

GENETICS

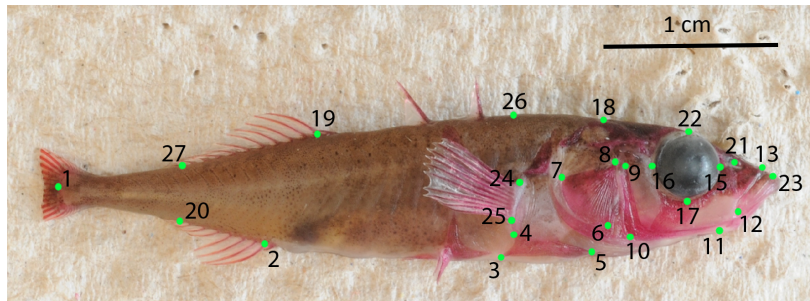
Supporting Information

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Extent of QTL Reuse During Repeated Phenotypic Divergence of Sympatric Threespine Stickleback

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Supplementary Material



Landmarks (x and y coordinates)

1. posterior midpoint of the caudal peduncle
2. anterior insertion of the anal fin at the first soft ray
3. posteroventral corner of the ectocoracoid bone
4. posterodorsal corner of the ectocoracoid bone
5. anterior-most corner of the ectocoracoid bone
6. anteroventral corner of the opercle
7. posterodorsal corner of the opercle
8. dorsal edge of the opercle-hyomandibular boundary
9. dorsal-most extent of the preopercle
10. posteroventral corner of the preopercle
11. anterior-most extent of the preopercle along the ventral silhouette
12. posteroventral extent of the maxilla
13. anterodorsal extent of the maxilla
14. *No landmark*
15. anterior margin of the orbit in line with the eye's midpoint
16. posterior margin of the orbit in line with the eye's midpoint
17. ventral margin of the orbit in line with the eye's midpoint
18. posterior extent of neurocranium (i.e., supraoccipital) along dorsal silhouette
19. anterior insertion of the dorsal fin at the first soft ray
20. posterior insertion of the anal fin at the first soft ray
21. edge of the lachrymal at the naris
22. dorsal margin of the orbit in line with the eye's midpoint
23. anterior-most extent of the premaxilla
24. dorsal insertion of the pectoral fin
25. ventral insertion of the pectoral fin
26. dorsum of the trunk over the pectoral fin midpoint
27. posterior insertion of the dorsal fin at the first soft ray

- centroid size (square root of the sum of squared distances of the 26 landmarks from their centroid)

Meristics

- lateral plate count
- 1st dorsal spine presence/absence
- 2nd dorsal spine presence/absence
- long gill raker count (on the first gill arch)
- short gill raker count (on the first gill arch)

Figure S1 All phenotypes scored

Landmark numbers were made consistent with those in Arnegard et al. (2014).

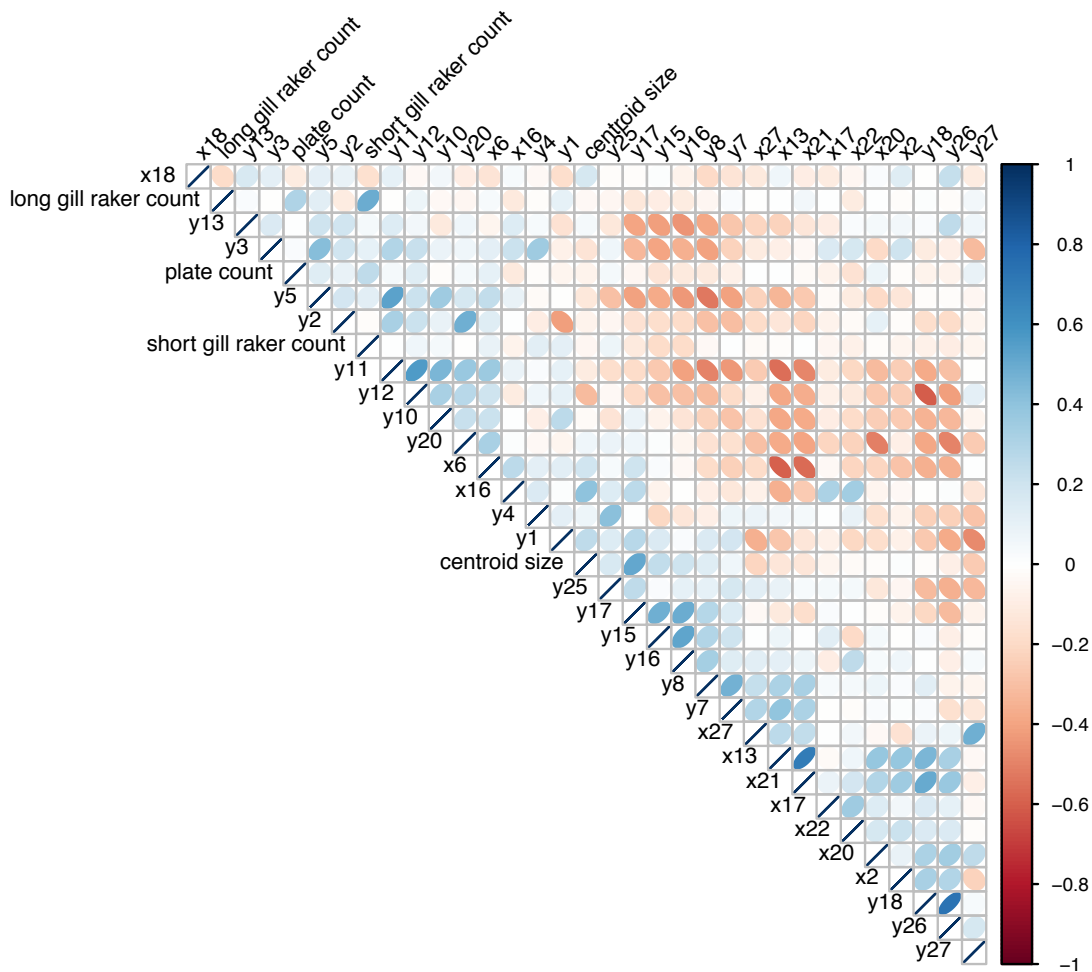


Figure S2 Correlations among parallel traits in Paxton Lake F₂s

The strength of correlation between pairs of parallel traits in Paxton Lake F₂s is indicated by both color and elongation of the ellipse. F₂ values were corrected for family and sex.

