4 S1: Supplementary for disappearances models

5 A summary of the raw data (available in S6) can be seen in Table 1.

Table 1: Overview of disappearances of each genotype per year.

Genotype	Year of birth	Total	Disappearances	Percentage
+/+	2004	13	7	0.538
+/+	2006	122	57	0.467
+/+	2007	522	354	0.678
+/+	2008	485	305	0.629
+/+	2009	508	211	0.415
+/+	2010	536	312	0.582
+/+	2011	491	209	0.426
+/t	2004	20	5	0.250
+/t	2006	65	43	0.662
+/t	2007	88	71	0.807
+/t	2008	48	39	0.813
+/t	2009	27	18	0.667
+/t	2010	7	5	0.714
+/t	2011	6	6	1.000

6 Full model comparisons

7 In Table 2, we present an extended version of Table 1 in the paper with all model comparisons

8 we made.

9 Effect estimates

10 We used the function *confint* of the R package *lme4* for parameter confidence intervals in

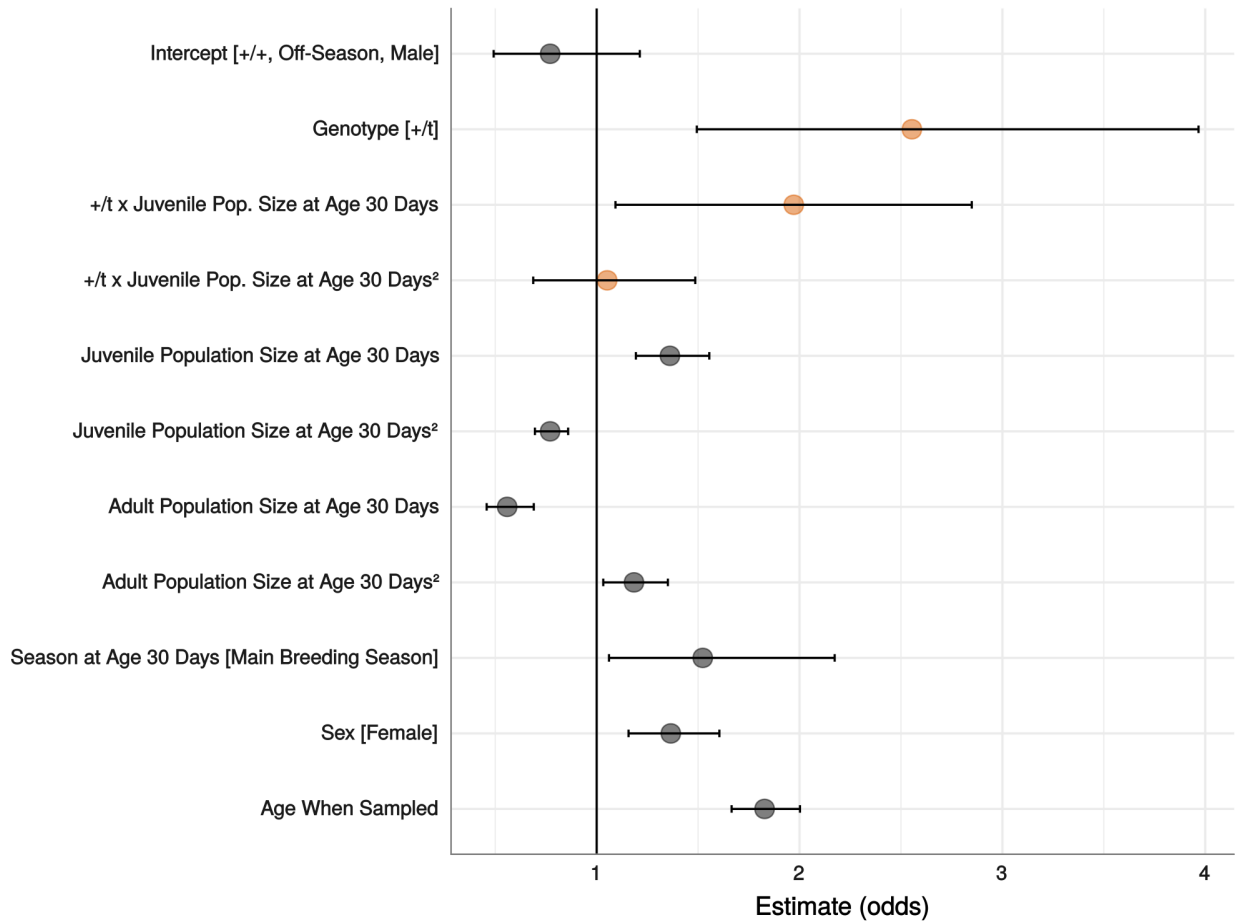11 Figure 1 with the built-in basic bootstrapping method and 1,000 simulations.

