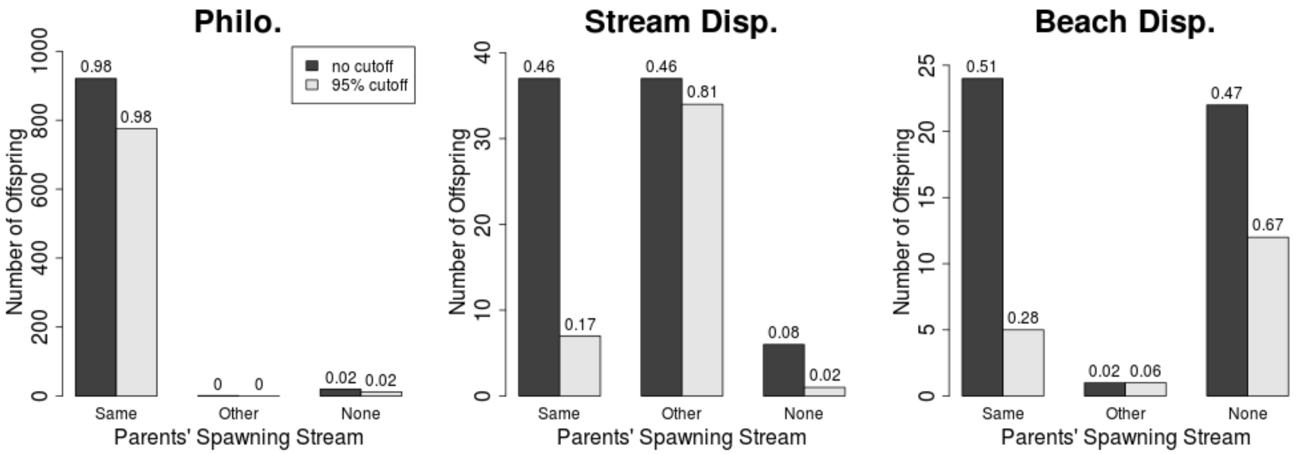
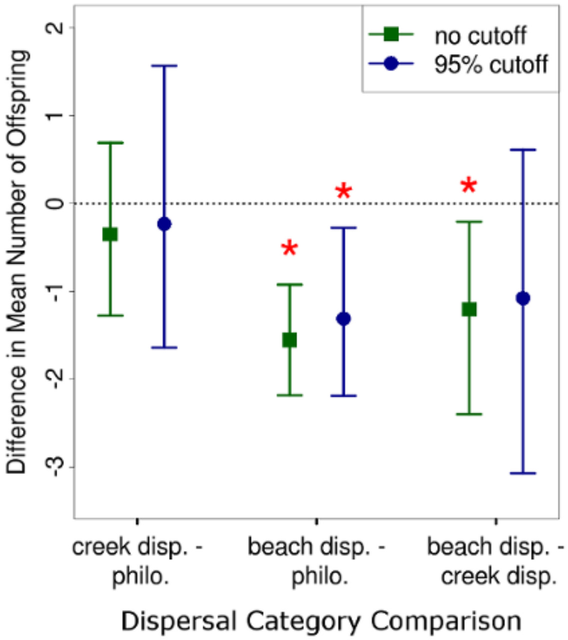
Supplementary Figure S1 | Verification of population assignment by parentage.



Bar height indicates the number of offspring with parents from the same creek in which the offspring were observed (true philopatric individuals), with parents from the other creek (true stream-to-stream dispersers), or with no parent assigned (either true immigrants from the beach population or individuals with neither stream-spawning parent sampled). Numbers above the bars indicate relative proportions. Distributions are plotted for individuals in each assigned disperal category ("Philo." = philopatric individuals, "Stream Disp." = between-stream dispersers, and "Beach Disp." = beach-to-stream dispersers).