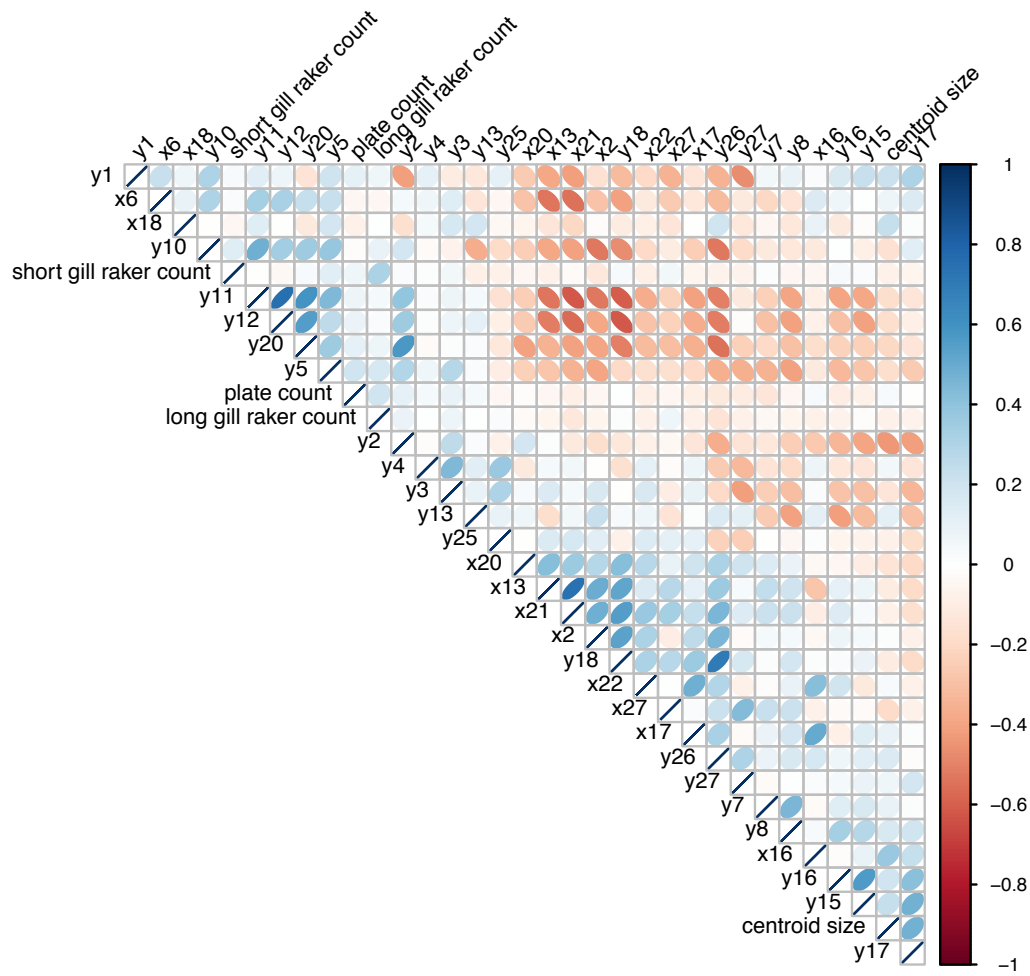


Figure S3 Correlations among parallel traits in Priest Lake F₂s

The strength of correlation between pairs of parallel traits in Priest Lake F₂s is indicated by both color and elongation of the ellipse. F₂ values were corrected for family and sex.

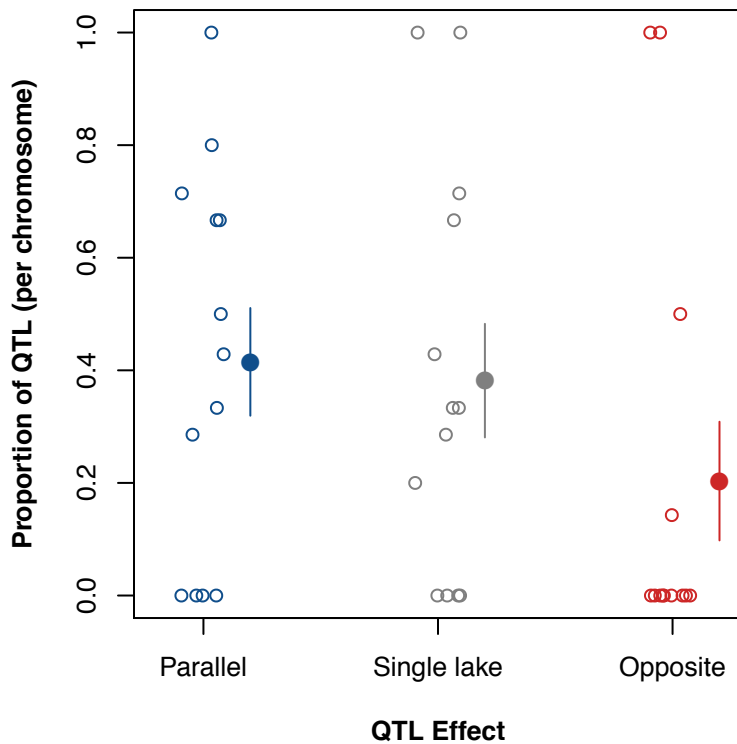


Figure S4 Proportions of QTL effect categories per chromosome

The proportion of parallel (blue), single lake (gray) and opposite QTL effects (red) on 13 chromosomes (Figure 2). Filled circles and vertical lines indicate the mean proportion and SE over the 13 chromosomes: 41.5% ± 9.6% SE parallel, 38.1% ± 10.1% SE single lake, and 20.3% ± 10.5% SE opposite effects.

