

new QTL in blue letters and the old QTL, which could not be confirmed, in red letters

Table 1. Evidence for QTL significant at the 5% chromosome-wise level for various meat quality traits by chromosome. Estimated significance levels (F value), location, gene effects and % of F2 variance explained by each QTL.

SSC	Trait	New Markers	F-value ^a old	F-value New	Location (cM) old	Location (cM) new	Add. effect ^b old	Add. effect ^b new	Domi. Effect old	Domi. Effect new	% var. ^c old
1	Marbling	3		5.17		33		-0.12		0.05	
1	Marbling	3	8.42*	8.62*	48	57	-0.16	-0.15	0.16	0.16	4.34
1	Total Lipid (%)	3	6.06	6.33	51	60	-0.28	-0.28	0.13	0.12	2.90
1	Drip Loss (%)	3	7.15	6.53	90	88	-0.53	-0.41	-0.13	-0.03	4.66
1	Lab Loin pH	3		5.32		95		0.03		-0.02	
1	Color Score	3		5.29		102		0.08		0.07	
2	Color Score	5	5.33	4.98	141	152	-0.10	-0.09	0.04	0.04	2.41
2	Hormel Loin Hunter	5		5.44		129		0.78		1.06	
2	Hormel Loin Minolta	5	5.90	5.78	77	89	0.91	0.91	-0.94	-0.93	3.83
2	Lab Loin Minolta	5	7.24	7.83	127	140	0.83	0.85	0.19	0.23	3.94
2	Lab Loin Hunter	5	6.33	6.96	128	141	0.80	0.83	0.18	0.25	3.39
2	Drip Loss (%)	5	5.07	8.31	40	54	0.44	0.49	0.12	0.17	3.22
2	Drip Loss (%)	5	5.68	5.81	122	137	0.43	0.43	-0.26	-0.23	3.53
2	Water Holding Cap.	5	5.90	5.32	71	83	0.03	0.03	0.01	0.00	2.94
2	Water Holding Cap.	5	5.85	6.43	139	154	0.03	0.02	-0.01	-0.01	2.67
2	Chewiness Score	5	6.76	6.81	143	157	0.20	0.19	0.07	0.10	2.62
2	Tenderness Score	5	7.99	8.01	143	157	-0.26	-0.25	-0.15	-0.17	3.08
2	Firmness	5		6.21		69		-0.14		-0.004	
2	Firmness	5	5.31	5.39	86	99	-0.11	-0.11	-0.09	-0.07	2.39
2	Flavor score	5	5.93	6.73	143	157	-0.35	-0.35	0.03	0.02	2.45
2	Off Flavor Score	5	5.84	10.0	45	59	0.50	0.49	0.03	0.28	4.18
2	Off Flavor Score	5	5.17	5.84	143	156	0.35	0.35	0.07	0.13	2.08
4	Lab Loin Hunter	2	6.15	5.92	130	146	0.54	0.52	0.67	0.65	2.66
4	Lab Loin Minolta	2	6.01	5.91	130	146	0.55	0.54	0.56	0.55	2.58