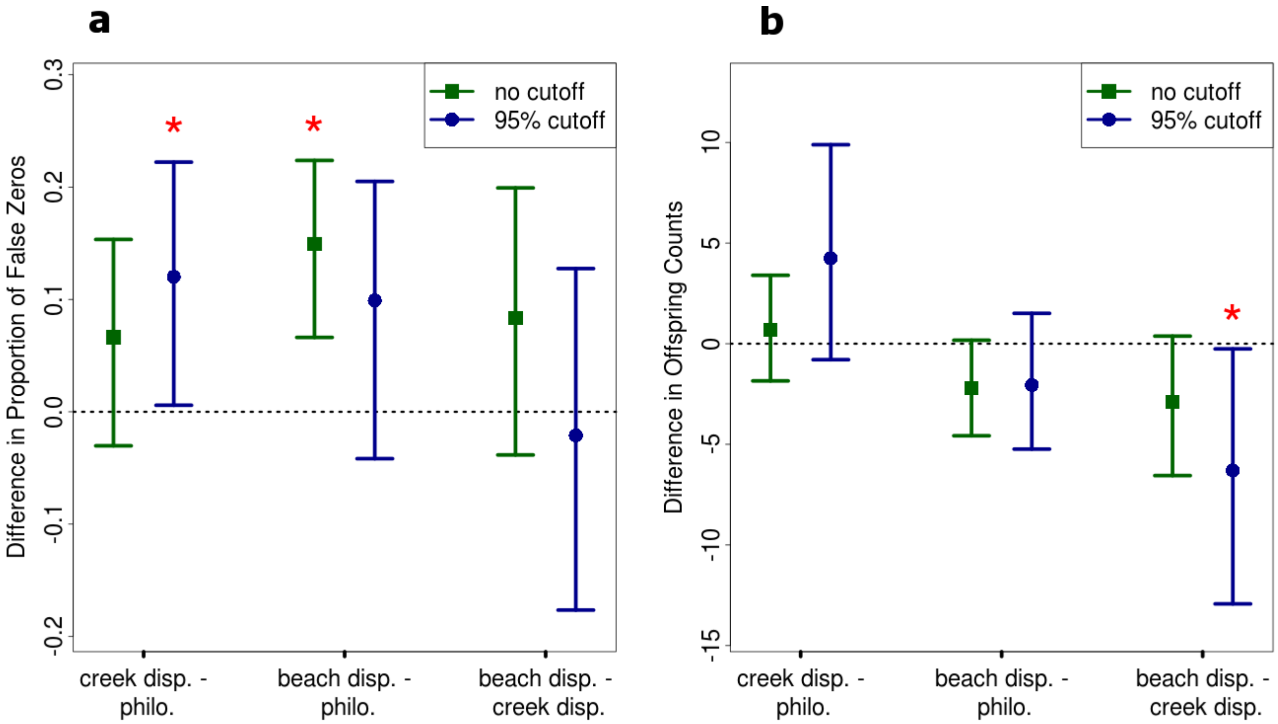
Supplementary Figure S2 | Difference in mean reproductive success of disperser categories with and without assignment cutoff.



Values represent the model-predicted effect of dispersal category on number of offspring after accounting for differences in reproductive success between sexes, spawning streams, and spawning years. Error bars indicate 95% confidence intervals.

* indicates a difference that is statistically significant after bootstrapping (95% CI does not include zero).