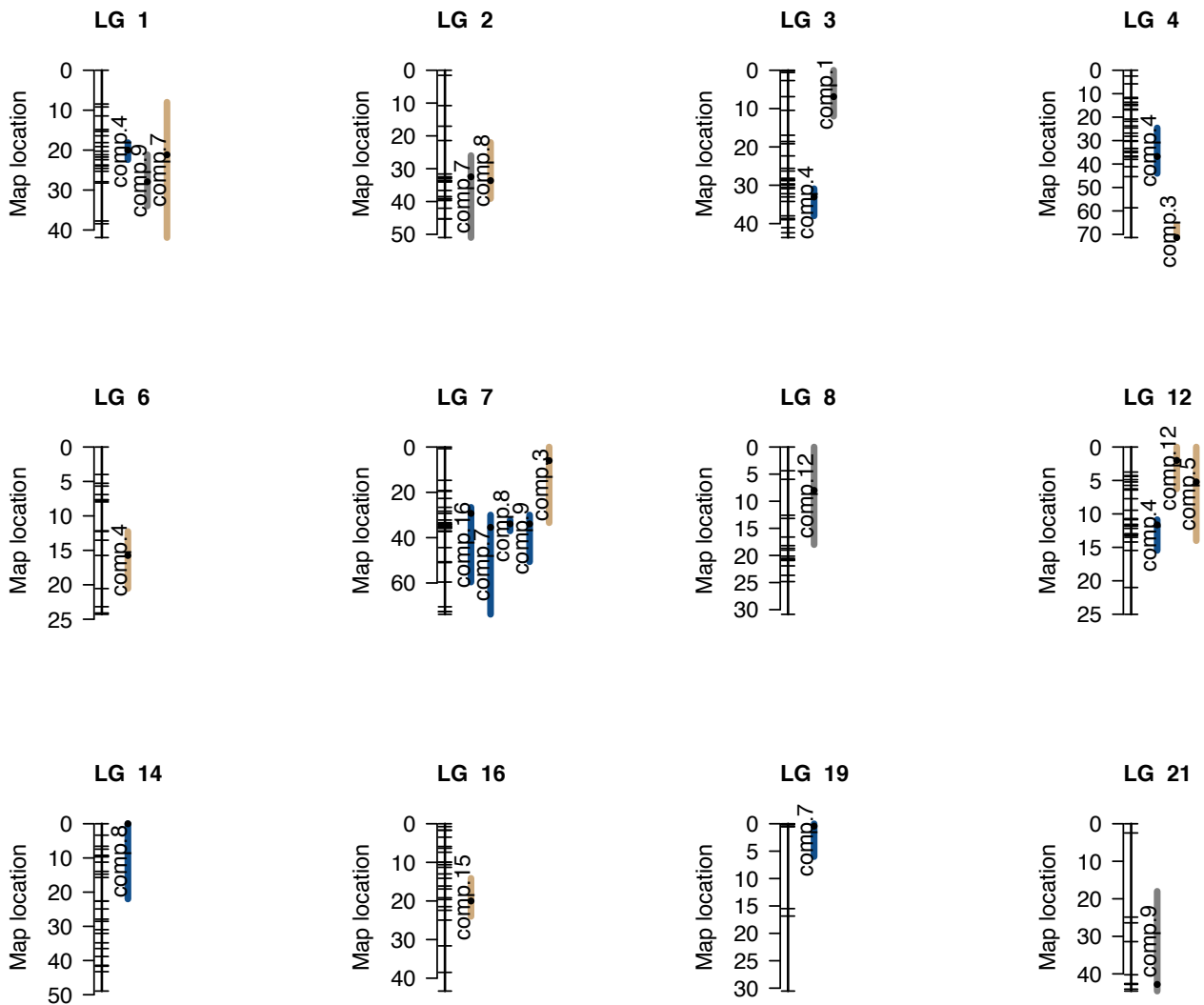


Figure S5 Map of Principal Component QTL

Map of 23 QTL (i.e. QTL with an effect in one or both lakes) underlying parallel principal components of parallel traits. Only QTL for principal components accounting for the first 90% of cumulative variance in F_2 phenotypes are shown. Linkage groups on which QTL were detected are shown. For each, the positions of SNP markers in the combined Paxton and Priest linkage map are depicted by tick marks on the left. Colored bars span the 1.5 LOD confidence intervals of QTL. Black dots within bars represent the peak marker position. The principal component phenotype affected by each QTL is indicated to the left its bar. Colors of bars represent the 'QTL Effect' category, as follows: parallel effects – blue; effect in only one lake – grey; opposite effects – red. Tan colored bars represent the candidate QTL for which more than one QTL effect category fit the data nearly equally well.

Table S1 Trait divergence categories

(Starts on next page) Trait divergence was considered 'parallel' when the best model of the species effect was either 'same effect' or was 'different effect' and the direction of divergence was 'same'. Trait divergence was considered 'single lake' when the best model of the species effect was either 'effect only in Paxton' or 'effect only in Priest'. Trait divergence was considered 'opposite' when the best model of species effect was 'different effect' and the direction of divergence was 'opposite'. The second best model of species effect and the delta AICc between it and the best model is also shown. When the delta AICc was less than two and the 2nd best model called for a different trait divergence category than the best model, we dropped the trait from further study (indicated by 'NA' in the "Trait divergence' based on AICc model selection' column), though detected QTL for all traits measured are shown in Tables S2 – S4.

Trait	'Trait divergence'		Best model of species effect	2nd best model of species effect	Delta AICc
	based on AICc model selection	Direction of divergence			
plate count	Parallel	same	different effect	same effect	35.62
gill raker count	Parallel	same	same effect	different effect	1.24
1st dorsal spine	Single lake	opposite	effect in Paxton only	different effect	2.14
2nd dorsal spine	NA	same	no effect	effect in Priest only	0.95
x1	NA	opposite	no effect	effect in Priest only	0.17
y1	Parallel	same	same effect	different effect	1.72
x2	Parallel	same	different effect	same effect	5.78
y2	Parallel	same	same effect	different effect	1.28
x3	Opposite	opposite	different effect	effect in Paxton only	3.97
y3	Parallel	same	different effect	same effect	1.14
x4	Single lake	opposite	effect in Priest only	different effect	2.12
y4	Parallel	same	different effect	same effect	31.59
x5	NA	opposite	effect in Priest only	different effect	0.02
y5	Parallel	same	different effect	same effect	2.77
x6	Parallel	same	same effect	different effect	2.20
y6	Opposite	opposite	different effect	effect in Priest only	5.36
x7	NA	opposite	different effect	effect in Priest only	1.47
y7	Parallel	same	same effect	different effect	1.90
x8	NA	opposite	effect in Paxton only	different effect	0.32
y8	Parallel	same	different effect	same effect	0.53
x9	NA	same	effect in Priest only	different effect	1.36
y9	NA	same	effect in Paxton only	different effect	0.26
x10	Single lake	same	effect in Priest only	different effect	2.18
y10	Parallel	same	same effect	different effect	1.01
x11	NA	same	effect in Paxton only	different effect	1.69
y11	Parallel	same	same effect	different effect	1.83
x12	Opposite	opposite	different effect	effect in Priest only	19.50
y12	Parallel	same	same effect	different effect	1.03
x13	Parallel	same	different effect	same effect	2.97
y13	Parallel	same	same effect	different effect	1.72
x15	NA	same	same effect	effect in Priest only	1.70
y15	Parallel	same	same effect	different effect	1.01
x16	Parallel	same	different effect	same effect	0.78
y16	Parallel	same	same effect	different effect	0.67
x17	Parallel	same	different effect	same effect	3.19
y17	Parallel	same	different effect	same effect	0.37
x18	Parallel	same	different effect	same effect	0.84
y18	Parallel	same	different effect	same effect	0.43
x19	NA	opposite	different effect	effect in Priest only	1.00
y19	Single lake	same	effect in Paxton only	different effect	2.13
x20	Parallel	same	different effect	effect in Priest only	3.10
y20	Parallel	same	different effect	same effect	17.17

Trait	'Trait divergence'		Best model of species effect	2nd best model of species effect	Delta AICc
	based on AICc model selection	Direction of divergence			
x21	Parallel	same	same effect	different effect	2.09
y21	NA	opposite	no effect	effect in Priest only	0.37
x22	Parallel	same	same effect	different effect	2.17
y22	NA	same	effect in Paxton only	different effect	0.27
x23	Opposite	opposite	different effect	effect in Paxton only	4.95
y23	NA	same	different effect	effect in Priest only	0.29
x24	NA	same	effect in Priest only	different effect	1.32
y24	Opposite	opposite	different effect	effect in Paxton only	17.01
x25	Single lake	same	effect in Priest only	different effect	2.19
y25	Parallel	same	different effect	effect in Paxton only	4.15
x26	NA	same	different effect	effect in Priest only	1.63
y26	Parallel	same	different effect	same effect	3.30
x27	Parallel	same	same effect	different effect	2.12
y27	Parallel	same	same effect	different effect	2.15
centroid	Parallel	same	different effect	effect in Paxton only	25.59

Table S2 Identities, map positions, and physical locations of SNPs

(Starts on next page) Identities, map positions, and physical locations of the 430 single nucleotide polymorphism (SNP) markers used in linkage and QTL analysis. The linkage group (LG) and map position in centimorgans (cM) are provided for each SNP. Each marker name is a combination of the chromosome number (before the colon) and the physical position in base pairs (after the colon) of the SNP in the reference stickleback genome assembly (Broad S1, Feb. 2006) (Jones et al. 2012). Markers identified from unassembled regions of the genome are indicated with 'chrUN'. In such cases, the position in base pairs is based on the composite chrUN in the UCSC genome browser. Marker information can be obtained from the Single Nucleotide Polymorphism Database (dbSNP, available at <http://www.ncbi.nlm.nih.gov/projects/SNP/>), which is hosted by the National Center for Biotechnology Information (NCBI) of the U.S. National Institutes of Health. Data for specific markers may be found by searches of the dbSNP using the submitted SNP ID numbers (ss#). Two SNPs are still awaiting ss# assignment.