SSC	Trait	New Markers	F-value ^a old	F-value New	Location (cM) old	Location (cM) new	Add. effect ^b old	Add. effect ^b new	Domi. Effect old	Domi. Effect new	% var. ^c old
5	Hormel Loin Minolta	2	6.88	5.51	112	120	0.64	0.61	-1.38	-1.00	4.11
5	Hormel Loin pH	2		5.01		90		-0.03		0.00	
5	Hormel Loin pH	2		5.26		112		-0.02		0.02	
5	Hormel Loin pH	2	8.56*	5.91	113	120	-0.03	-0.02	0.05	0.03	4.85
5	Lab Loin Hunter	2	7.41	5.36	113	120	0.48	0.46	-1.09	-0.75	4.30
5	Lab Loin Minolta	2	7.95	5.84	113	120	0.49	0.48	-1.07	-0.73	4.59
5	Lab Loin pH	2	6.20	6.46	81	81	-0.04	-0.04	0.01	0.00	3.38
5	Lab Loin pH	2		5.68		105		0.01		0.03	
5	Water holding Cap.	2		7.00		118		0.02		-0.02	
6	Chewiness Score	1		6.15		48		-0.11		-0.28	
6	Hormel Ham pH	1	6.82	7.48	53	53	-0.03	-0.02	0.05	0.05	2.90
7	Lab Loin Minolta	2		6.87		82		0.54		-0.66	
7	Lab Loin Hunter	2	5.83	7.06	80	82	0.52	0.54	-0.79	-0.74	3.00
8	Fiber Type I	1	5.97	5.42	52	54	-0.03	-0.02	-0.01	-0.01	2.88
8	Marbling	1	5.92	6.05	40	52	-0.14	-0.11	0.16	0.16	3.61
8	Hamm Minolta	1		5.00		77		-0.38		0.74	
9	Off Flavor Score	4		6.05		79		-0.31		-0.42	
10	Star Probe Force	1		5.36		45		-0.15		-0.17	
10	Star Probe Force	1	5.83	8.29	71	70	-0.20	-0.20	-0.06	-0.08	3.82
10	Marbling	1	5.11	5.04	3	3	-0.14	-0.13	-0.13	-0.12	3.24
11	Drip Loss (%)	1	5.95	5.71	7	0	0.44	0.34	0.59	-0.21	6.01
11	Drip Loss (%)	1	5.90	4.49	24	30	0.46	0.40	0.23	0.14	3.93
11	Glycogen ($\mu\text{mol/g}$)	1	4.73	4.18	0	0	0.65	0.54	-0.12	-0.22	2.33
11	Glycolytic Potential	1	5.91	4.56	0	0	3.36	2.68	-1.54	-1.79	2.68
12	Chewiness Score	1	5.13	4.08	73	56	0.10	0.07	0.43	0.29	6.63
12	Color Score	1	8.33*	5.66	73	60	-0.14	-0.10	-0.22	-0.10	10.13
13	Lab Loin Hunter	2		5.02		81		-0.39		-0.78	
13	Lab Loin Minolta	2		4.97		81		-0.40		-0.70	
13	Water Holding Cap.	2	6.14	6.04	43	45	0.03	0.02	0.09	0.00	2.75

SSC	Trait	New Markers	F-value ^a old	F-value New	Location (cM) old	Location (cM) new	Add. effect ^b old	Add. effect ^b new	Domi. Effect old	Domi. Effect new	% var. ^c old
14	Star Probe Force	2		6.14		35		-0.13		0.16	
14	Hormel Ham Hunter	2	5.16	5.26	0	0	-0.21	-0.22	-1.06	-1.06	3.19
14	Hormel Ham pH	2	5.79	3.72	110	111	-0.05	0.00	0.01	-0.04	3.59
14	Pcnt Cooking Loss	2	7.14	7.56	31	37	-1.03	-1.01	-0.40	-0.06	3.29
14	Tenderness Score	2	5.77	5.80	70	75	0.28	0.21	0.23	0.23	2.83
15	Hormel Loin Hunter	3	6.31	6.39	96	100	-1.07	-1.05	0.62	0.69	3.16
15	Lab Loin Hunter	3	5.04	6.28	66	70	-0.68	-0.73	0.17	0.17	2.46
15	Lab Loin Minolta	3	6.30	7.60	66	70	-0.73	-0.77	0.17	0.15	3.05
15	Hormel Ham pH	3	8.42*	7.92	72	79	0.05	0.05	-0.02	-0.01	4.00
15	Hormel Loin pH	3	12.15**	13.02**	76	79	0.05	0.05	-0.01	0.00	5.61
15	Lab Loin pH	3	9.05*	9.37*	45	43	0.04	0.04	-0.04	-0.03	5.14
15	Glycogen (umol/g)	3	8.25*	8.83*	65	71	-0.77	-0.75	0.71	0.67	4.27
15	Glycolytic Potential	3	6.21	6.36	67	74	-3.67	-3.57	0.77	0.39	2.95
15	Tenderness Score	3	5.22	6.69	44	50	0.24	0.29	-0.20	-0.08	3.00
15	Star Probe Force	3	5.25	7.94	42	49	-0.17	-0.21	0.09	0.09	2.88
15	Flavor score	3	6.41	6.49	91	96	0.36	0.33	-0.37	-0.35	3.73
15	Drip Loss (%)	3		7.58		52		-0.35		0.36	
15	Off Flavor Score	3		5.84		53		-0.37		0.24	
17	Color score	2	8.75*	8.57*	82	86	0.11	0.10	-0.09	-0.08	3.63
17	Lab Loin Hunter	2	9.11*	9.14*	82	86	-0.83	-0.83	0.22	0.24	3.73
17	Lab Loin Minolta	2	9.91*	9.90**	82	85	-0.83	-0.83	0.25	0.27	4.04
17	Lactate (umol/g)	2	6.40	6.32	82	85	-1.48	-1.49	3.37	3.44	2.80
17	Glycolytic Potential	2	5.01	4.94	82	84	-1.47	-1.48	4.05	4.32	2.22
17	Juiciness Score	2	6.36	4.02	30	18	0.23	0.17	-0.70	-0.38	8.03
18	Hormel Loin Minolta	2	6.40	6.45	26	28	0.12	0.06	-1.58	-1.51	3.82
18	Cholesterol	2	4.67	4.05	26	21	-0.15	-0.20	2.60	2.03	2.62
X	Off Flavor Score	1	4.90	4.51	69	66	-0.58	-0.57	-0.12	-0.12	5.78

