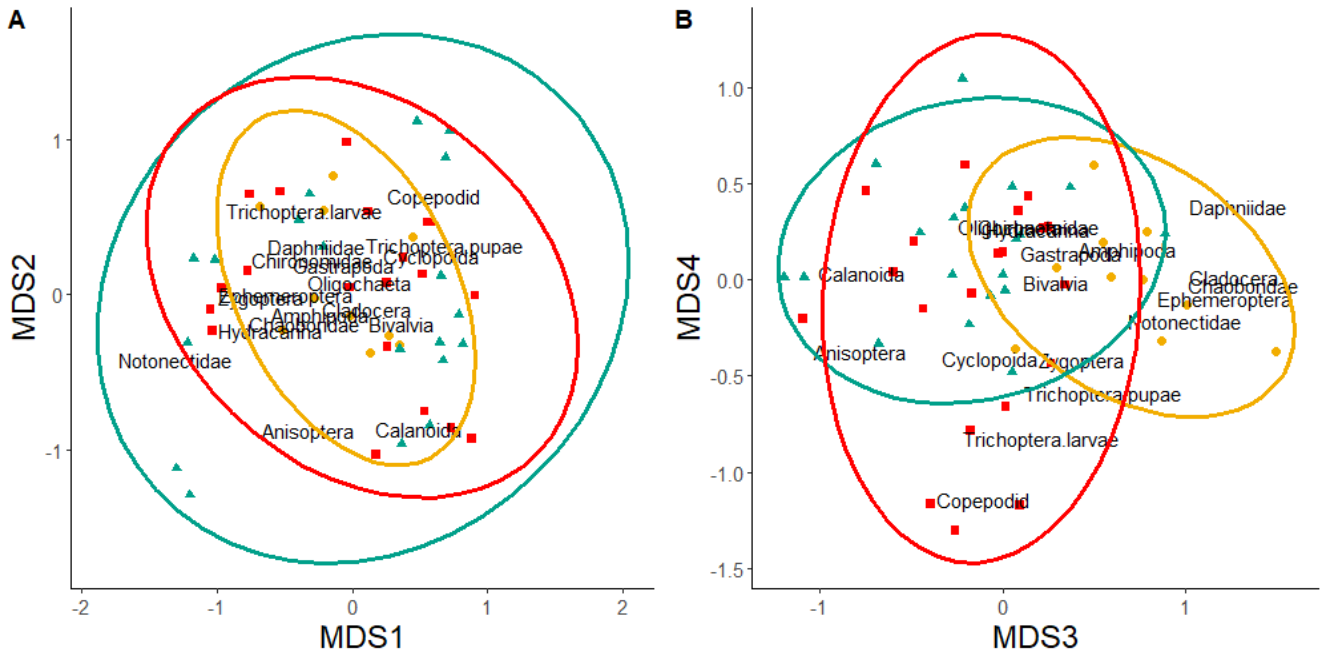1 **Supplementary Figures**

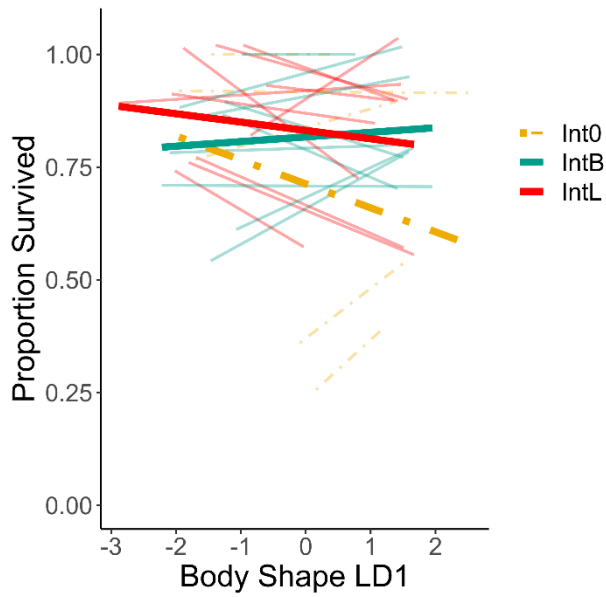2

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4

5 *Fig. S1*. NMDS of invertebrate community composition. Each point represents one mesocosm, with

6 colour indicating treatment (Int$_0$ = yellow circle, Int$_B$ = green triangle, Int$_L$ = red square). Ellipses

7 represent a 95% confidence interval for each treatment. Labels indicate the ordination of invertebrate

8 taxa.