Linkage Group	Map Position (cM)	Marker name (chromosome: position)	NCBI submitted SNP ID numbers (ss#)	Linkage Group	Map Position (cM)	Marker name (chromosome: position)	NCBI submitted SNP ID numbers (ss#)
1	0	chrI:27642534	418642015	2	45.24	chrII:919438	244222781
1	8.45	chrUn:18660323	418642624	2	45.324	chrUn:23384875	418642627
1	9.18	chrI:22716347	418642010	2	50.981	chrII:533883	120258418
1	11.439	chrI:3310077	244222768	3	0	chrUn:30223426	418642641
1	14.833	chrI:19946499	418642005	3	0.219	chrUn:27149198	418642632
1	15.322	chrI:2718044	418641984	3	0.593	chrUn:27040022	418642631
1	16.421	chrI:4219350	244222770	3	2.685	chrUn:30323959	418642642
1	18.111	chrI:3494580	120258412	3	6.884	chrIII:16463929	244222796
1	19.109	chrI:14261764	418641998	3	10.455	chrIII:16251071	120258431
1	20.267	chrI:15145305	418642000	3	16.956	chrIII:15793968	418642089
1	21.162	chrI:4171190	244222769	3	18.59	chrIII:15185662	418642088
1	21.745	chrI:17306554	418642003	3	19.173	chrIII:15157782	418642087
1	22.395	chrI:7545826	418641993	3	22.347	chrIII:14892994	244222794
1	23.715	chrI:20584613	418642006	3	25.596	chrIII:13397314	418642078
1	23.959	chrI:22899825	418642011	3	26.289	chrIII:13520975	252841102
1	24.572	chrI:22361077	120258417	3	28.19	chrIII:14393183	418642084
1	25.305	chrI:3538018	418641987	3	28.59	chrIII:14048561	252841058
1	27.917	chrI:26879230	244222777	3	28.741	chrIII:13911180	418642080
1	28.238	chrI:25560380	418642013	3	28.761	chrIII:11836494	418642072
1	37.745	chrI:1550	418641979	3	29.684	chrIII:13699701	418642079
1	38.432	chrUn:37631434	244223001	3	29.727	chrIII:12930427	418642076
1	41.893	chrI:913033	120258411	3	29.906	chrIII:14135608	418642081
2	0	chrII:22443700	244222787	3	30.523	chrIII:14456990	252841063
2	1.55	chrII:22644752	418642054	3	30.9	chrIII:14248039	418642083
2	10.77	chrII:21231538	244222786	3	32.208	chrIII:11302839	418642071
2	17.049	chrII:21013052	418642052	3	33.049	chrIII:2376699	418642065
2	21.421	chrII:19985741	244222785	3	34.228	chrIII:1968625	418642063
2	31.618	chrII:5914538	418642030	3	37.992	chrIII:1198125	120258428
2	32.478	chrII:10092618	418642034	3	38.662	chrIII:639237	418642059
2	32.693	chrII:8305286	418642033	3	38.988	chrIII:1651721	252841079
2	33.053	chrII:6475468	244222782	3	41.069	chrIII:269753	418642057
2	33.629	chrII:17453243	418642042	3	42.403	chrIII:105665	418642055
2	33.653	chrII:5935944	252841148	3	43.645	chrIII:186390	418642056
2	33.707	chrII:12292176	120258425	4	0	chrUn:27478064	244222993
2	33.978	chrII:14611516	244222784	4	2.47	chrUn:27589750	418642633
2	34.026	chrII:17312835	418642041	4	5.799	chrUn:27402745	252841068
2	36.632	chrII:4530808	120258423	4	11.6	chrIV:32592491	418642150
2	38.498	chrII:19324477	418642044	4	12.021	chrIV:32487875	244222812
2	39.102	chrII:3931852	418642025	4	13.638	chrIV:32387818	120258447
2	39.262	chrII:4157699	252841112	4	14.49	chrIV:32277841	418642146
2	39.701	chrII:3516452	120258422	4	15.02	chrIV:32236655	418642145
2	42.057	chrII:3384330	120258421	4	16.56	chrIV:32092919	252841132

Linkage Group	Map Position (cM)	Marker name (chromosome: position)	NCBI submitted SNP ID numbers (ss#)	Linkage Group	Map Position (cM)	Marker name (chromosome: position)	NCBI submitted SNP ID numbers (ss#)
4	16.927	chrIV:32005807	120258445	5	46.025	chrV:7791830	252841093
4	20.838	chrIV:31740478	244222809	5	50.516	chrUn:10540032	418642614
4	21.77	chrIV:31350187	418642140	5	53.473	chrUn:10213240	418642613
4	23.776	chrIV:29763654	120258443	5	53.596	chrUn:11980918	252841136
4	24.599	chrIV:31611147	252841084	5	56.444	chrUn:12390868	120258569
4	26.831	chrIV:30568387	252841083	6	0	chrVI:487411	418642183
4	28.149	chrIV:5165268	418642111	6	3.991	chrVI:6312798	418642187
4	30.064	chrIV:21232476	418642127	6	5.262	chrVI:1440771	244222823
4	30.311	chrIV:21605258	252841082	6	5.672	chrVI:10415741	418641920
4	33.352	chrIV:15721538	244222806	6	6.903	chrVI:11954719	418642192
4	33.352	chrIV:15737291	244222807	6	7.644	chrVI:13220597	252841044
4	34.536	chrIV:15530121	244222805	6	7.721	chrVI:11873663	120258454
4	35.12	chrIV:15052901	244222804	6	7.97	chrVI:12427477	418642193
4	36.67	chrIV:10997988	244222801	6	12.157	chrVI:3116218	244222825
4	36.782	chrIV:9220132	418642120	6	12.259	chrVI:16870159	244222834
4	36.984	chrIV:8545605	418642119	6	13.529	chrVI:218630	244222820
4	38.029	chrIV:11367975	120258435	6	15.74	chrVI:14571427	418642200
4	41.136	chrIV:4065598	244222799	6	20.547	chrVI:15413799	418642203
4	45.377	chrIV:3334208	418642103	6	23.176	chrVI:14976508	418642201
4	58.662	chrIV:2045971	418642099	6	24.097	chrVI:15654034	418642204
4	71.359	chrIV:219384	418642093	6	24.282	chrVI:15692312	418642205
5	0	chrUn:25831365	418642629	7	0	chrVII:27918897	418642257
5	2.542	chrUn:25946639	244222990	7	0.743	chrUn:29400087	418642638
5	8.438	chrV:11316476	252841077	7	14.707	chrVII:26769148	418642251
5	9.302	chrV:11368893	418642177	7	19.214	chrVII:26538823	244222842
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5	17.208	chrV:11642284	418642179	7	22.7	chrVII:26227403	120258461
5	19.847	chrV:11722274	418642180	7	26.614	chrVII:25662266	120258460
5	20.126	chrV:10649179	252841089	7	28.341	chrVII:25193081	418642246
5	23.802	chrV:10674055	418642173	7	29.302	chrVII:24988330	
5	30.785	chrV:10028353	418642167	7	32.219	chrVII:24217606	418642245
5	31.771	chrV:9884672	418642164	7	33.407	chrVII:19857837	418642237
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5	34.423	chrV:9157076	244222818	7	34.209	chrVII:23703797	418642243
5	40.776	chrV:8327818	244222816	7	34.447	chrVII:22798737	418642240
5	42.038	chrV:1238066	120258448	7	34.985	chrVII:21302029	418642238
5	43.017	chrV:1727383	418642153	7	35.124	chrVII:20883742	252841067
5	43.695	chrV:2528528	244222814	7	35.45	chrVII:18353106	244222839
5	44.689	chrUn:11085407	418642615	7	35.809	chrVII:13452516	244222836
5	45.499	chrV:5064057	418642160	7	35.815	chrVII:5552972	252841066
5	45.501	chrV:4819972	418642158	7	37.029	chrVII:5936068	120258457