Figure 1: Effect estimates in odds with 95% confidence intervals of the most informative juvenile disappearance model ($N = 2938$). The level of a categorical variable for which the effect is calculated is given in square brackets. Continuous variables are scaled. Interactions are indicated with an 'x' between the variables. Quadratic terms are indicated with a superscripted '2'. t main effect and interactions with t are highlighted in orange.

Table 2: Overview of models of juvenile disappearances (DM) out of the study population. The 'x' in model terms indicates interactions. Quadratic terms are indicated with a superscripted '2'. Comparison shows against which other model the model in the row was evaluated. LRT indicates the likelihood ratio test statistic of the observed dataset. The p-value is the fraction of simulated datasets with LRT larger than the observed LRT (see Methods). Runs indicate the absolute values on which the p is based. The ΔAIC is given for comparison with other statistical approaches. The star indicates that these models were restricted by removing individuals without data on pup body mass (see Methods).

Models	Formula	Comparison	LRT	p	Runs	ΔAIC
Null model with covariates	$\sim$ juvenile population size + juvenile population size^2 + adult population size + adult population size^2 + season + sex + age when sampled	NA	NA	NA	NA	NA
DM1	$\sim$ genotype + null model variables	Null model	16.00	0.0003	1/5869	-14.0
DM2	$\sim$ genotype x juv. pop. size + genotype x juv. pop. size^2 + DM1 variables	DM1	11.62	0.005	26/5815	-7.62
DM3	$\sim$ genotype x ad. pop. size + genotype x ad. pop. size^2 + DM1 variables	DM1	4.24	0.10	884/8512	-0.24
DM4	$\sim$ genotype x ad. pop. size + genotype x ad. pop. size^2 + DM2 variables	DM2	0.79	0.70	5402/7681	+3.21
DM5	$\sim$ genotype x season + DM2 variables	DM2	0.03	0.96	7092/7355	+1.97
DM6	$\sim$ genotype x sex + DM2 variables	DM2	1.12	0.41	2807/6912	+0.88
DM7	$\sim$ pup body mass + null model variables	Null model*	0.97	0.38	3160/8359	+1.03
DM8	$\sim$ pup body mass + DM2 variables	DM2*	1.34	0.46	3770/8150	+0.66

Full model outputs

The full model outputs of the juvenile disappearances models (DM) can be found in Table 3. The models labelled DM 1-8 refer to the disappearances models with the respective numbers from Table 2. Null* is the null model without missing pup body masses used to compare disappearances model 7 against. DM D50 uses the same variables as the disappearance model 2, but is based on population size calculations using 50 instead of 30 days until an individual counts as an adult (see Methods section of the manuscript).

Table 3: Full model outputs of the juvenile disappearances models. Quadratic terms are indicated with a superscripted '2'. All numerical variables are scaled and centred. An 'x' indicates an interaction term. The parameter coefficient is provided followed by the standard error in brackets.