9
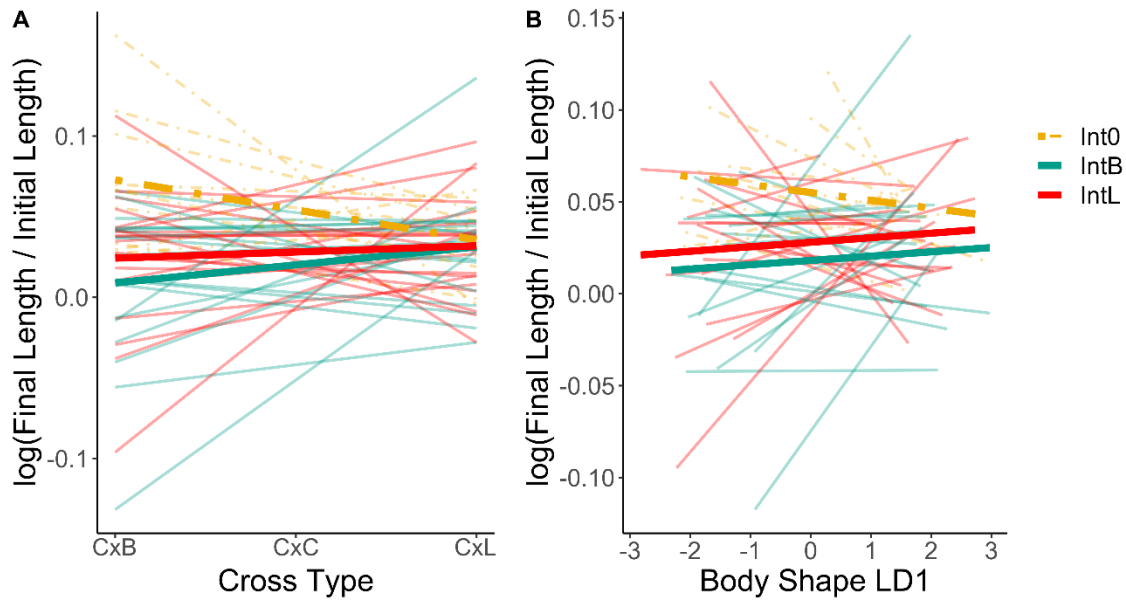
10

Fig. S2. Target population survival in contrasting frequency distributions of phenotypes of

individually-marked fish. Each line represents one mesocosm. More negative LD1 values indicate a

more benthic-like body shape while fish with more positive LD1 values have a more limnetic-like body

shape.

16

17 *Fig. S3.* Target population growth in contrasting frequency distributions of phenotypes of both

18 individually- and batch-marked fish. Each line represents one mesocosm. In (A) cross was converted to

19 a numeric value, with CxB = -1, CxC = 0, and CxL = 1. In (B), more negative LD1 values indicate a

20 more benthic-like body shape while fish with more positive LD1 values have a more limnetic-like body

21 shape.

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23

Fig. S4. Target population growth in contrasting frequency distributions of phenotypes of individually-
marked fish. Each line represents one mesocosm. More negative LD1 values indicate a more benthic-
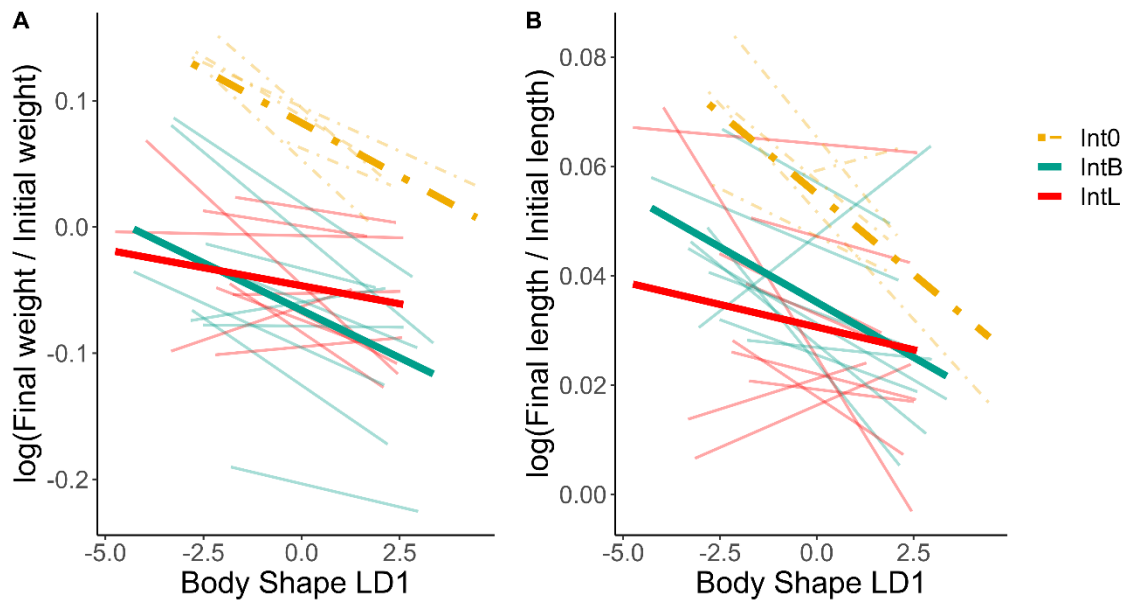like body shape while fish with more positive LD1 values have a more limnetic-like body shape.