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7	37.322	chrVII:4310181	418642225	9	32.728	chrIX:13852312	418642311
7	44.369	chrVII:2559099	418642220	9	33.542	chrIX:803523	252841065
7	50.636	chrVII:1569236	418642218	9	33.594	chrIX:16779825	244222869
7	50.989	chrVII:1481322	418642217	9	36.679	chrIX:2360337	244222859
7	59.593	chrVII:835236	252841091	9	37.317	chrIX:2310926	418642299
7	70.492	chrUn:29087782	244222996	9	39.339	chrIX:2089567	244222858
7	72.645	chrVII:537136	252841113	9	43.455	chrIX:1273244	244222857
7	72.679	chrVII:393417	418642213	9	45.903	chrIX:1417909	418642292
7	73.819	chrUn:28671327	244222995	9	46.308	chrIX:1571056	418642294
8	0	chrVIII:19282658	418642286	9	52.345	chrIX:639609	244222856
8	4.379	chrVIII:868226	418642258	10	0	chrX:1275840	418642326
8	5.961	chrVIII:18760705	244222855	10	4.412	chrX:14831394	418642358
8	12.586	chrVIII:2505620	418642263	10	4.526	chrX:14456479	252841100
8	13.173	chrVIII:1929053	244222843	10	4.527	chrX:14549101	252841122
8	16.606	chrVIII:2257915	418642261	10	6.198	chrX:14265366	120258486
8	18.186	chrVIII:3765115	418642265	10	7.06	chrUn:14127611	418642619
8	18.689	chrVIII:3627706	244222844	10	8.977	chrUn:14043112	418642618
8	19.011	chrVIII:3987295	120258464	10	9.768	chrUn:24511995	418642628
8	20.132	chrVIII:6680213	418642268	10	10.14	chrUn:29017220	418642637
8	20.538	chrVIII:8858242	418642273	10	10.338	chrX:13132917	418642352
8	20.747	chrVIII:14278829	418642277	10	16.368	chrX:10080391	418642338
8	20.771	chrVIII:12472630	252841158	10	16.858	chrX:11139448	252841128
8	20.929	chrVIII:13412707	244222846	10	17.302	chrX:4696470	418642330
8	21.923	chrVIII:15261158	418642279	10	19.902	chrX:8703061	120258485
8	23.667	chrVIII:13577518	252841097	10	20.486	chrX:7113953	120258483
8	24.825	chrVIII:14472465	244222848	10	22.444	chrX:11252137	244222875
8	30.855	chrVIII:16843576	418642285	10	24.019	chrX:12844036	418642350
9	0	chrIX:19781202	244222870	10	28.446	chrX:12507632	244222877
9	0.675	chrIX:20090929	244222871	11	0	chrXI:16701186	244222888
9	7.45	chrIX:19745222	418642321	11	0.287	chrXI:16655205	120258495
9	17.662	chrIX:18494397	418642317	11	8.458	chrXI:15154801	418642382
9	19.295	chrIX:18826248	418642319	11	15.6	chrUn:32523521	418642646
9	19.628	chrIX:19322448	418642320	11	20.238	chrXI:14631875	418642379
9	24.547	chrIX:5109672	244222860	11	20.482	chrXI:14691162	418642380
9	25.033	chrIX:4882924	120258472	11	20.626	chrXI:14830913	244222885
9	27.249	chrIX:5403530	120258474	11	23.738	chrXI:15005173	244222886
9	28.314	chrIX:5568375	244222863	11	31.588	chrXI:12097498	418642375
9	30.384	chrIX:12933483	244222865	11	31.877	chrXI:10976029	244222883
9	30.606	chrIX:7146708	418642304	11	34.655	chrXI:9039275	252841094
9	31.139	chrIX:15670033	244222868	11	35.303	chrXI:7355052	418642370
9	31.408	chrIX:7893416	418642306	11	37.738	chrXI:12746496	244222884
9	31.862	chrIX:13553866	252841127	11	38.425	chrXI:3120961	244222880

Linkage Group	Map Position (cM)	Marker name (chromosome: position)	NCBI submitted SNP ID numbers (ss#)	Linkage Group	Map Position (cM)	Marker name (chromosome: position)	NCBI submitted SNP ID numbers (ss#)
11	42.418	chrXI:1017481	120258488	13	21.03	chrXIII:2632698	244222901
11	43.126	chrXI:1449684	120258489	13	22.175	chrXIII:2523163	120258505
11	43.715	chrXI:1266618	418642362	13	23.993	chrXIII:1909687	244222900
11	46.473	chrXI:234849	120258487	13	24.529	chrXIII:1698554	418642421
12	0	chrXII:17758877	244222897	13	27.703	chrXIII:1001571	120258503
12	3.744	chrXII:16628544	418642412	13	28.789	chrXIII:2105469	418642423
12	4.281	chrXII:2242677	418642394	14	0	chrXIV:14049917	252841090
12	4.39	chrUn:26305459	244222991	14	3.337	chrUn:21213332	120258571
12	4.88	chrXII:16877465	418642413	14	6.577	chrXIV:11054767	120258517
12	5.223	chrXII:3026329	418642398	14	7.427	chrXIV:9742642	418642458
12	5.738	chrXII:18221941	244222899	14	9.222	chrXIV:6992838	418642456
12	6.258	chrXII:4123972	418642400	14	9.409	chrXIV:15137805	418642462
12	6.422	chrUn:30606854	244222997	14	9.506	chrXIV:6641188	418642455
12	7.731	chrUn:38378170	120258576	14	9.686	chrXIV:7313827	418642457
12	9.452	chrXII:3810254	418642399	14	11.233	chrXIV:15033103	418642461
12	10.731	chrXII:6012527	418642404	14	13.935	chrXIV:3414352	120258514
12	10.731	chrXII:5828898	418642403	14	14.748	chrXIV:3598443	418642452
12	10.863	chrXII:5521301	418642402	14	15.715	chrXIV:3534175	120258515
12	11.573	chrXII:6399147	252841133	14	22.579	chrXIV:2084777	418642446
12	11.61	chrXII:6924609	418642405	14	22.648	chrXIV:1798136	418642443
12	11.639	chrXII:6745006	244222892	14	24.911	chrXIV:1713227	120258513
12	11.825	chrXII:6913126	120258500	14	27.904	chrXIV:1641269	418642442
12	12.164	chrXII:7504339	418642406	14	28.549	chrXIV:1442872	120258512
12	13.016	chrXII:16454328	418642411	14	30.976	chrXIV:1383447	244222908
12	13.016	chrXII:1589655	120258497	14	32.066	chrXIV:1311694	418642441
12	13.016	chrXII:2157795	418642393	14	34.828	chrXIV:1087388	418642439
12	13.016	chrXII:15046849	418642410	14	36.498	chrXIV:800076	418642438
12	13.24	chrXII:11472159	418642407	14	38.817	chrXIV:721170	244222907
12	13.498	chrXII:13045611	244222894	14	41.408	chrXIV:451065	120258511
12	14.199	chrXII:14223760	244222895	14	41.654	chrXIV:348659	418642435
12	15.462	chrXII:1483544	244222889	14	43.257	chrUn:35285565	418642649
12	20.999	chrXII:880748	418642389	14	48.931	chrUn:36334731	244223000
12	25.007	chrXII:548804	252841119	15	0	chrXV:13047331	418642481
13	0	chrXIII:18470329	252841124	15	0.602	chrXV:12281774	418642480
13	8.132	chrXIII:17392141	120258510	15	3.131	chrXV:6446874	418642477
13	8.48	chrXIII:17249562	418642432	15	6.668	chrXV:2507809	244222914
13	16.245	chrXIII:8085851	418642430	15	7.328	chrXV:3703641	418642475
13	17.207	chrXIII:4401535	418642425	15	9.649	chrXV:2169610	244222912
13	18.717	chrXIII:4868788	418642428	15	12.33	chrXV:1902350	244222911
13	19.246	chrXIII:4621027	418642426	15	13.521	chrXV:1800560	418642468
13	20.037	chrXIII:2969182	418642424	15	19.973	chrXV:414608	120258519
13	20.712	chrXIII:3109522	120258506	15	20.789	chrXV:505537	418642465