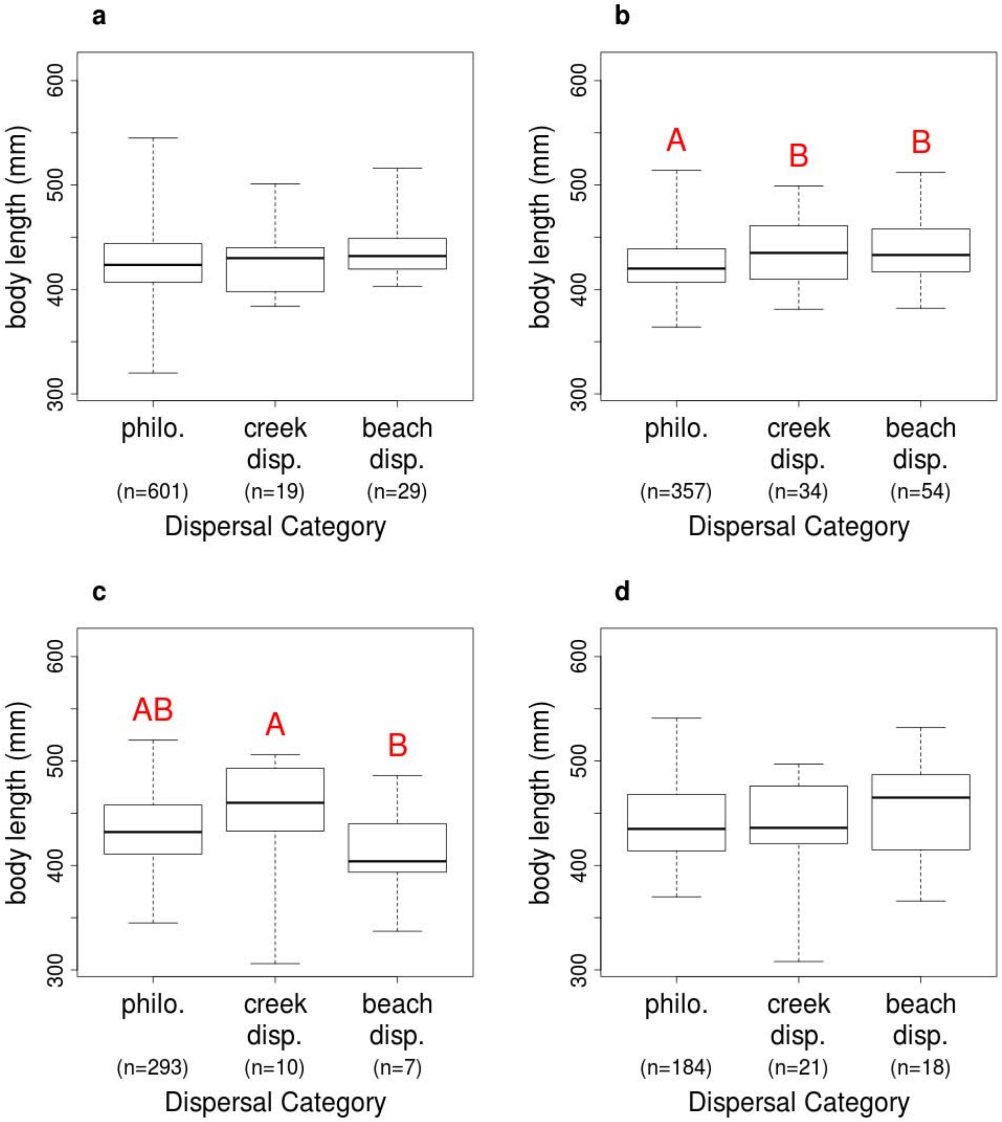
Supplementary Figure S3 | Differences in mean reproductive success between diseperser categories – zeros and counts.



a, Differences in estimated proportions of individuals producing zero offspring from the zero inflation portion of the ZINB model ("false zeros"). **b**, Differences in estimated mean offspring counts from the negative binomial distribution in the ZINB model ("counts"). Values represent the model-predicted effect of dispersal category on reproductive success after accounting for differences in reproductive success between sexes, spawning streams, and spawning years. Error bars indicate 95% confidence intervals.

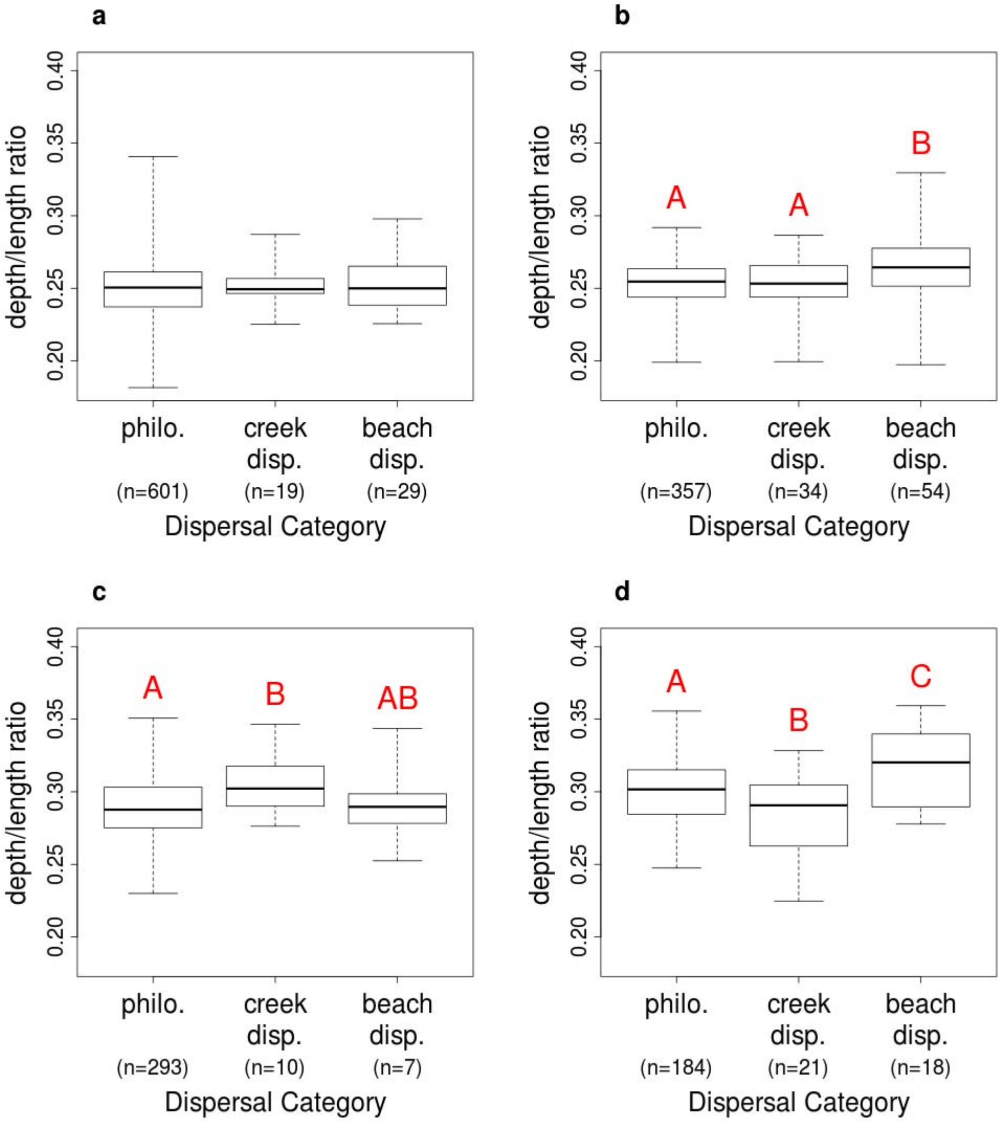
* indicates a difference that is statistically significant after bootstrapping (95% CI does not include zero).

