

Supplementary Table 2. Phenotype means of fish with different allele combinations at most closely linked microsatellite

<u>Genotype</u>	<u>Gill raker number</u>		<u>Lateral plate number</u>		<u>Dorsal spine 1 length</u>		<u>Dorsal spine 2 length</u>		<u>Pelvic spine length</u>	
	<u>Mean</u>	<u>N</u>	<u>Mean</u>	<u>N</u>	<u>Mean</u>	<u>N</u>	<u>Mean</u>	<u>N</u>	<u>Mean</u>	<u>N</u>
L ₁ B ₂	15.4 (0.94)	17	8.5 (1.66)	17	1.53 (0.73)	19	2.72 (0.43)	21	3.35 (0.49)	20
B ₁ B ₂	14.3 (1.17)	27	8.6 (1.55)	25	0.49 (0.75)	15	2.59 (0.50)	13	3.41 (0.39)	12
L ₁ B ₃	13.8 (1.20)	17	10.6 (1.62)	23	1.00 (0.91)	25	2.31 (0.46)	24	2.91 (0.49)	21
B ₁ B ₃	13.8 (1.03)	21	8.4 (1.75)	16	0.57 (0.81)	25	2.35 (0.32)	20	2.84 (0.49)	19
L ₁ vs. B ₁	P = 0.0285*		P = 0.0152*		P = 0.0003*		P = 0.7341		P = 0.8859	
B ₂ vs. B ₃	P = 0.0002*		P = 0.0216*		P = 0.1830		P = 0.0009*		P < 0.0001*	
Interaction	P = 0.0213*		P = 0.0020*		P = 0.1024		P = 0.4003		P = 0.5868	
<u>QTL-b</u>										
L ₁ B ₂	14.9 (1.35)	23	10.0 (1.81)	23	1.42 (0.77)	23	2.57 (0.46)	17		
B ₁ B ₂	13.2 (1.26)	18	8.2 (1.01)	19	0.73 (0.93)	22	2.65 (0.42)	28		
L ₁ B ₃	14.4 (1.05)	22	9.6 (2.09)	20	0.97 (0.86)	20	2.22 (0.42)	19		
B ₁ B ₃	14.3 (0.66)	20	8.0 (1.59)	16	0.13 (0.36)	16	2.39 (0.47)	23		
L ₁ vs. B ₁	P < 0.0010*		P < 0.0001*		P < 0.0001*		P = 0.1938			
B ₂ vs. B ₃	P = 0.3999		P = 0.4472		P = 0.0041*		P = 0.0022*			
Interaction	P = 0.0019*		P = 0.7547		P = 0.6621		P = 0.6519			

Mean phenotype, standard deviation (in parenthesis), and sample size (N) of animals having a particular allele combination at the microsatellite marker nearest each QTL. Contribution of within and between species genetic variation to differences between phenotype means was estimated using two-factor ANOVA. The first (between species) factor represented the effect on mean phenotype of alternate alleles inherited from the F1 male parent (L₁ vs. B₁). The second (within species) factor represented the effect of alternate alleles inherited from the benthic female parent (B₂ vs. B₃). P-values for these tests are based on the two-factor model lacking an interaction term. Interaction of within and between species effects was subsequently tested by determining whether inclusion of the interaction term significantly improved the fit to the data. *P<0.05.

Supplementary Table 3. Estimated effect of increased number of limnetic alleles across pairs of QTLs.

<u>Genotype</u>		<u>Gill raker number</u>		<u>Lateral plate number</u>		<u>Dorsal spine 1 length</u>		<u>Dorsal spine 2 length</u>	
<u>QTL-a</u>	<u>QTL-b</u>	<u>Mean</u>	<u>N</u>	<u>Mean</u>	<u>N</u>	<u>Mean</u>	<u>N</u>	<u>Mean</u>	<u>N</u>
B ₁ B ₂	B ₁ B ₂	13.6 (1.39)	7	8.2 (0.84)	5	0.31 (0.62)	4	2.66 (0.85)	4
B ₁ B ₂	B ₁ B ₃	14.4 (0.79)	7	7.9 (1.36)	8	0.00 (0.00)	4	3.12	1
B ₁ B ₃	B ₁ B ₂	13.2 (0.45)	5	7.3 (0.96)	4	0.00 (0.00)	6	2.26 (0.27)	5
B ₁ B ₃	B ₁ B ₃	14.0 (0.63)	6	8.0 (0.00)	3	0.18 (0.43)	6	2.43 (0.28)	8
0 limnetic alleles		13.8 (0.99)	25	7.9 (1.04)	20	0.12 (0.36)	20	2.47 (0.47)	18
L ₁ B ₂	B ₁ B ₂		0	8.6 (1.13)	7	1.52 (0.93)	5	2.53 (0.39)	7
L ₁ B ₂	B ₁ B ₃	14.8 (0.50)	4	7.7 (1.53)	3	0.00	1	2.92 (0.54)	8
L ₁ B ₃	B ₁ B ₂	13.2 (1.48)	5	8.5 (0.71)	2	1.11 (1.07)	5	2.32 (0.27)	5
L ₁ B ₃	B ₁ B ₃	14.0 (0.00)	3	12.0	1	0.26 (0.51)	4	2.53 (0.32)	7
B ₁ B ₂	L ₁ B ₂	15.0 (1.41)	6	9.1 (1.86)	7	1.64 (0.65)	2	2.40 (0.18)	5
B ₁ B ₃	L ₁ B ₂	13.0 (1.00)	3	9.0 (2.65)	3	1.37 (0.91)	5	2.30 (0.41)	5
B ₁ B ₂	L ₁ B ₃	14.3 (0.82)	6	9.6 (1.52)	5	0.39 (0.68)	3	2.86	1
B ₁ B ₃	L ₁ B ₃	14.7 (1.21)	6	9.3 (2.50)	4	0.86 (0.91)	6	2.35 (0.58)	2
1 limnetic allele		14.2 (1.23)	33	9.0 (1.74)	32	1.00 (0.91)	31	2.53 (0.42)	40
L ₁ B ₂	L ₁ B ₂	15.7 (1.11)	9	11.0 (1.00)	3	1.80 (0.24)	8	2.82 (0.11)	2
L ₁ B ₂	L ₁ B ₃	15.3 (0.58)	3	7.0 (0.00)	2	1.76 (0.36)	3	2.61 (0.32)	4
L ₁ B ₃	L ₁ B ₂	14.8 (0.50)	4	10.6 (1.51)	10	1.20 (0.91)	6	1.80 (0.29)	4
L ₁ B ₃	L ₁ B ₃	13.8 (1.26)	4	11.2 (1.72)	6	0.95 (0.81)	6	2.48 (0.61)	6
2 limnetic alleles		15.1 (1.19)	20	10.5 (1.81)	21	1.42 (0.74)	23	2.39 (0.54)	16
		P < 0.0001*		P < 0.0001*		P < 0.0001*		P = 0.6083	

Phenotype means, standard deviations (in parentheses) and sample size of animals having 0, 1 or 2 limnetic alleles at the microsatellite markers nearest each of the two detected QTLs affecting each trait. P-values indicate significance of the relationship between number of limnetic alleles and phenotype, tested using linear regression. P-values were similar when categories of individuals having 0, 1, or 2 limnetic alleles were compared using single-factor ANOVA instead. Pelvic spine length is not included because only a single QTL was detected. *P<0.05.