Linkage Group	Map Position (cM)	Marker name (chromosome: position)	NCBI submitted SNP ID numbers (ss#)	Linkage Group	Map Position (cM)	Marker name (chromosome: position)	NCBI submitted SNP ID numbers (ss#)
15	26.144	chrXV:979445	418642466	17	27.817	chrXVII:12022612	120258536
15	28.551	chrXV:215800	418642464	17	29.614	chrXVII:1264852	418642508
15	29.834	chrXV:11818	418642463	17	30.48	chrXVII:12528572	252841151
16	0	chrXVI:2764206	120258523	17	34.32	chrXVII:769372	244222939
16	0.74	chrXVI:2650854	244222922	17	34.515	chrXVII:645029	418642506
16	1.67	chrXVI:2392758	244222921	17	41.148	chrXVII:14127979	418642528
16	1.674	chrXVI:2483136	252841051	18	0	chrXVIII:15478444	120258549
16	3.48	chrXVI:3206769	244222923	18	19.259	chrXVIII:13773116	418642545
16	5.889	chrXVI:13588796	244222930	18	23.155	chrXVIII:13753579	244222958
16	6.329	chrXVI:14093156	244222931	18	24.456	chrXVIII:13193140	244222957
16	7.378	chrXVI:14963879	244222933	18	24.798	chrXVIII:12818939	120258545
16	9.956	chrXVI:12996432	244222929	18	26.138	chrXVIII:12273872	252841150
16	9.978	chrXVI:5562355	244222924	18	26.312	chrXVIII:11896010	244222954
16	10.609	chrXVI:6415385	418642487	18	27.539	chrXVIII:11765327	120258543
16	11.281	chrXVI:9428786	244222926	18	27.765	chrXVIII:11702469	418642543
16	12.994	chrXVI:13148331	418642492	18	27.765	chrXVIII:11641450	244222953
16	14.134	chrXVI:14283264	244222932	18	28.292	chrXVIII:11504306	418642542
16	16.126	chrXVI:15039503	418642494	18	29.831	chrXVIII:13352631	120258546
16	16.894	chrXVI:16058672	252841101	18	31.323	chrXVIII:5765162	120258540
16	19.173	chrXVI:17471373	418642502	18	31.327	chrXVIII:4836241	120258539
16	19.623	chrXVI:18106789	120258529	18	34.367	chrXVIII:3137228	
16	21.464	chrXVI:17895677	244222938	18	41.287	chrXVIII:1211531	418642530
16	22.417	chrXVI:17405918	418642501	19	0	chrXIX:8190806	120258554
16	24.961	chrXVI:17236926	244222936	19	0.054	chrXIX:14650559	418641975
16	31.626	chrXVI:16673569	120258528	19	0.099	chrXIX:18045399	120258558
16	38.499	chrUn:37016121	418642651	19	0.102	CH213.119K16:14070	418641977
16	43.334	chrUn:26389255	244222992	19	0.102	CH213.21C23:188808	418641953
17	0	chrXVII:1733515	418642509	19	0.434	chrXIX:3737235	418641965
17	8.642	chrXVII:12666712	418642526	19	0.554	chrXIX:18043409	252841059
17	10.714	chrXVII:2664810	244222940	19	15.488	chrXIX:1546489	418641958
17	11.707	chrXVII:2626658	418642511	19	16.847	chrXIX:1472847	120258551
17	13.517	chrXVII:2872553	418642512	19	30.53	chrXIX:897343	418641956
17	18.03	chrXVII:3906379	244222942	20	0	chrXX:12622695	244222966
17	18.272	chrXVII:10329401	418642524	20	0	chrXX:12810044	252841048
17	18.272	chrXVII:9697366	244222947	20	0.278	chrXX:14562943	418642569
17	19.473	chrXVII:3843835	120258534	20	0.588	chrXX:14462157	244222968
17	20.238	chrXVII:4909843	244222944	20	0.724	chrXX:14859034	418642571
17	20.598	chrUn:2474754	418642603	20	1.646	chrXX:5734841	418642558
17	20.713	chrUn:2776586	120258568	20	3.948	chrXX:15996390	418642573
17	20.713	chrUn:2632376	252841074	20	8.045	chrXX:16253512	252841060
17	21.65	chrXVII:2999556	418642513	20	16.409	chrXX:2080510	418642553
17	23.546	chrXVII:9881295	418642523	20	22.695	chrUn:30545876	120258573

Linkage Group	Map Position (cM)	Marker name (chromosome: position)	NCBI submitted SNP ID numbers (ss#)	Linkage Group	Map Position (cM)	Marker name (chromosome: position)	NCBI submitted SNP ID numbers (ss#)
21	0	chrUn:31339987	244222998				
21	2.453	chrUn:28158103	418642634				
21	24.879	chrXXI:11060209	120258566				
21	26.406	chrXXI:10969152	244222981				
21	31.416	chrUn:23042966	418642626				
21	40.24	chrXXI:9820534	418642589				
21	42.589	chrXXI:7002178	244222977				
21	42.816	chrXXI:5737465	244222973				
21	44.076	chrXXI:3082227	418642585				
21	44.583	chrUn:6720054	244222987				

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

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 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	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)

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

Table S6 QTL effects of candidate QTL

(Starts on next page) QTL effect was considered 'parallel' when either the best model of the QTL effect was 'same effect', or when the best model of QTL effect was 'different effect' but the direction of additive effects were 'same'. QTL effect was considered only in a 'single lake' when the best model of the QTL effect was either 'effect in Paxton only' or 'effect in Priest only'. QTL effect was considered 'opposite' when the best model of QTL effect was 'different effect' and the direction of additive effects were 'opposite'. The second best model of QTL effect and the delta AICc between it and the best model is also shown. When the delta AICc was less than two and the 2nd best model called for a different QTL effect category than the best model did, we dropped the QTL from any analysis in which QTL effect category was a variable study (indicated by 'NA' in the "QTL effect based on AICc model selection" column). PVE for each QTL in each lake was determined using 'single QTL, single lake linear models'. The 'Priest Entropy' and 'Paxton Entropy' columns show the entropy values (an index of genotype information content, where lower values indicate greater information content), in each lake's cross at the QTL's peak marker.