Supplementary Tables

Table S1. Tests of the difference between treatment fish presence (Int_L and Int_B) and absence (Int_0). For

dataset = 1, all mesocosms were included. For dataset = 2, we included only mesocosms where all four

treatment stage fish were recovered.

variable	fish	dataset	meso-cosms	t-stat	df	p-value	Cohen's D
log(final length / initial length)	batch-marked and indi-vidually-marked	1	48	2.8	16.62	0.01	0.94
log(final length / initial length)	batch-marked and indi-vidually-marked	2	34	3.15	21.25	<0.01	1.13
log(final length / initial length)	individually-marked only	1	25	4.99	9.05	<0.01	2.19
log(final length / initial length)	individually-marked only	2	18	4.77	11.22	<0.01	2.28
log(final weight / initial weight)	individually-marked only	1	25	8.89	23	<0.01	3.01
log(final weight / initial weight)	individually-marked only	2	18	8.07	15.22	<0.01	3.32
proportion sur-vived	individually-marked only	1	25	-0.9	4.32	0.42	-0.54
proportion sur-vived	individually-marked only	2	18	-1.08	4.53	0.34	-0.65

Table S2. Tests of frequency-dependent selection. For tests where slope predictor is "cross type", CxB

individuals were coded as -1, CxC individuals were coded as 0, and CxL individuals were coded as 1.

For dataset = 1, all mesocosms were included. For dataset = 2, we included only mesocosms where all

four treatment stage fish were recovered.

slope pre-dictor	slope response	fish	dataset	meso-cosms	t-stat	df	p-value	Co-hen's D
body shape (LD1)	log(final length / initial length)	batch-marked and indi-vidually-marked	1	37	1.09	32.15	0.28	0.36
body shape (LD1)	log(final length / initial length)	batch-marked and indi-vidually-marked	2	23	0.52	20.31	0.61	0.22
cross type	log(final length / initial length)	batch-marked and indi-vidually-marked	1	38	0.78	35.87	0.44	0.25
cross type	log(final length / initial length)	batch-marked and indi-vidually-marked	2	24	0.28	21.88	0.78	0.12
body shape (LD1)	log(final length / initial length)	individually-marked only	1	19	-0.33	16.91	0.74	-0.15
body shape (LD1)	log(final length / initial length)	individually-marked only	2	13	-0.5	10.67	0.62	-0.28
body shape (LD1)	log(final weight / initial weight)	individually-marked only	1	19	-0.84	16.95	0.41	-0.38
body shape (LD1)	log(final weight / initial weight)	individually-marked only	2	13	-0.65	10.86	0.53	-0.36

slope predictor	slope response	fish	dataset	mesocosms	t-stat	df	p-value	Cohen's D
cross type	log(final length / initial length)	individually-marked only	1	20	-0.04	14.32	0.97	-0.02
cross type	log(final length / initial length)	individually-marked only	2	13	-0.99	9.84	0.35	-0.54
cross type	log(final weight / initial weight)	individually-marked only	1	20	1.25	16.93	0.23	0.56
cross type	log(final weight / initial weight)	individually-marked only	2	13	0.8	10.97	0.44	0.44
mean LD1 for each cross type	proportion survived	individually-marked only	1	19	1.96	16.89	0.07	0.89
mean LD1 for each cross type	proportion survived	individually-marked only	2	13	1.06	9.94	0.31	0.58
cross type	proportion survived	individually-marked only	1	20	2.34	14.69	0.03	1.05
cross type	proportion survived	individually-marked only	2	13	1.45	8.92	0.18	0.79