Supplementary Figure S4 | Body length distributions by dispersal category.



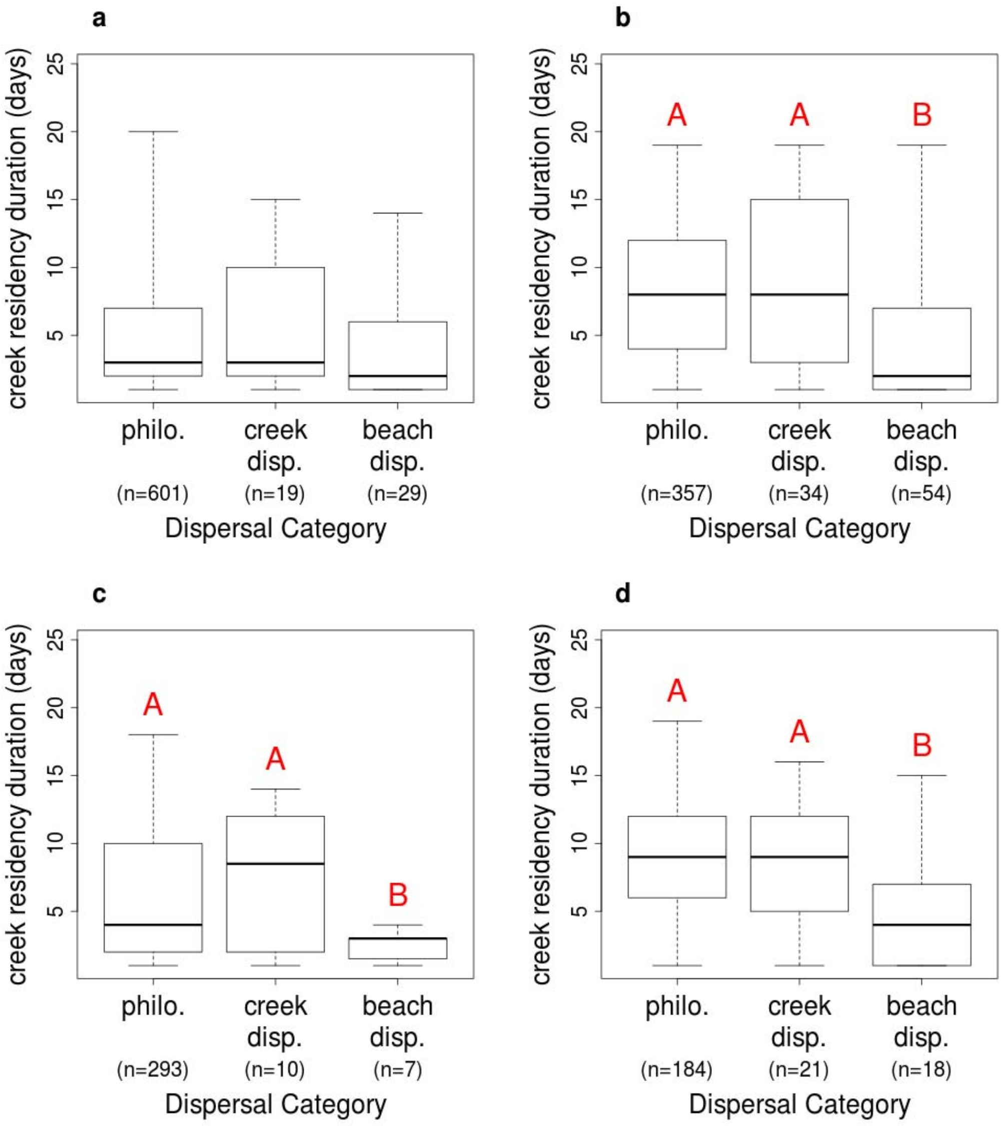
a, A Creek females. **b**, C Creek females. **c**, A Creek males. **d**, C Creek males. “Philo.” = philopatric individuals, “Stream Disp.” = between-stream dispersers, and “Beach Disp.” = beach-to-stream dispersers. Boxplots show the median (dark horizontal line), 25% and 75% quartiles (the box) and the entire range (the whiskers). Letters indicate significantly different groups based on generalized linear models assuming a gamma distribution.