	Null	DM1	DM2	DM3	DM4	DM5	DM6	Null*	DM7	DM8	DM D50
Genotype (+/t)		0.660 (0.170)	0.938 (0.245)	0.930 (0.265)	0.833 (0.300)	0.943 (0.247)	1.144 (0.320)			0.922 (0.260)	1.053 (0.259)
Juv. Pop. Size at Age 30 Days	0.325 (0.066)	0.327 (0.066)	0.308 (0.066)	0.331 (0.066)	0.308 (0.066)	0.307 (0.066)	0.308 (0.066)	0.298 (0.066)	0.302 (0.066)	0.291 (0.066)	0.518 (0.066)
Juv. Pop. Size at Age 30 Days²	−0.279 (0.052)	−0.273 (0.052)	−0.261 (0.052)	−0.270 (0.052)	−0.260 (0.052)	−0.260 (0.052)	−0.261 (0.052)	−0.263 (0.053)	−0.262 (0.053)	−0.242 (0.052)	−0.276 (0.051)
Adu. Pop. Size at Age 30 Days	−0.642 (0.120)	−0.568 (0.122)	−0.582 (0.105)	−0.613 (0.120)	−0.581 (0.108)	−0.583 (0.106)	−0.587 (0.107)	−0.799 (0.178)	−0.805 (0.180)	−0.691 (0.152)	−0.543 (0.107)
Adu. Pop. Size at Age 30 Days²	0.175 (0.068)	0.141 (0.070)	0.169 (0.066)	0.188 (0.071)	0.171 (0.069)	0.170 (0.066)	0.172 (0.066)	0.289 (0.088)	0.298 (0.090)	0.265 (0.082)	0.277 (0.069)
Season at Age 30 Days (Off-Season)	−0.432 (0.177)	−0.439 (0.177)	−0.421 (0.176)	−0.430 (0.177)	−0.419 (0.176)	−0.428 (0.181)	−0.419 (0.177)	−0.378 (0.186)	−0.382 (0.186)	−0.398 (0.183)	0.182 (0.143)
Sex (Male)	−0.307 (0.083)	−0.299 (0.083)	−0.312 (0.083)	−0.304 (0.083)	−0.312 (0.083)	−0.312 (0.083)	−0.289 (0.086)	−0.316 (0.083)	−0.316 (0.083)	−0.319 (0.084)	−0.317 (0.083)
Pup Body Mass								−0.043 (0.043)	−0.050 (0.043)		
Age When Sampled	0.600 (0.046)	0.609 (0.046)	0.603 (0.046)	0.607 (0.046)	0.603 (0.046)	0.603 (0.046)	0.602 (0.046)	0.594 (0.047)	0.599 (0.047)	0.602 (0.047)	0.591 (0.046)
+/t x Off-Season						0.103 (0.575)					
+/t x Male							−0.361 (0.343)				
+/t x Juv. Pop. Size			0.679 (0.268)		0.707 (0.298)	0.693 (0.278)	0.711 (0.271)			0.692 (0.280)	0.781 (0.245)
+/t x Juv. Pop. Size²			0.051 (0.199)		0.059 (0.208)	0.031 (0.226)	0.047 (0.199)			0.069 (0.236)	0.021 (0.197)
+/t x Adu. Pop. Size				−0.139 (0.363)	−0.367 (0.413)						
+/t x Adu. Pop. Size²				−0.333 (0.203)	−0.167 (0.230)						
Intercept	0.511 (0.193)	0.470 (0.203)	0.472 (0.172)	0.447 (0.184)	0.471 (0.171)	0.472 (0.171)	0.456 (0.174)	0.393 (0.226)	0.379 (0.231)	0.368 (0.201)	0.250 (0.184)
Observations	2,938	2,938	2,938	2,938	2,938	2,938	2,938	2,898	2,898	2,898	2,938
Log Likelihood	−1,733.969	−1,725.967	−1,720.159	−1,723.848	−1,719.763	−1,720.142	−1,719.597	−1,707.272	−1,706.788	−1,693.613	−1,719.158
Akaike Inf. Crit.	3,485.938	3,471.934	3,464.317	3,471.697	3,467.526	3,466.285	3,465.193	3,432.544	3,433.575	3,413.226	3,462.316
Bayesian Inf. Crit.	3,539.807	3,531.788	3,536.143	3,543.522	3,551.323	3,544.096	3,543.004	3,486.290	3,493.293	3,490.859	3,534.142

S2: Supplementary concerning local adult population sizes as a predictor

We considered further subdividing the adult population size into local adult population sizes in the four sectors. This way, we could control for population size in the sector where each individual was last seen in as a pup, which could be a measure of population density that better reflects what is relevant for the individual. However, we decided against including it in the main paper for three reasons. 1) In contrast to the stark difference between juvenile and adult population sizes ($R^2 = 0.08$), the local adult population sizes are much more similar to the adult population sizes (the R^2 of each of the four sector densities separately explaining the total adult population size ranges from 0.49 to 0.75, with a mean of 0.64). 2) The interpretation of the biological significance of the local adult population size was complicated by the fact that we did not know whether an individual was still at this location at the age that we analysed (30 days). We could have therefore either taken the local population size on the date the individual was found in that sector (at circa 13 days of age) or assumed that the individual remained in that sector until disappearance. 3) After adding the local adult population sizes to the disappearances model, we discovered that they explained a lot of variance, but did not change the results we were mainly interested in. The local adult population size x genotype interaction was not an informative addition to the null model (see Table 1). In the within-population migration model, local adult population size fits better than total adult population size as a non-interacting predictor (AIC of model LPMM7 (S2) = 520.14, AIC of MM7 (S5) = 530.09), but did also not change the general

