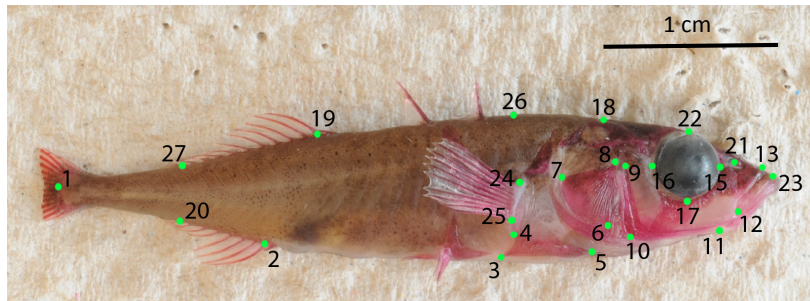# Supplementary Material



**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
- $1^{st}$ dorsal spine presence/absence
- $2^{nd}$ 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 F$_2$s**

The strength of correlation between pairs of parallel traits in Paxton Lake F$_2$s is indicated by both color and elongation of the ellipse. F$_2$ values were corrected for family and sex.
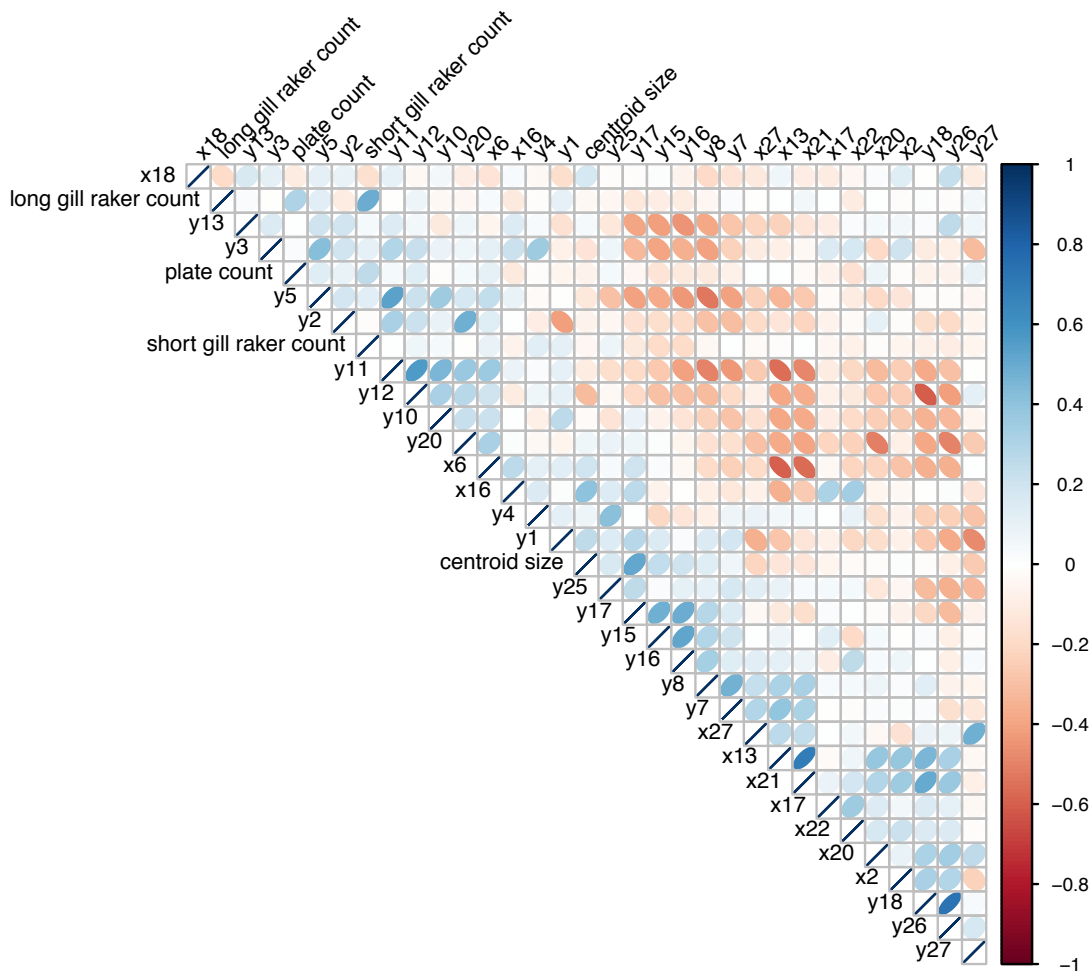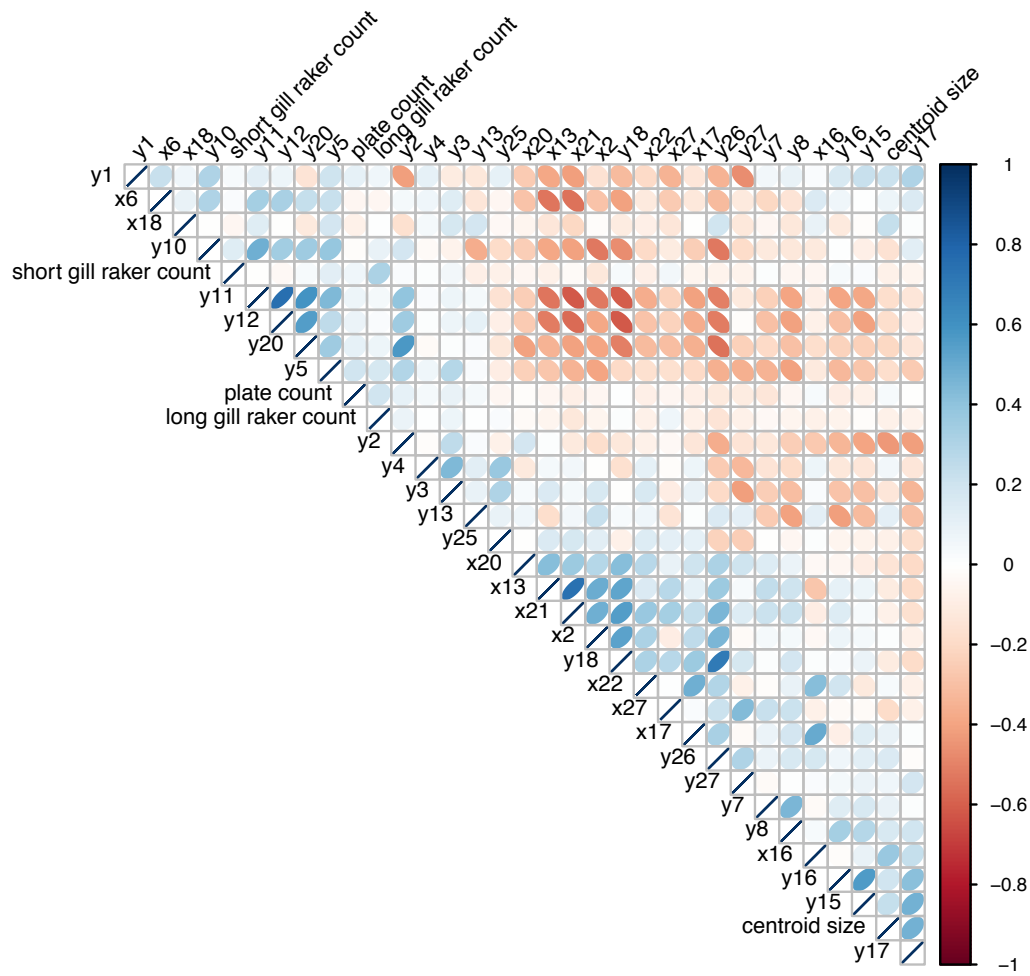
**Figure S3   Correlations among parallel traits in Priest Lake F₂s**