Supplementary Figure S5 | Body shape distributions by dispersal category.



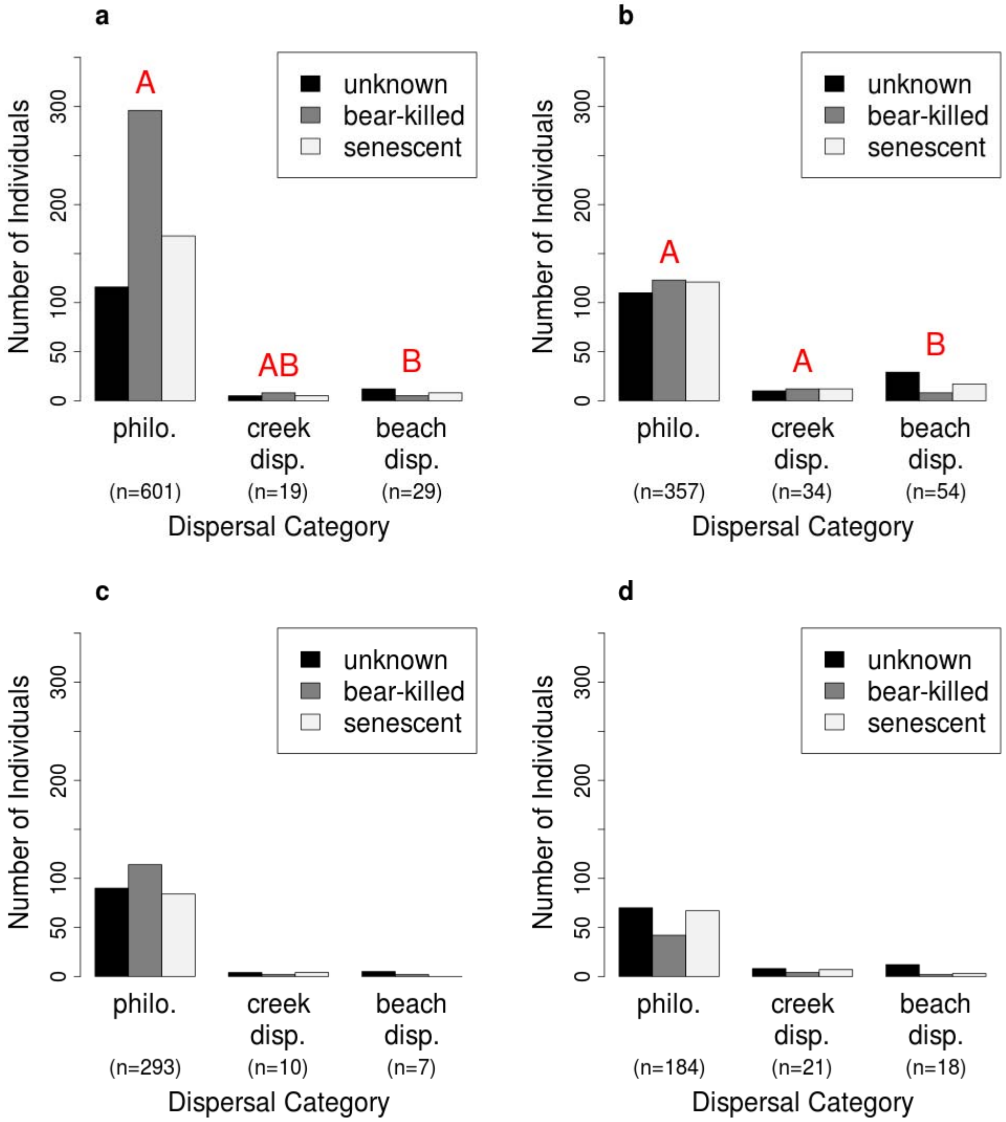
a, A Creek females. **b**, C Creek females. **c**, A Creek males. **d**, C Creek males. "Philo." = philopatric individuals, "Stream Disp." = between-stream dispersers, and "Beach Disp." = beach-to-stream dispersers. Boxplots show the median (dark horizontal line), 25% and 75% quartiles (the box) and the entire range (the whiskers). Letters indicate significantly different groups based on generalized linear models assuming a gamma distribution.