²⁵ results (i.e. in all population size interactions, male $+/t$ are most likely to migrate in low

²⁶ sizes). Furthermore, the juvenile population size x genotype interaction that was found to

²⁷ be most informative in absence of local adult population sizes (MM7, S5) remained most

²⁸ informative when including local adult population sizes (AIC of LPMM8 = 522.08 vs AIC

²⁹ of LPMM7 = 520.14). In the interest of focusing on our hypothesis in the paper, we decided

³⁰ to present the data here instead.

³¹ The variable "local adult population size" represents the adult population size of the sector

³² the focal individual was in at the age of 13 days. It is calculated by using the last known

³³ location of all adults still alive in the barn on that day. Those that were last seen in the

³⁴ same sector as the focal individual were counted towards this local population size.

³⁵ Disappearances models

³⁶ In Table 1, we present similar model comparisons as in the paper (and S1), but here we

³⁷ tested the informativeness of local adult population size as a predictor for disappearances.

³⁸ These models are called "local adult population size disappearances models" (LPDM) 0-3

³⁹ here. We also tested whether it provides a more informative interaction with the genotype

⁴⁰ than the juvenile population size. We concluded that the local adult population size is an

⁴¹ informative predictor for disappearances (in addition to total juvenile and adult population

⁴² sizes). However, it did not provide a more informative interaction with the genotype, which

⁴³ is why we present the results here instead of the paper. The full model outputs can be seen

⁴⁴ in Table 2. The low number of simulation runs of the comparison LPDM2 vs DM2* indicates

⁴⁵ that almost all of the 10,000 simulation runs were discarded because the LRT in those runs

⁴⁶ was negative (see Methods of paper). It is conservative to exclude those runs, thus the *p*-

⁴⁷ value is much higher in that comparison that it would be with many more simulation runs

⁴⁸ (given the very large LRT and ΔAIC), but it was already clear that local adult population

⁴⁹ size explains a lot of variance if it is modelled as a non-interacting predictor.

Table 1: Overview of model comparisons of juvenile disappearances with local adult population sizes (LPDM). The star indicates that this model from the paper has been restricted to individuals with known birth sector (S1). The 'x' indicates model term interactions. A superscripted '2' indicates quadratic terms

Models	Formula	Comparison	LRT	p	Runs	ΔAIC
LPDM0	$\sim$ genotype $+$ juv. pop. size $+$ juv. pop. size^2 $+$ adu. pop. size $+$ adu. pop. size^2 $+$ loc. adu. pop. size $+$ loc. adu. pop. size^2 $+$ season $+$ sex $+$ age when sampled	NA	NA	NA	NA	NA
DM2*	$\sim$ genotype $+$ juv. pop. size $+$ juv. pop. size^2 $+$ adu. pop. size $+$ adu. pop. size^2 $+$ season $+$ sex $+$ age when sampled $+$ genotype x juv. pop. size $+$ genotype x juv. pop. size^2	NA	NA	NA	NA	NA
LPDM1	$\sim$ genotype x loc. adu. pop. size $+$ genotype x loc. adu. pop. size^2 $+$ LPDM0 variables	LPDM0	5.06	0.08	662/8008	-1.06
LPDM2	$\sim$ loc. adu. pop size $+$ loc. adu. pop. size^2 $+$ DM2* variables	DM2*	679.74	0.04	0/26	-675.74
LPDM3	$\sim$ genotype x loc. adu. pop. size $+$ genotype x loc. adu. pop. size^2 $+$ LPDM2 variables	LPDM2	0.69	0.77	6437/8327	+3.31

Table 2: Full model outputs of the juvenile disappearances models using local adult population sizes (LPDM). The parameter coefficient is provided followed by the standard error in brackets. The star indicates that this model from the main manuscript has been restricted to individuals with known birth sector. Interactions are indicated with an 'x' between model terms. Superscripted '2' indicates quadratic terms.