The strength of correlation between pairs of parallel traits in Priest Lake F$_2$s is indicated by both color and elongation of the ellipse. F$_2$ 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.
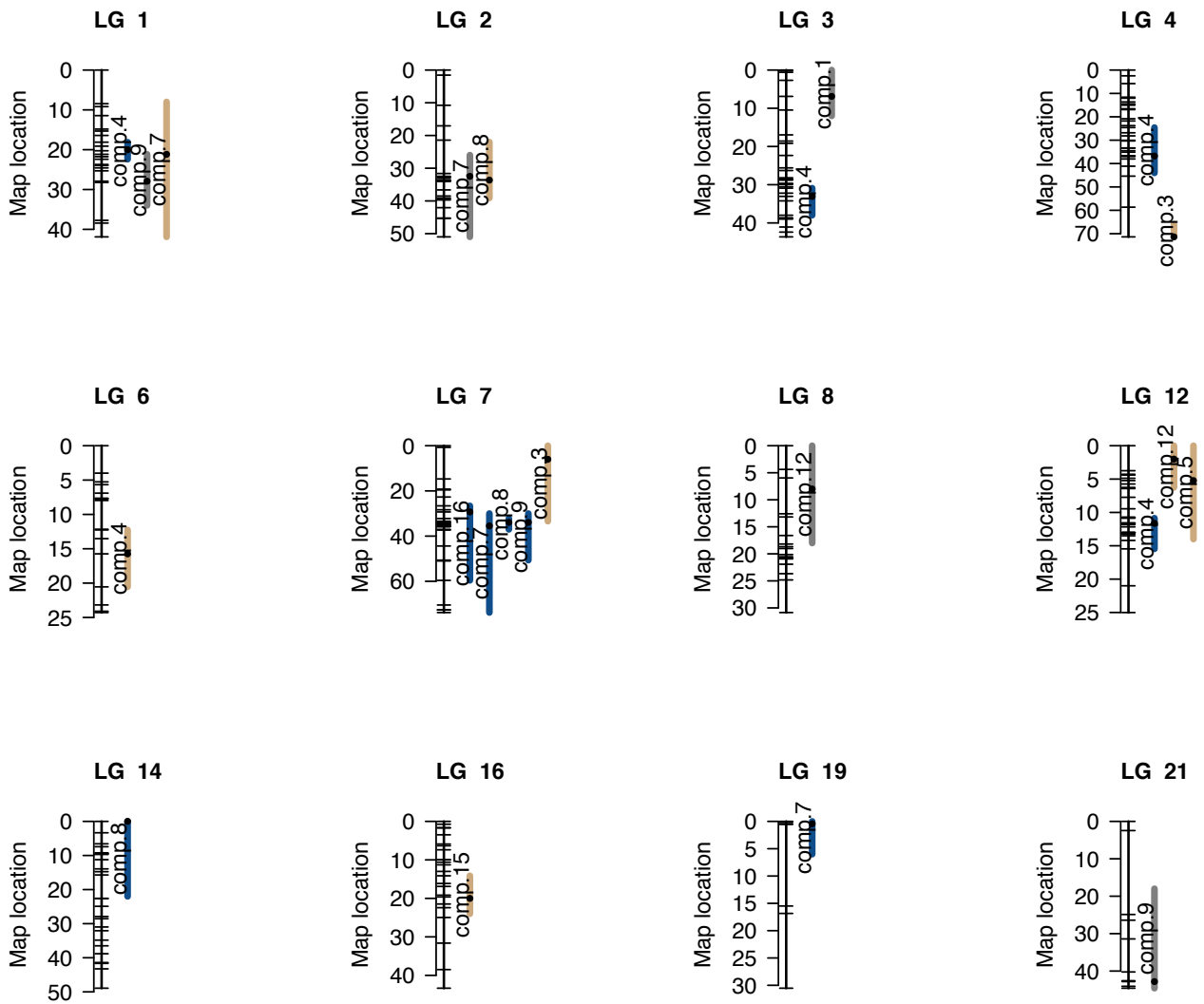
**Figure S5   Map of Principal Component QTL**