Trait	Scan QTL was detected in	Linkage group	Peak Marker Position (cM)	Direction of additive effects	'QTL Effect' based on AICc model selection	Best model of QTL effect	2nd best model of QTL effect	Delta AICc	PVE in Priest	PVE in Paxton	Priest entropy	Paxton entropy
plate count	combined	2	24	same	Parallel	same effect	different effect	2.21	4.9	1.32	0.28	0.27
plate count	combined	7	33.93	same	Parallel	different effect	same effect	0.94	9.1	12.09	0.04	0.03
plate count	combined	16	9.98	opposite	Opposite	different effect	effect in Priest only	2.03	6.06	0.73	0.06	0.17
long gill raker count	combined	7	35.12	same	Parallel	same effect	different effect	2.26	6.51	6.3	0.01	0.08
long gill raker count	combined	3	36	same	NA	effect in Paxton only	different effect	1.12	1.08	5	0.14	0.14
short gill raker count	combined	1	21.16	same	Parallel	same effect	different effect	2.72	4.13	4.32	0.07	0.17
short gill raker count	combined	7	34.99	same	Parallel	same effect	different effect	0.68	1.67	3.97	0	0.08
y1	combined	8	18	same	Single lake	effect in Paxton only	same effect	4.14	1.58	4.18	0.09	0.12
x2	combined	4	23.78	same	Parallel	same effect	different effect	2.99	1.48	1.13	0.08	0.21
x2	Paxton	7	0	same	NA	effect in Paxton only	same effect	0.58	0.07	2.39	0.71	0.05
x2	Priest	14	38.82	opposite	NA	effect in Priest only	different effect	0.39	1.92	0.37	0.08	0.16
y3	combined	4	71.36	opposite	NA	different effect	effect in Priest only	1.38	5.29	0.9	0.06	0.88
y3	combined	7	6	opposite	Single lake	effect in Paxton only	different effect	2.49	0.13	8.86	0.5	0.13
y4	combined	7	34.99	same	Parallel	same effect	different effect	2	1.56	4.08	0	0.08
y5	combined	7	35.45	same	Parallel	same effect	different effect	2.42	4.34	2.51	0	0.12
y5	Paxton	19	2	same	Parallel	same effect	different effect	0.42	0.21	3.63	0.19	0.05
x6	combined	7	34.21	opposite	NA	different effect	effect in Paxton only	0.92	0.68	3.4	0.02	0.05
x6	Priest	4	20.84	same	Parallel	same effect	different effect	1.81	3.09	0.7	0.05	0.2
x6	Priest	13	27.7	same	Single lake	effect in Priest only	same effect	7.08	3.15	0.08	0.1	0.2
y7	combined	7	35.45	same	NA	effect in Priest only	different effect	0.94	5.9	0.52	0	0.12
y7	combined	2	33.63	opposite	Opposite	different effect	effect in Paxton only	5.61	2.41	3.14	0.03	0.04
y7	Priest	9	10	same	Single lake	effect in Priest only	same effect	3.44	4.61	0.59	0.35	0.34
y10	combined	1	19.11	opposite	Opposite	different effect	effect in Priest only	9.03	2.77	1.63	0	0.01
y10	combined	14	12	same	Parallel	same effect	different effect	0.31	1.23	4.22	0.06	0.2
y10	Paxton	4	58	opposite	Single lake	effect in Paxton only	different effect	2.57	0.09	3.76	0.03	0.74
y11	combined	11	28	same	NA	effect in Priest only	different effect	0.57	2.45	0.37	0.13	0.12
y11	combined	1	21.16	opposite	Single lake	effect in Paxton only	different effect	5.1	0.35	3.49	0.07	0.17
y11	combined	4	30	same	Single lake	effect in Paxton only	different effect	2.4	0.38	4.13	0.01	0.24
y12	combined	19	0	same	Single lake	effect in Priest only	different effect	13.99	2.03	3.11	0.22	0.03
y12	combined	13	27.7	same	Parallel	same effect	different effect	3.01	1.96	1.58	0.1	0.2
y12	Paxton	4	28.15	same	Single lake	effect in Paxton only	different effect	2.77	0.55	2.81	0.06	0.19
x13	combined	7	28	opposite	NA	same effect	different effect	0.23	2.3	1.91	0.09	0.22

Trait	Scan QTL was detected in	Linkage group	Peak Marker Position (cM)	Direction of additive effects	'QTL Effect' based on AICc model selection	Best model of QTL effect	2nd best model of QTL effect	Delta AICc	PVE in Priest	PVE in Paxton	Priest entropy	Paxton entropy
x13	combined	1	18.11	same	Parallel	same effect	different effect	0.31	0.57	3.71	0.08	0.17
x16	combined	1	21.75	same	Parallel	same effect	different effect	2.97	6.19	3.32	0.11	0.2
x16	combined	12	5.22	same	Parallel	different effect	same effect	0.87	5.45	1.36	0.06	0.16
x16	Paxton	13	20.04	same	Parallel	different effect	same effect	1.02	0.98	3.39	0.05	0.07
y16	combined	13	28.79	opposite	NA	different effect	same effect	0.83	3.55	2.08	0.16	0.26
y16	Priest	21	42.82	same	NA	same effect	effect in Priest only	0.34	4.22	0.54	0.01	0.87
x17	combined	12	6.42	opposite	Single lake	effect in Priest only	different effect	3.69	6.84	0.01	0.16	0.22
x17	Priest	14	34.83	same	Single lake	effect in Priest only	different effect	2.58	4.52	0.29	0	0.22
x18	combined	7	32.22	opposite	Single lake	effect in Paxton only	different effect	4.02	2.06	3.84	0.06	0.11
y18	combined	11	34	same	Parallel	same effect	different effect	1.45	2.71	1.27	0.03	0.03
y18	Paxton	4	36	opposite	Single lake	effect in Paxton only	different effect	9.02	0.16	2.85	0.02	0.04
x20	combined	4	20	opposite	Single lake	effect in Priest only	effect in Paxton only	3.16	3.58	2.15	0.04	0.19
x20	Paxton	1	25.31	same	NA	different effect	effect in Paxton only	1.62	1.18	3.32	0.13	0.15
x20	Priest	12	4.39	opposite	NA	different effect	effect in Priest only	1.21	4.34	0.75	0.05	0.17
x21	Paxton	1	20	same	Single lake	effect in Paxton only	same effect	2.57	0.25	2.51	0.01	0.01
x22	Paxton	7	33.93	same	NA	different effect	effect in Paxton only	0.06	0.73	3.94	0.04	0.03
y25	combined	12	13.24	same	Parallel	same effect	different effect	2.88	4.71	5.64	0.02	0.04
y26	combined	1	21.75	opposite	Single lake	effect in Priest only	different effect	2.66	4.71	0.07	0.11	0.2
y26	combined	12	13.24	same	Parallel	same effect	different effect	2.36	3.17	2.57	0.02	0.04
y26	combined	19	0.55	same	Parallel	different effect	effect in Priest only	5.04	1.18	2.79	0.19	0.04
y26	Priest	14	36.5	opposite	Single lake	effect in Priest only	different effect	6.62	2.83	0.05	0.07	0.18
y27	combined	12	13.24	same	Parallel	same effect	different effect	2.55	4.16	2.91	0.02	0.04
y27	combined	17	21.65	opposite	Opposite	different effect	effect in Priest only	10.7	4.81	2.95	0.11	0.1
y27	combined	8	19.01	same	Single lake	effect in Paxton only	effect in Priest only	1.4	2.76	2.53	0.01	0.1
centroid	combined	1	24.57	same	NA	effect in Priest only	different effect	1.14	6.4	0.91	0.07	0.13
centroid	Paxton	19	0.1	opposite	NA	effect in Priest only	same effect	1.28	1.24	2.96	0.21	0.02

Table S7 Principal components of parallel traits

32 principal components of 32 parallel traits in Paxton and Priest Lake F₂ individuals. Classification of the species divergence of each principal component (based on model selection technique described in the 'Identifying parallel phenotypic evolution' subsection of the Methods) as parallel, single lake, opposite or not able to be classified (-) is shown under 'PC divergence category'. The number of QTL detected for parallel principal components is also shown. For the effect categories of QTL that underlie parallel principal components that explain up to 90 percent of the cumulative variance, refer to Figure S5.

