

Table S5 'Combined' QTL scan results

(Starts on next page) The QTL scan results for all QTL detected in our 'combined scan' (i.e. Paxton and Priest Lakes, and including a genotype by lake interaction covariate) are shown. Together, the '1.5 LOD C.I. low (cM)' and '1.5 LOD C.I. high (cM)' columns indicate the range of the 1.5 LOD confidence interval of the genomic location of the QTL. The 'LOD' column indicates the LOD score at the peak marker for the QTL (the marker at which genotypes showed the strongest association with phenotypes). The 'p-value' column indicates the genome-wide significance of the peak marker's LOD score for the associated trait. When QTL were not included in the 'candidate QTL' dataset, the reason is indicated ("trait not parallel" means that the associated trait was not determined to have diverged in parallel and therefore was not a focus of the study.)

Trait	Linkage group	Peak Marker Position (cM)	1.5 LOD		LOD	p-value	Candidate QTL?
			C.I. low (cM)	C.I. high (cM)			
plate count	2	24	18	39.1	5.59	5.27E-02	yes
plate count	7	33.93	33.41	34.99	24.81	<1.00E-04	yes
plate count	16	9.98	4	22	5.66	4.68E-02	yes
long gill raker count	3	36	30.9	42	7.29	2.30E-03	yes
long gill raker count	7	35.12	33.41	35.81	14.12	<1.00E-04	yes
short gill raker count	1	21.16	14	23.72	9.43	2.00E-04	yes
short gill raker count	7	34.99	32.22	35.81	6.67	9.40E-03	yes
1st dorsal spine	2	33.63	24	39.26	10.39	<1.00E-04	no (trait not parallel)
x1	2	26	18	33.05	10.61	<1.00E-04	no (trait not parallel)
y1	8	18	10	30.86	5.97	3.45E-02	yes
x2	4	23.78	14.49	26.83	5.97	5.01E-02	yes
x3	1	21.16	16.42	22.4	8.16	1.40E-03	no (trait not parallel)
x3	5	50.52	30	56.44	6.4	1.57E-02	no (trait not parallel)
x3	12	18	8	25.01	8.57	6.00E-04	no (trait not parallel)
y3	4	71.36	66	71.36	5.8	4.04E-02	yes
y3	7	6	0	14	10.65	<1.00E-04	yes
x4	7	33.93	26.61	35.81	8.4	1.10E-03	no (trait not parallel)
y4	7	34.99	32.22	37.03	5.81	4.95E-02	yes
y5	7	35.45	34.21	42	9.77	<1.00E-04	yes
x6	7	34.21	30	50.99	6.18	1.92E-02	yes
y6	7	37.32	26.61	44	6.86	6.80E-03	no (trait not parallel)
y6	13	12	0	23.99	7.32	2.80E-03	no (trait not parallel)
y6	19	0	0	4	11.42	<1.00E-04	no (trait not parallel)
x7	3	6	0.22	12	7.61	1.70E-03	no (trait not parallel)
y7	2	33.63	30	38	6.05	2.52E-02	yes
y7	7	35.45	32.22	56	6.41	1.36E-02	yes
x9	3	4	0	10	5.89	3.10E-02	no (trait not parallel)
x10	2	36.63	28	42	5.71	4.66E-02	no (trait not parallel)
y10	1	19.11	18.11	26	8.36	5.00E-04	yes
y10	14	12	0	22	10.43	<1.00E-04	yes
x11	1	21.16	16.42	23.72	5.96	3.77E-02	no (trait not parallel)
y11	1	21.16	15.32	26	5.86	5.35E-02	yes
y11	4	30	26.83	71.36	6.31	2.86E-02	yes
y11	11	28	10	37.74	6.7	1.58E-02	yes
x12	19	0.55	0	6	6.12	4.57E-02	no (trait not parallel)
y12	13	27.7	24.53	28.79	6	4.21E-02	yes
y12	19	0	0	10	6.85	1.28E-02	yes
x13	1	18.11	16	30	6.51	2.34E-02	yes
x13	7	28	24	33.41	6.87	1.37E-02	yes
x16	1	21.75	18.11	23.72	9.67	<1.00E-04	yes
x16	12	5.22	2	15.46	6.92	5.60E-03	yes
y16	13	28.79	24	28.79	6.18	2.02E-02	yes

Trait	Linkage group	Peak Marker Position (cM)	1.5 LOD		LOD	p-value	Candidate QTL?
			C.I. low (cM)	C.I. high (cM)			
x17	12	6.42	4	15.46	6.87	9.50E-03	yes
x18	7	32.22	29.3	37.03	6.51	1.12E-02	yes
y18	11	34	28	42	6.44	1.24E-02	yes
y19	1	21.75	14	41.89	6.25	2.17E-02	no (trait not parallel)
y19	4	34.54	30.31	38	6.7	1.02E-02	no (trait not parallel)
y19	8	26	19.01	30.86	6.97	6.50E-03	no (trait not parallel)
y19	12	12.16	10.86	15.46	9.25	1.00E-04	no (trait not parallel)
y19	14	11.23	0	36	6.01	3.22E-02	no (trait not parallel)
y19	19	0	0	6	6.19	2.46E-02	no (trait not parallel)
x20	4	20	15.02	23.78	6.42	1.28E-02	yes
y22	1	18	15.32	20.27	6.71	9.20E-03	no (trait not parallel)
x23	1	21.16	16.42	23.72	6.75	1.67E-02	no (trait not parallel)
x23	3	6	0	10.46	8.19	2.00E-03	no (trait not parallel)
y25	12	13.24	10.86	21	11.06	<1.00E-04	yes
y26	1	21.75	18.11	34	7.91	9.00E-04	yes
y26	12	13.24	10.86	22	9.37	<1.00E-04	yes
y26	19	0.55	0	6	6.83	9.00E-03	yes
y27	8	19.01	16.61	30.86	5.54	5.42E-02	yes
y27	12	13.24	10.73	24	7.51	2.90E-03	yes
y27	17	21.65	12	27.82	7.15	4.40E-03	yes
centroid	1	24.57	2	32	9.64	3.00E-04	yes