5.13
15	57.4 (54.4;57.4)	28.9	36.6	bw6	2.4	0.38	0.28	-0.26	0.37	57.4	8.9	2.4	0.38	0.28	-0.26	0.37	0.17
				afw	4.3	0.001	0.01	-0.03	0.02	57.4	8.5	4.3	0.001	0.01	-0.03	0.02	0.99
				afp	7.0	-0.02	0.04	-0.13	0.10	57.4	8.6	7.0	-0.02	0.04	-0.13	0.05	2.14
				mw	2.2	0.003	0.003	-0.01	0.004	12.4	8.5	3.8	0.01	0.004	0.004	0.01	0.76
				liv	5.0	-0.02	0.02	-0.07	0.03	57.4	8.8	5.0	-0.02	0.02	-0.07	0.03	1.27
				kid	9.5	0.01	0.01	-0.01	0.01	57.4	8.6	9.5	0.01	0.01	-0.01	0.01	3.16
				spl	7.6	0.002	0.003	-0.01	0.004	55.4	8.6	7.7	0.002	0.003	-0.01	0.004	2.45
17	27.5 (17.5;32.5)	29.3	64.4	bw6	6.8	0.70	0.28	-0.54	0.45	27.5	9.5	6.8	0.70	0.28	-0.54	0.45	2.06
				afw	7.2	-0.01	0.01	-0.04	0.02	34.5	9.5	8.9	-0.02	0.01	-0.05	0.02	2.93
				afp	13.0	-0.09	0.04	-0.13	0.06	33.5	9.2	14.7	-0.11	0.04	-0.15	0.07	5.32
				mw	2.9	0.004	0.003	-0.01	0.01	16.5	9.6	3.2	0.004	0.003	-0.01	0.01	0.51
				liv	10.5	0.07	0.02	-0.08	0.04	23.5	9.7	11.3	0.07	0.02	-0.06	0.03	3.91
				kid	23.1	0.02	0.01	-0.01	0.01	21.5	9.3	24.2	0.02	0.004	-0.01	0.01	9.08
				spl	2.6	0.004	0.003	0.002	0.004	6.5	9.0	5.0	0.004	0.002	-0.01	0.003	1.22
19	34 (22;47)	29.3	49.3	bw6	0.7	-0.06	0.29	-0.41	0.51	44	8.7	4.2	-0.23	0.25	-0.70	0.38	0.94
				afw	11.0	0.04	0.01	-0.01	0.02	20	8.8	15.3	0.04	0.01	0.01	0.02	5.55
				afp	15.5	0.15	0.04	-0.003	0.07	24	9.1	18.7	0.15	0.04	-0.01	0.06	6.91
				mw	6.1	-0.01	0.004	-0.001	0.01	51	9.0	10.8	-0.01	0.003	-0.003	0.01	3.69
				liv	3.5	-0.02	0.02	-0.07	0.04	46	8.8	5.8	-0.04	0.02	-0.06	0.03	1.61
				kid	3.1	-0.01	0.01	0.01	0.01	50	8.7	8.1	-0.01	0.004	0.003	0.01	2.57
				spl	1.2	0.003	0.003	0.002	0.01	6	8.5	7.4	0.01	0.003	0.003	0.003	2.28

Abbreviations and indices as in Table 1 and Supplementary Table 1.

^b The genome-wide 1% and 5% likelihood ratio thresholds are 43.9 and 38.9, respectively. Highly significant likelihood ratios are given in **bold** type and significant likelihood ratios in **bold italic**.

* Negative variance estimates are legitimate when using analysis of variance (when using maximum likelihood (ML) or restricted maximum likelihood (REML) they are often constrained to be greater than zero). If a non-existent random effect is fitted in an ANOVA, 50% of the time you expect a negative estimate and 50% a positive around a mean of zero. The negative variance components were obtained when there was no evidence for a single QTL.