Supplementary Figure S6 | In-creek residency period distributions by dispersal category.



a, A Creek females. **b**, C Creek females. **c**, A Creek males. **d**, C Creek males. "Philo." = philopatric individuals, "Stream Disp." = between-stream dispersers, and "Beach Disp." = beach-to-stream dispersers. Boxplots show the median (dark horizontal line), 25% and 75% quartiles (the box) and the entire range (the whiskers). Letters indicate significantly different groups based on generalized linear models assuming a gamma distribution.

Supplementary Figure S7 | Death fates by dispersal category.



a, A Creek females. **b**, C Creek females. **c**, A Creek males. **d**, C Creek males. “Philo.” = philopatric individuals, “Stream Disp.” = between-stream dispersers, and “Beach Disp.” = beach-to-stream dispersers. Letters indicate significantly different distributions (Fisher’s exact tests).

Supplementary Table S1 | Microsatellite data.

Locus	Conc. (μM)	Panel	T_A (°C)	H_E	# All	F_{IS}	Dropout	False	Null
ONE100a	0.10	1a	63	0.853	23	0.137	0.022	0.000	0.073
ONE102	0.05	3	57.5	0.845	17	-0.013	0.014	0.000	0.007
ONE103	0.08	1b	58.5	0.926	43	0.018	0.007	0.007	0.007
ONE106	0.05	1b	58.5	0.874	32	0.097	0.068	0.021	0.047
ONE108	0.05	3	57.5	0.864	24	0.015	0.002	0.006	0.010
ONE109	0.05	2	60	0.802	16	0.010	0.021	0.003	0.011
ONE110c	0.08	1a	63	0.833	19	0.001	0.004	0.000	0.003
ONE111	0.05	2	60	0.755	30	-0.009	0.021	0.000	0.004
ONE114	0.05	2	60	0.880	25	0.009	0.006	0.000	0.005
ONE115a	0.05	3	57.5	0.896	19	0.179	0.015	0.019	0.101
OTS103	0.05	1a	63	0.859	18	-0.005	0.011	0.004	0.004
Average				0.853	24.2	0.040	0.017	0.005	0.024

Conc., final PCR concentration of forward and reverse primers; T_A, annealing temperature, H_E, expected heterozygosity; # All, total number of observed alleles; F_{IS}, average of F_{IS} estimates from each population and year (FSTAT); Dropout, estimated large allele dropout rate (Pedant); False, estimated false allele rate (Pedant); Null, estimated null allele frequency (ML-NullFreq). Primer references given in ref. 43. Panels 1a and 1b were amplified separately but run together for fragment size analysis.

Supplementary Table S2 | Reproductive success by population and dispersal category.

a

Population	sex	year	*N* philo	*N* creek disp	*N* beach disp	rep. success philo	rep. success creek disp	rep success. beach disp
A Creek	f	2004	342	11	9	0.67	0.73	0.22
A Creek	f	2005	259	8	20	2.59	1.88	1.45
A Creek	m	2004	136	2	3	1.56	0	2.67
A Creek	m	2005	157	8	4	4.38	3.5	0
C Creek	f	2004	232	17	22	1.72	1.35	1.55
C Creek	f	2005	125	17	32	2.56	2.65	0.72
C Creek	m	2004	82	6	7	4.65	4.33	0.43
C Creek	m	2005	102	15	11	3.48	3.33	2

b

Population	sex	year	*N* philo	*N* creek disp	*N* beach disp	rep. success philo	rep. success creek disp	rep success. beach disp
A Creek	f	2004	356	4	2	0.65	1	1
A Creek	f	2005	270	3	14	2.51	2.67	2.07
A Creek	m	2004	139	0	2	1.53	-	4
A Creek	m	2005	167	1	1	4.22	12	0
C Creek	f	2004	250	13	8	1.80	0.31	0.13
C Creek	f	2005	150	9	15	2.35	2.56	0.8
C Creek	m	2004	87	5	3	4.43	4.8	0.33
C Creek	m	2005	107	11	10	3.46	3.18	2.2

a, without 95% assignment cutoff. **b**, with 95% assignment cutoff.