^a Chromosome-wise F-statistic thresholds at the 5% level, as determined by permutation test were as follows: **old / new** (1) 5.08 / 5.09, (2) 5.12 / 5.50, (3) 5.14 (no markers added), (4) 5.14 / 5.21, (5) 4.99 / 5.00, (6) 5.32 / 5.25, (7) 5.25 / 5.14, (8) 5.03 / 4.97, (9) 5.09 / 5.25, (10) 5.11 / 5.00, (11) 4.59 / 4.53, (12) 4.78 / 4.68, (13) 5.03 / 4.95, (14) 5.02 / 4.94, (15) 5.02 / 4.99, (16) 4.34 (no markers added), (17) 4.86 / 4.88, (18) 4.45 / 4.39, (X) 4.80 / 4.84.

^b Additive (a) and dominance (d) QTL effects correspond to genotype values of +a, d, and -a for, respectively, individuals having inherited two Berkshire alleles, heterozygotes, and individuals with two Yorkshire alleles. Positive additive effects indicate that Berkshire alleles increased the trait, negative that the Berkshire alleles decreased it. Dominance effects are relative to the mean of the two homozygotes.

^c % variance = genetic variance at the QTL based on estimated additive and dominance effects and allele frequencies of 1/2, as a percent of the residual variance in the F2.

Significant at the 10% genome-wise level: (F>7.42)

* Significant at the 5% genome-wise level (F>8.22 / 8.21)

** Significant at the 1% genome-wise level (F> 9.96 / 9.88)

Table 2. Evidence for QTL significant at the 5% chromosome-wise level for various growth and composition traits by chromosome. Estimated significance levels (F value), location, gene effects and % of F2 variance explained by each QTL.

