Table S4 Priest Lake QTL scan results

(Starts on next page) The QTL scan results for all QTL detected in our Priest 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 maker 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 C.I. low (cM)	1.5 LOD C.I. high (cM)	LOD	p-value	Candidate QTL?
plate count	2	26	18	44	4.41	2.34E-02	no (combined scan)
plate count	7	35.45	30	42	8.58	<1.00E-04	no (combined scan)
plate count	16	14	6.33	22	5.5	2.70E-03	no (combined scan)
long gill raker count	7	46	32.22	58	6.13	1.70E-03	no (combined scan)
short gill raker count	1	14.83	6	32	4.67	1.69E-02	no (combined scan)
x1	2	24	18	33.63	9.52	<1.00E-04	no (trait not parallel)
x2	14	38.82	30.98	48.93	4.04	4.88E-02	yes
x3	14	38.82	28.55	48.93	4.38	2.47E-02	no (trait not parallel)
y3	4	71.36	66	71.36	4.67	1.51E-02	no (combined scan)
y5	7	40	34.21	56	6.16	1.40E-03	no (combined scan)
x6	4	20.84	14.49	32	3.99	5.35E-02	yes
x6	13	27.7	22.18	28.79	4.06	4.64E-02	yes
x7	3	6	0	14	5.32	4.80E-03	no (trait not parallel)
y7	7	35.45	30	50.64	5.58	3.50E-03	no (combined scan)
y7	9	10	0	17.66	4.32	2.97E-02	yes
y10	1	23.96	4	27.92	5.8	1.80E-03	no (combined scan)
y11	11	30	8.46	37.74	4.86	8.30E-03	no (combined scan)
x15	3	2.69	0	12	4.2	3.39E-02	no (trait not parallel)
x16	1	21.75	18.11	34	5.4	3.20E-03	no (combined scan)
x16	12	13.5	2	15.46	5.68	1.70E-03	no (combined scan)
y16	21	42.82	26	44.58	4.19	4.17E-02	yes
x17	12	6.42	4	13.24	6.31	7.00E-04	no (combined scan)
x17	14	34.83	24	48.93	4.1	4.36E-02	yes
y18	11	34.66	28	40	4.31	3.04E-02	no (combined scan)
y19	1	22	16	37.75	5.87	9.00E-04	no (trait not parallel)
y19	12	12.16	0	24	4.3	3.20E-02	no (trait not parallel)
y19	14	34.83	0	41.41	4.53	2.15E-02	no (trait not parallel)
x20	12	4.39	0	15.46	4.56	1.86E-02	yes
x23	3	4	0	12	4.69	1.54E-02	no (trait not parallel)
y23	21	44	20	44.58	5.35	4.70E-03	no (trait not parallel)
y25	12	11.57	9.45	15.46	4.09	4.82E-02	no (combined scan)
y26	1	21.75	18.11	30	7.02	<1.00E-04	no (combined scan)
y26	12	15.46	3.74	25.01	4.7	1.42E-02	no (combined scan)
y26	14	36.5	12	48.93	4.13	3.94E-02	yes
y27	12	4.39	0	15.46	4.47	2.19E-02	no (combined scan)
y27	17	21.65	0	27.82	4.29	2.99E-02	no (combined scan)
centroid	1	24.57	22.4	32	6.74	3.00E-04	no (combined scan)