Supplementary Table S3 | Results of assignment simulation.

a

	Assigned to		
True pop.	A Creek	Beach	C Creek
A Creek	0.949	0.019	0.033
	(0.005)	(0.003)	(0.005)
Beach	0.018	0.910	0.072
	(0.006)	(0.015)	(0.013)
C Creek	0.055	0.065	0.880
	(0.006)	(0.010)	(0.010)

b

	Assigned to		
True pop.	A Creek	Beach	C Creek
A Creek	0.949	0.008	0.042
	(0.006)	(0.005)	(0.006)
Beach	0.008	0.928	0.065
	(0.005)	(0.020)	(0.017)
C Creek	0.080	0.045	0.875
	(0.013)	(0.009)	(0.018)

c

	Assigned to		
True pop.	A Creek	Beach	C Creek
A Creek	0.982	0.009	0.009
	(0.003)	(0.002)	(0.003)
Beach	0.010	0.972	0.018
	(0.007)	(0.015)	(0.011)
C Creek	0.026	0.029	0.945
	(0.008)	(0.007)	(0.010)

d

	Assigned to		
True pop.	A Creek	Beach	C Creek
A Creek	0.989	0.002	0.009
	(0.003)	(0.002)	(0.002)
Beach	0.005	0.980	0.015
	(0.004)	(0.009)	(0.009)
C Creek	0.043	0.022	0.935
	(0.008)	(0.007)	(0.009)

a, F0 Cohort (2004 & 2005), no assignment cutoff. **b**, F1 Cohort (2009), no assignment cutoff. **c**, F0 Cohort (2004 & 2005), 95% assignment cutoff. **d**, F1 Cohort (2009), 95% assignment cutoff. Cell values are the means of ten iterations of the simulation, with standard deviations in parentheses. Of the three F1 cohorts, we assessed the assignment accuracy in 2009 because we had both parental cohorts for those offspring, allowing verification of the assignment accuracy with parentage.

Supplementary Methods and Results

Error Checking. Of the 4639 individuals sampled, 4377 were fin-clipped and 4350 were successfully genotyped at eight or more loci. Ninety-two individuals genotyped at fewer than 8 of 11 loci were removed from the dataset because parentage assignments were not reliable in this group. Departures from Hardy-Weinberg equilibrium were found in 100 of the 132 tests, probably because of small population sizes. There was evidence for null alleles at three loci (One100a, One106, and One115a; as found by supplementary ref. 41). Linkage disequilibrium was statistically significant for all pairs of loci within each stream subpopulation, but only 3 of 55 locus pairs were significantly linked in the beach population. Estimated effective population sizes (N_e) were lower for the stream subpopulations than for the beach subpopulation. The ratios of the estimated N_e values to the census sizes (0.13-0.44) are similar to those reported for other salmonid populations[42], suggesting that the observed linkage is caused by small N_e rather than physical linkage between loci.

Pedigree Reconstruction. Colony accounts for the fact that not all parents may be sampled, and we conservatively set the estimated probability of a stream-spawning parent being sampled at 0.7, the proportion of adults sampled in 2008 assigned to parents that were sampled in 2004 in the A Creek population by supplementary ref. 41. A sensitivity analysis of the proportion of sampled parents indicated that this parameter had negligible effects on the parentage assignments.

Of 711 F1 individuals sampled in 2008, 461 (65%) were assigned to a parent pair and 124 (17%) were assigned to a single parent. Of 1167 F1 individuals sampled in 2009, 1031 (88%) were assigned to a parent pair and 89 (8%) were assigned to a single parent. Of 725 F1 individuals sampled in 2010, 179 (25%) were assigned to a parent pair and 58 (8%) were assigned to a single parent, likely because the 4-year-old cohort (whose parents returning in 2006 were not genotyped) dominated in this year.