SSC	Trait	New Markers	F-value ^a old	F-value ^a new	Location (cM) (old)	Location (cM) (new)	Additive Effect ^b old	Additive Effect ^b new	Dominance effect old	Dominance effect new	% var ^c old
1	Average Back Fat (cm)	3	6.79	4.82	29	32	-0.09	-0.08	-0.12	-0.09	2.83
1	Average Back Fat (cm)	3	6.46	6.54	63	73	-0.12	-0.11	-0.07	-0.07	2.87
1	Tenth Rib Back Fat (cm)	3	11.32**	9.12*	29	32	-0.11	-0.10	-0.23	-0.20	4.78
1	Last Rib Back Fat (cm)	3	6.61	6.63	66	74	-0.13	-0.13	-0.01	-0.02	3.03
1	Lumbar Back Fat(cm)	3	6.96	6.94	64	73	-0.15	-0.15	-0.08	-0.08	3.12
1	Loin Eye Area (cm2)	3	10.34**	9.17*	29	32	1.11	1.02	1.33	1.26	4.21
1	Loin Eye Area (cm2)	3	5.71	5.74	105	108	1.36	1.11	-0.58	-0.54	4.00
2	16 Day Weight	5		5.77		77		-0.004		0.44	
2	Ave Daily Gain b-w	5		6.27		78		-0.009		0.02	
2	Ave Daily Gain on Test	5	8.31*	8.15	87	100	0.015	0.014	0.010	0.009	3.65
2	Average Back Fat (cm)	5		9.52*		1		0.14		-0.01	
2	Last Rib Back Fat (cm)	5		7.39		1		0.12		-0.003	
2	Lumbar Back Fat(cm)	5		9.70*		0		0.17		-0.03	
2	Tenth Rib Backfat (cm)	5		5.79		1		0.13		-0.009	
3	Birth Weight (kg)	0	5.20		19		-0.02		-0.09		2.88
4	Ave Daily Gain on Test	2	8.87*	5.70	97	120	-0.006	-0.007	0.03	0.01	5.71
4	Carcass Weight (kg)	2	11.76**	11.45**	123	140	0.71	0.70	0.41	0.35	5.97
4	Loin Eye Area (cm2)	2	7.87	7.84	92	98	1.38	1.48	-0.64	0.03	4.20
4	Last Rib Back Fat (cm)	2	5.86	6.83	101	116	-0.03	-0.05	0.19	0.19	3.18
4	Lumbar Back Fat(cm)	2	5.29	6.16	107	122	-0.03	-0.03	0.27	0.21	2.92
5	Average Back Fat (cm)	2	7.35	10.81**	113	117	0.15	0.16	-0.002	0.04	3.75
5	Last Rib Back Fat (cm)	2	9.51*	10.64**	113	114	0.17	0.16	0.04	-0.07	4.83

5	Lumbar Back Fat(cm)	2	7.25	10.91**	107	116	0.17	0.19	0.11	0.10	3.79
6	10th Rib Back Fat (cm)	1	6.14	6.07	128	128	-0.14	-0.13	0.15	0.15	3.63
6	Carcass Length (cm)	1	5.44	5.47	141	142	0.46	0.44	0.05	0.05	2.59
SSC	Trait	New Markers	F-value ^a old	F-value ^a new	Location (cM) (old)	Location (cM) (new)	Additive Effect ^b old	Additive Effect ^b new	Dominance effect old	Dominance effect new	% var ^c old
7	Ave Back Fat (cm)	2	11.10**	10.64**	58	56	0.17	0.16	0.05	0.05	5.34
7	Ave Back Fat (cm)	2	10.36**	8.71*	91	87	0.16	0.13	-0.09	-0.06	5.39
7	Ave Back Fat (cm)	2		8.92*		104		0.15		-0.08	
7	Lumbar Back Fat (cm)	2	13.81**	13.46**	72	57	0.24	0.23	-0.07	0.03	6.88
7	Lumbar Back Fat (cm)	2	12.51**	9.60*	91	103	0.22	0.20	-0.11	-0.07	6.39
7	10 th Rib Back Fat (cm)	2	5.60	5.22	58	55	0.14	0.13	0.09	0.09	2.83
7	10 th Rib Back Fat (cm)	2	5.42	5.45	89	88	0.14	0.04	-0.08	-0.08	2.77
7	10 th Rib Back Fat (cm)	2		5.52		104		0.14		-0.11	
7	Last Rib Back Fat (cm)	2		6.71		56		0.13		0.02	
7	Last Rib Back Fat (cm)	2	7.27	6.46	74	87	0.14	0.11	-0.04	-0.04	3.69
7	Last Rib Back Fat (cm)	2	6.97	6.35	90	107	0.13	0.13	-0.08	-0.03	3.64
7	Carcass Weight (kg)	2	6.87	6.68	7	7	0.48	0.47	-0.64	-0.63	4.34
7	Carcass Weight (kg)	2	7.69	4.58	95	98	0.41	0.35	-0.77	-0.54	4.68
8	Ave Daily Gain Test	1	6.28	5.63	48	49	-0.014	-0.013	0.005	-0.002	2.76
8	Carcass Weight (kg)	1	7.33	7.92	48	48	-0.34	-0.34	0.67	0.68	3.36
9	ADG to Wean.	4	6.38	7.88	37	37	0.008	0.007	0.023	0.02	3.66
9	Average Daily Gain Test	4	5.32	5.75	116	120	0.014	0.013	-0.002	-0.002	2.86
9	16 Day Weight	4		6.09		139		0.18		0.34	
9	Loin Eye Area (cm2)	4		5.99		37		-0.69		-1.45	

