

Table S3 Paxton Lake QTL scan results

(Starts on next page) The QTL scan results for all QTL detected in our Paxton Lake scan 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 ("combined scan" means that a co-locating QTL was discovered in the combined scan, which we used instead; "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	7	33.93	33.41	34.99	16.65	<1.00E-04	no (combined scan)
long gill raker count	3	36	30.9	42	6.43	1.70E-03	no (combined scan)
long gill raker count	7	34.01	32.22	35.81	8.66	<1.00E-04	no (combined scan)
short gill raker count	1	21.16	16	23.72	6.05	3.50E-03	no (combined scan)
short gill raker count	7	34.99	32.22	35.81	5.54	7.60E-03	no (combined scan)
1st dorsal spine	2	33.63	22	39.26	8.11	<1.00E-04	no (trait not parallel)
2nd dorsal spine	20	1.65	0	22.7	4.39	3.68E-02	no (trait not parallel)
x1	1	20	16.42	21.75	5.05	1.86E-02	no (trait not parallel)
y1	8	18.19	10	30	5.12	1.58E-02	no (combined scan)
x2	7	0	0	14	6.38	1.70E-03	yes
x3	1	21.16	16.42	23.72	9.14	<1.00E-04	no (trait not parallel)
x3	5	52	26	56.44	5.65	6.60E-03	no (trait not parallel)
x3	12	13.5	12.16	24	10.23	<1.00E-04	no (trait not parallel)
y3	7	6	0	14	11.12	<1.00E-04	no (combined scan)
x4	3	10	4	16	5.68	5.20E-03	no (trait not parallel)
x4	7	34.21	32.22	35.81	7.61	4.00E-04	no (trait not parallel)
x4	12	20	7.73	25.01	5.09	1.50E-02	no (trait not parallel)
y4	7	34.99	32	37.03	5.27	1.08E-02	no (combined scan)
y5	19	2	0	10	5.11	1.55E-02	yes
x6	7	35.45	30	54	5.61	5.50E-03	no (combined scan)
y6	7	35.45	14.71	40	4.47	4.79E-02	no (trait not parallel)
y6	13	18.72	0	24.53	5.1	1.80E-02	no (trait not parallel)
y6	19	0.1	0	4	11.3	<1.00E-04	no (trait not parallel)
x10	7	40	34.45	50	5.54	7.80E-03	no (trait not parallel)
y10	4	58	35.12	71.36	6.47	1.10E-03	yes
y10	14	11.23	0	22	7.32	2.00E-04	no (combined scan)
x11	1	21.16	16.42	23.72	5.94	3.90E-03	no (trait not parallel)
y11	1	21.75	16.42	23.72	6.82	9.00E-04	no (combined scan)
y11	4	30	26.83	71.36	8.11	3.00E-04	no (combined scan)
x12	1	19.11	16	23.72	4.71	2.95E-02	no (trait not parallel)
y12	4	28.15	26	71.36	4.62	3.74E-02	yes
y12	19	0.1	0	8	5.13	1.59E-02	no (combined scan)
x13	1	19.11	16.42	27.92	7.15	3.00E-04	no (combined scan)
x13	7	35.12	24	40	4.58	4.24E-02	no (combined scan)
x16	1	19.11	16.42	27.92	4.76	2.85E-02	no (combined scan)
x16	13	20.04	8.48	27.7	4.44	4.93E-02	yes
x18	7	32.22	26.61	33.93	4.84	2.52E-02	no (combined scan)
y18	4	36	30.31	71.36	4.53	4.11E-02	yes
x19	10	8	6.2	24	4.96	2.00E-02	no (trait not parallel)
y19	8	26	19.01	30.86	6.83	1.00E-03	no (trait not parallel)
y19	12	12.16	10	25.01	4.84	2.73E-02	no (trait not parallel)
x20	1	25.31	24	34	4.36	5.30E-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)			
x21	1	20	16.42	22.4	4.9	2.32E-02	yes
x22	7	33.93	24	35.45	4.62	4.06E-02	yes
x23	1	19.11	16.42	27.92	8.51	<1.00E-04	no (trait not parallel)
x24	1	19.11	16	26	5.62	6.40E-03	no (trait not parallel)
x25	1	20	16	26	4.53	4.33E-02	no (trait not parallel)
x25	16	12.99	0	24	4.48	4.74E-02	no (trait not parallel)
y25	12	18	12.16	25.01	7.67	<1.00E-04	no (combined scan)
x26	1	19.11	16	26	5.13	1.47E-02	no (trait not parallel)
y26	19	0.1	0	6	4.85	2.63E-02	no (combined scan)
centroid	19	0.1	0	6	4.67	3.42E-02	yes