Identification of Dispersers. The accuracy of the assignment method was assessed by simulation: 10 pools of simulated genotypes of the same size as the original data set were produced and source populations were assigned to each individual using the leave-one-out Bayesian assignment method. Simulated genotypes were produced by combining multilocus haploid "gametes" from random individuals within each population, thereby preserving any linkage disequilibrium present in the data (as in supplementary ref. 43). The assignment algorithm in GeneClass2 produces a probability of each multilocus genotype belonging to each population, which was used as a confidence score for each assignment. The accuracy of the assignment method for simulated individuals from each population was quantified by calculating the proportion of individuals assigned to each of the three populations under two approaches: 1) accepting the most likely population of origin for each individual regardless of statistical confidence and 2) only accepting the most likely population of origin when it was assigned with 95% confidence or greater.

Individuals assigned to all three potential source populations were sampled in both streams in 2004 and 2005, and 83% of assignments were given confidence scores of at least 95% (Supplementary Table S2). In simulations 88-95% of population assignments were correct with no confidence cutoff, and 95-99% were correct with the 95% confidence cutoff (Supplementary Table S3).

Because of the likelihood that philopatric fish would greatly outnumber dispersers, we were concerned that even low misassignment rates of philopatric individuals could produce a large ratio of spurious dispersers to true dispersers. We therefore conducted a second verification of the dispersal category assignment method by comparing the results of population assignments in an offspring cohort with the results of our parentage analysis. Parentage reconstruction is often a much more accurate method to identify dispersers (in the offspring generation) between genetically similar populations than population assignment tests[44], so it offers an excellent empirical assessment of the validity of our dispersal assignments[45]. We compared parentage with dispersal assignments in the 2009 cohort because both 4 and 5 year old fish should have sampled parents (2004 and 2005), and so almost all fish should have parents assigned if they spawned in the streams. We therefore evaluated the accuracy and power of the dispersal categories inferred from the population assignment method by calculating, for each assigned dispersal category, the number of individuals with two parents from the same stream (true philopatric individuals), two parents from the other stream (true stream-to-stream dispersers), or zero parents assigned (either true immigrants from the beach population or offspring with neither stream-spawning parent sampled). Parents were expected to be from the same creek for putative philopatric individuals and from the other stream for putative stream dispersers. No parents were expected to be assigned for putative beach dispersers. Offspring were included only if they were sampled in A or C Creek and had neither or both parents assigned.

Our results indicated that using the 95% assignment cutoff produced dispersal category assignments with a higher proportion of individuals with parents that spawned in the expected locations (Supplementary Figure S1). However, this increased accuracy came at the cost of sample size – many true dispersers were eliminated by the cutoff, particularly those from the beach population. Because we did not expect a bias from misassignments, but only a decrease in power to differentiate reproductive success between dispersal categories, we ran further analyses using the full dataset. Nevertheless, using the assignment cutoff does not substantially affect the results (Supplementary Figure S2).

Differences Between Dispersal Groups in Morphological and Behavioral Traits. The three dispersal groups were compared in the following traits: sex ratio, body length, body shape (body depth / body length ratio[46], residency period on the spawning grounds (total number of days observed in the stream) and death fate (bear-killed, senescent or unknown). The dataset was divided by sex and stream to create four groups, within each of which trait distributions were compared between dispersal categories. Significant differences between dispersal categories in mean trait values were evaluated with Fisher's exact tests for categorical variables and generalized linear models for continuous variables. In the case of the glms, the morphological or behavioral trait of interest was the response variable and dispersal category was the predictor variable. The best distribution for each continuous trait was chosen by evaluating the AIC for models assuming normal, Poisson, and gamma distributions and a simple intercept as the only predictor.

Beach dispersers differed from philopatric individuals in many traits, but stream dispersers were indistinguishable at most traits from philopatric individuals (Supplementary Figures S4-S7). We used the gamma distribution for all traits because it always produced the lowest AIC. The only differences observed between stream dispersers and philopatric individuals were in body shape (C Creek males were deeper than A Creek males) and stream entry date (C Creek fish entered earlier than A Creek fish). Beach dispersers were longer and deeper-bodied, had shorter residency periods in the stream, and entered later than philopatric individuals. Few differences were observed between beach dispersers and philopatric individuals in the number of missing observations, daily movement or stream position. The distributions of death fates were not significantly different between stream dispersers and philopatric individuals, but beach dispersers were less likely to be killed by bears and more likely to have an unknown fate (relative to the proportion dying of senescence) than philopatric individuals (although this difference was only statistically significant for females).

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