SSC	Trait	New Markers	F-value ^a old	F-value ^a New	Location (cM) (old)	Location (cM) (new)	Additive Effect ^b old	Additive Effect ^b new	Dominance effect old	Dominance effect new	% variance ^c old
10	Carcass Weight (kg)	1		5.49		73		0.42		-0.51	
10	Last Rib Back Fat (cm)	1		5.12		74		0.10		-0.11	
11	Carcass Length (cm)	1	5.72	4.39	13	16	-0.36	-0.28	0.60	0.47	4.06
12	Last Rib Back Fat (cm)	1	4.78	3.59	81	7	-0.14	-0.07	-0.12	0.11	4.52
12	Carcass weight (kg)	1		4.90		96		0.19		0.71	
13	Average Back Fat (cm)	2	5.84	5.82	27	28	0.09	0.08	-0.13	-0.12	2.81
13	Tenth Rib Back Fat (cm)	2	7.08	7.00	23	24	0.12	0.11	-0.14	-0.14	3.05
13	Last Rib Back Fat (cm)	2	5.35	5.43	36	38	0.07	0.06	-0.15	-0.15	2.69
13	Carcass Weight (kg)	2	5.52	5.43	54	56	-0.19	-0.19	-0.67	-0.66	2.61
14	Last Rib Back Fat (cm)	2	5.29	5.30	57	61	-0.04	-0.04	0.14	0.14	2.09
14	Carcass Weight (kg)	2	5.51	5.40	58	62	0.19	0.19	0.62	0.62	2.30
15	Tenth Rib Back Fat (cm)	3		6.85		69		-0.10		-0.14	
18	Average Back Fat (cm)	2	4.46	4.53	5	5	-0.12	-0.11	0.02	0.01	2.33
X	Carcass Length (cm)	1	5.17	5.60	75	72	0.55	0.57	-0.02	-0.04	3.95

^a Chromosome-wise F-statistic thresholds at the 5% level, as determined by permutation test were as follows: old / new (1) 5.08 / 5.09, (2) 5.12 / 5.50, (3) 5.14 (no markers added), (4) 5.14 / 5.21, (5) 4.99 / 5.00, (6) 5.32 / 5.25, (7) 5.25 / 5.14, (8) 5.03 / 4.97, (9) 5.09 / 5.25, (10) 5.11 / 5.00, (11) 4.59 / 4.53, (12) 4.78 / 4.68, (13) 5.03 / 4.95, (14) 5.02 / 4.94, (15) 5.02 / 4.99, (16) 4.34 (no markers added), (17) 4.86 / 4.88, (18) 4.45 / 4.39, (X) 4.80 / 4.84.

^b Additive (a) and dominance (d) QTL effects correspond to genotype values of +a, d, and -a for, respectively, individuals having inherited two Berkshire alleles, heterozygotes, and individuals with two Yorkshire alleles. Positive additive effects indicate that Berkshire alleles increased the trait, negative that the Berkshire alleles decreased it. Dominance effects are relative to the mean of the two homozygotes.

^c % variance = genetic variance at the QTL based on estimated additive and dominance effects and allele frequencies of ½, as a percent of the residual variance in the F2.

Significant at the 10% genome-wise level: (F>7.42)

* Significant at the 5% genome-wise level (F>8.22 / 8.21)

** Significant at the 1% genome-wise level (F> 9.96 / 9.88)

Summary

significant QTL for growth and composition traits

	5% Chr-wise	5% Gen-wise	1% Gen-wise
Old scan (125 markers)	43	10	7
New scan (160 markers)	51	13	6
Number lost	5	2	4
Number added	13	5	3

significant QTL for meat quality traits

	5% Chr-wise	5% Gen-wise	1% Gen-wise
Old scan (125 markers)	61	10	1
New scan (160 markers)	72	9	3
Number lost	8	3	0
Number added	19	2	2