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39 Table S3. Tests of differences in slope between fish presence and absences. For tests where slope

40 predictor is "cross type", CxB individuals were coded as -1, CxC individuals were coded as 0, and CxL

41 individuals were coded as 1. For dataset = 1, all mesocosms were included. For dataset = 2, we

42 included only mesocosms where all four treatment stage fish were recovered.

slope predictor	slope response	fish	dataset	mesocosms	t-stat	df	p-value	Cohen's D
body shape (LD1)	log(final length / initial length)	batch-marked and individually-marked	1	47	-2.39	13.50	0.03	-0.87
body shape (LD1)	log(final length / initial length)	batch-marked and individually-marked	2	33	-1.85	16.72	0.08	-0.70
cross type	log(final length / initial length)	batch-marked and individually-marked	1	48	-2.60	15.34	0.02	-0.90
cross type	log(final length / initial length)	batch-marked and individually-marked	2	34	-2.03	20.13	0.056	-0.74
body shape (LD1)	log(final length / initial length)	individually-marked only	1	24	-1.06	5.87	0.33	-0.55
body shape (LD1)	log(final length / initial length)	individually-marked only	2	18	-0.95	7.93	0.37	-0.49
body shape (LD1)	log(final weight / initial weight)	individually-marked only	1	24	-2.63	9.66	0.03	-1.16
body shape (LD1)	log(final weight / initial weight)	individually-marked only	2	18	-2.11	12.82	0.05	-0.98
cross type	log(final length / initial length)	individually-marked only	1	25	-0.54	5.95	0.61	-0.28
cross type	log(final length / initial length)	individually-marked only	2	18	-0.61	7.22	0.56	-0.32
cross type	log(final weight / initial weight)	individually-marked only	1	25	1.06	12.60	0.31	0.43
cross type	log(final weight / initial weight)	individually-marked only	2	18	1.12	15.20	0.28	0.49

mean LD1 for each cross type	proportion survived	individually-marked only	1		24	2.25	5.85	0.07	1.17
mean LD1 for each cross type	proportion survived	individually-marked only	2		18	2.27	6.06	0.06	1.25
cross type	proportion survived	individually-marked only	1		25	2.30	7.81	0.05	1.06
cross type	proportion survived	individually-marked only	2		18	2.18	9.40	0.06	1.08

43

44 Table S4. Population history and number of treatment fish recovered between treatment and target

45 population phases.

Mesocosm	Treatment	Lake	Recovered
T1-3	IntB	Bullocks	4
T3-6	IntB	Bullocks	4
T3-8	IntB	Bullocks	4
T4-7	IntB	Bullocks	4
T5-1	IntB	Bullocks	4
T6-3	IntB	Bullocks	4
T1-7	IntB	Bullocks	3
T2-8	IntB	Bullocks	3
T4-8	IntB	Bullocks	2
T4-5	IntB	Bullocks	1
T1-2	IntB	Hoggan	4
T4-3	IntB	Hoggan	4
T4-6	IntB	Hoggan	4
T4-9	IntB	Hoggan	4
T5-2	IntB	Hoggan	4
T5-4	IntB	Hoggan	4
T1-5	IntB	Hoggan	3
T2-4	IntB	Hoggan	0
T2-5	IntB	Hoggan	0
T6-1	IntB	Hoggan	0
T2-7	IntL	Ambrose	4
T4-2	IntL	Ambrose	4
T5-9	IntL	Ambrose	4
T6-2	IntL	Ambrose	2
T2-2	IntL	Garden Bay	4
T1-4	IntL	Little Quarry	4
T5-7	IntL	Little Quarry	4
T2-10	IntL	Little Quarry	3
T4-1	IntL	Little Quarry	3

T2-1	IntL	North	4
T3-4	IntL	North	4
T5-8	IntL	North	4
T2-3	IntL	North	3
T2-9	IntL	North	3
T3-9	IntL	Paq	4
T4-4	IntL	Paq	4
T1-9	IntL	Paq	3
T1-6	IntL	Paq	2
T3-5	IntL	Priest	4
T3-7	IntL	Priest	4