Principal component	Standard deviation	Percent of variance	Cumulative percent of variance	PC divergence category	Number of QTL detected
Comp.1	2.516	19.8	19.8	Parallel	1
Comp.2	1.939	11.7	31.5	Parallel	0
Comp.3	1.601	8.0	39.5	Parallel	2
Comp.4	1.502	7.0	46.6	Parallel	5
Comp.5	1.303	5.3	51.9	Parallel	1
Comp.6	1.223	4.7	56.6	-	-
Comp.7	1.185	4.4	60.9	Parallel	4
Comp.8	1.125	4.0	64.9	Parallel	3
Comp.9	1.053	3.5	68.4	Parallel	3
Comp.10	0.998	3.1	71.5	Single lake	-
Comp.11	0.992	3.1	74.5	-	-
Comp.12	0.907	2.6	77.1	Parallel	2
Comp.13	0.869	2.4	79.5	-	-
Comp.14	0.849	2.2	81.7	Parallel	0
Comp.15	0.839	2.2	83.9	Parallel	1
Comp.16	0.799	2.0	85.9	Parallel	1
Comp.17	0.745	1.7	87.7	Parallel	0
Comp.18	0.718	1.6	89.3	-	-
Comp.19	0.658	1.4	90.6	Parallel	0
Comp.20	0.639	1.3	91.9	Opposite	-
Comp.21	0.619	1.2	93.1	Parallel	2
Comp.22	0.574	1.0	94.1	-	-
Comp.23	0.543	0.9	95.0	-	-
Comp.24	0.534	0.9	95.9	Single lake	-
Comp.25	0.516	0.8	96.8	Parallel	0
Comp.26	0.474	0.7	97.5	-	-
Comp.27	0.432	0.6	98.0	-	-
Comp.28	0.407	0.5	98.6	-	-
Comp.29	0.388	0.5	99.0	-	-
Comp.30	0.373	0.4	99.5	-	-
Comp.31	0.337	0.4	99.8	Parallel	0
Comp.32	0.235	0.2	100.0	Single lake	-

Table S8 Proportional similarity of QTL use underlying parallel traits

(Starts on next page) For each QTL, 'PVE in Priest' and 'PVE in Paxton' were determined using a 'multiple QTL linear model' containing genotypic effects of each QTL affecting the same trait (as well as family identity and sex as covariates). These models were run for each lake separately. If the QTL genotype (both additive and dominant components) did not show a significant effect when dropped from a 'single lake, single QTL linear model' then it was not entered in the multiple QTL model for that lake. In this case, the PVE column is left blank. In each lake, proportional contributions of QTL to traits were calculated by scaling the PVEs of all QTL affecting the same trait so that they summed to 1. The proportional similarity of a QTL was taken as the overlap in the proportional contributions of that QTL in the two lakes. The 'proportional similarity of QTL use' underlying any given trait is then the sum of the proportional similarities of all QTL affecting that trait.

Trait	QTL	Proportional		Proportional		Proportional Similarity
	(LG # @ position (cM))	PVE in Priest	Contribution in Priest	PVE in Paxton	Contribution in Paxton	
plate count	16@10.0	4.79	0.31			0.00
plate count	2@24.0	3.39	0.22	1.28	0.10	0.10
plate count	7@33.9	7.32	0.47	12.04	0.90	0.47
long gill raker count	7@35.1	6.51	1.00	6.23	0.56	0.56
long gill raker count	3@36.0			4.93	0.44	0.00
short gill raker count	1@21.2	4.13	1.00	4.89	0.52	0.52
short gill raker count	7@35.0			4.54	0.48	0.00
y1	8@18.0	1.58	1.00	4.18	1.00	1.00
x2	14@38.8	1.70	0.57			0.00
x2	4@23.8	1.26	0.43	1.11	0.32	0.32
x2	7@0.0			2.38	0.68	0.00
y3	4@71.4	5.29	1.00			0.00
y3	7@6.0			8.86	1.00	0.00
y4	7@35.0			4.08	1.00	0.00
y5	7@35.5	4.34	1.00	2.44	0.41	0.41
y5	19@2.0			3.57	0.59	0.00
x6	13@27.7	3.11	0.50			0.00
x6	4@20.8	3.06	0.50			0.00
x6	7@34.2			3.40	1.00	0.00
y7	2@33.6	1.43	0.12	3.14	1.00	0.12
y7	7@35.5	5.98	0.49			0.00
y7	9@10.0	4.74	0.39			0.00
y10	1@19.1	2.61	0.71	0.73	0.11	0.11
y10	14@12.0	1.07	0.29	3.51	0.51	0.29
y10	4@58.0			2.68	0.39	0.00
y11	11@28.0	2.45	1.00			0.00
y11	1@21.2			2.60	0.44	0.00
y11	4@30.0			3.24	0.56	0.00
y12	13@27.7	1.54	0.49	1.35	0.19	0.19
y12	19@0.0	1.61	0.51	3.14	0.44	0.44
y12	4@28.1			2.69	0.37	0.00
x13	7@28.0	2.30	1.00	1.31	0.30	0.30
x13	1@18.1			3.11	0.70	0.00
x16	1@21.7	4.53	0.54	2.31	0.37	0.37
x16	12@5.2	3.79	0.46	1.16	0.18	0.18
x16	13@20.0			2.83	0.45	0.00
y16	13@28.8	3.03	0.45	2.08	1.00	0.45
y16	21@42.8	3.70	0.55			0.00
x17	12@6.4	6.00	0.62			0.00

Trait	QTL (LG # @ position (cM))	Proportional		Proportional		Proportional Similarity
		PVE in Priest	Contribution in Priest	PVE in Paxton	Contribution in Paxton	
x17	14@34.8	3.68	0.38			0.00
x18	7@32.2	2.06	1.00	3.84	1.00	1.00
y18	11@34.0	2.71	1.00	0.88	0.26	0.26
y18	4@36.0			2.47	0.74	0.00
x20	12@4.4	4.15	0.55			0.00
x20	4@20.0	3.40	0.45	1.61	0.37	0.37
x20	1@25.3			2.78	0.63	0.00
x21	1@20.0			2.51	1.00	0.00
x22	7@33.9			3.94	1.00	0.00
y25	12@13.2	4.71	1.00	5.64	1.00	1.00
y26	1@21.7	3.02	0.38			0.00
y26	12@13.2	2.07	0.26	3.00	0.48	0.26
y26	14@36.5	1.62	0.20			0.00
y26	19@0.6	1.21	0.15	3.22	0.52	0.15
y27	12@13.2	3.47	0.34	2.87	0.35	0.34
y27	17@21.7	4.36	0.43	3.17	0.38	0.38
y27	8@19.0	2.36	0.23	2.21	0.27	0.23
centroid size	1@24.6	6.40	1.00			0.00
centroid size	19@0.1			2.96	1.00	0.00

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