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 co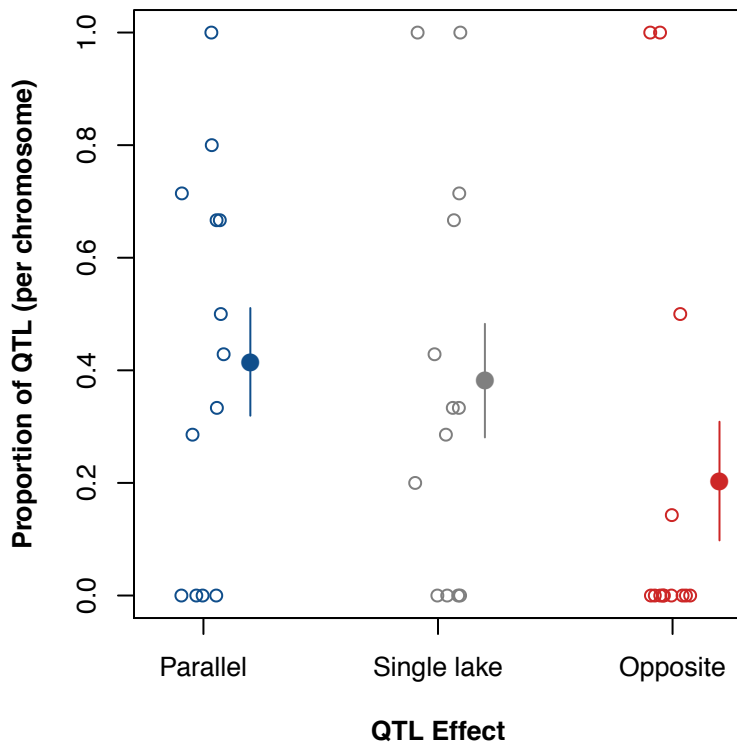mponents accounting for the first 90% of cumulative variance in $F_2$ phenotypes are shown. Linkage groups on which QTL were detected are shown. For each, the positions of SNPs markers in the combined Paxton and Priest linkage map are depicted by tick marks on the left. Colored bars span the 1.5 LOD 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' based on AICc model selection | Direction of divergence | Best model of species effect | 2nd best model of species effect | Delta AICc |
|---|---|---|---|---|---|
| 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' based on AICc model selection | Direction of divergence | Best model of species effect | 2nd best model of species effect | Delta AICc |
|---|---|---|---|---|---|
| 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 |
| 5 | 13.732 | chrV:11509827 | 418642178 | 7 | 19.55 | chrVII:26448674 | 252841125 |
| 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 |
| 5 | 31.771 | chrV:9911653 | 418642165 | 7 | 33.931 | chrVII:16848769 | 418642232 |
| 5 | 32.969 | chrV:9768052 | 252841108 | 7 | 34.008 | chrVII:24203557 | 120258459 |
| 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 |

| 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#) |
|---|---|---|---|---|---|---|---|
| 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 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 | 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 C.I. low (cM) | 1.5 LOD C.I. high (cM) | LOD | p-value | Candidate QTL? |
|---|---|---|---|---|---|---|---|
| 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 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) |

# 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 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 ("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 | 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 C.I. low (cM) | 1.5 LOD C.I. high (cM) | LOD | p-value | Candidate QTL? |
|---|---|---|---|---|---|---|---|
| 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 $F_2$ 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 (LG # @ position (cM)) | PVE in Priest | Proportional Contribution in Priest | PVE in Paxton | Proportional Contribution in Paxton | Proportional Similarity |
|---|---|---|---|---|---|---|
| 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)) | PVE in Priest | Proportional Contribution in Priest | PVE in Paxton | Proportional Contribution in Paxton | Proportional Similarity |
|---|---|---|---|---|---|---|
| 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 |

## References

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