	LPDM0	DM2*	LPDM1	LPDM2	LPDM3
Genotype $+/t$	0.784	1.002	1.200	1.161	1.244
	(0.200)	(0.258)	(0.277)	(0.296)	(0.330)
Juv. Pop. Size at Age 30 Days	0.359	0.291	0.361	0.340	0.342
	(0.075)	(0.066)	(0.075)	(0.075)	(0.076)
Juv. Pop. Size at Age 30 Days^2	-0.101	-0.226	-0.101	-0.085	-0.087
	(0.066)	(0.051)	(0.066)	(0.066)	(0.067)
Adu. Pop. Size at Age 30 Days	-0.117	-0.598	-0.147	-0.090	-0.106
	(0.200)	(0.109)	(0.201)	(0.203)	(0.205)
Adu. Pop. Size at Age 30 Days	0.359	0.225	0.389	0.359	0.371
	(0.105)	(0.070)	(0.106)	(0.106)	(0.107)
Season at 30 Days (Breeding Season)	0.483	0.516	0.483	0.488	0.487
	(0.218)	(0.179)	(0.219)	(0.219)	(0.219)
Sex (Female)	0.387	0.319	0.393	0.399	0.400
	(0.097)	(0.084)	(0.098)	(0.098)	(0.098)
Age When Sampled	0.705	0.600	0.707	0.703	0.705
	(0.057)	(0.047)	(0.057)	(0.056)	(0.057)
Local. Adu. Pop. Size at Age 13 Days	-2.721		-2.768	-2.713	-2.729
	(0.131)		(0.134)	(0.131)	(0.134)
Local. Adu. Pop. Size at Age 13 Days^2	0.614		0.636	0.613	0.621
	(0.060)		(0.060)	(0.059)	(0.060)
$+/t$ x Juv. Pop. Size		0.696		0.667	0.599
		(0.266)		(0.301)	(0.332)
$+/t$ x Juv. Pop. Size^2		-0.023		-0.133	-0.097
		(0.211)		(0.267)	(0.270)
$+/t$ x Loc. Adu. Pop. Size			0.299		-0.025
			(0.339)		(0.402)
$+/t$ x Loc. Adu. Pop. Size^2			-0.390		-0.227
			(0.248)		(0.273)
Intercept	-2.602	-0.407	-2.495	-2.374	-2.365
	(1.226)	(0.231)	(1.128)	(1.062)	(1.047)
Observations	2,863	2,863	2,863	2,863	2,863
Log Likelihood	$-1,335.372$	$-1,670.280$	$-1,332.842$	$-1,330.412$	$-1,330.069$
Akaike Inf. Crit.	2,694.744	3,364.561	2,693.684	2,688.824	2,692.138
Bayesian Inf. Crit.	2,766.260	3,436.076	2,777.119	2,772.258	2,787.492

Within-population migration models

The comparisons of the local adult population size within-population migration models (LPMM) shown in Table 3 revealed that the interaction of local adult population size with the genotype is an informative predictor for within-population migration. It is similarly informative as the interaction with juvenile population size we describe in the paper and S5, but does not change our conclusions (the lowest density has the highest migration propensity for $+/t$). In contrast to the disappearances models shown above, here we replaced the total adult population size with the local adult population size, because they explained similar parts of the variance, which is more relevant with the smaller sample size of the within-population migration models in comparison with the disappearance models. The full model outputs of the LPMM can be found in Table 4.

Table 3: Overview of comparisons of juvenile within-population migration models using local adult population size as a predictor (LPMM). The numbering of the models is comparable to the numbering of within-population models without local adult population size in S5. A superscripted '2' indicates a quadratic term while an 'x' indicates model term interactions

Models	Formula	Comparison	LRT	p	Runs	ΔAIC
Null model with covariates	$\sim$ juvenile population size $+$ juvenile population size^2 $+$ local adult population size $+$ local adult population size^2 $+$ season $+$ sex $+$ age when sampled	NA	NA	NA	NA	NA
LPMM1	$\sim$ genotype $+$ null model variables	Null model	0.21	0.65	6548/10000	+1.79
LPMM2	$\sim$ genotype x juv. pop. size $+$ genotype x juv. pop. size^2 $+$ LPMM1 variables	LPMM1	8.09	0.03	314/10000	-4.09
LPMM3	$\sim$ genotype x l. ad. pop. size $+$ genotype x l. ad. pop. size^2 $+$ LPMM1 variables	LPMM1	9.18	0.02	173/10000	-5.18
LPMM4	$\sim$ genotype x juv. pop. size $+$ genotype x juv. pop. size^2 $+$ LPMM3 variables	LPMM3	6.44	0.09	878/9939	-2.44
LPMM5	$\sim$ genotype x season $+$ LPMM1 variables	LPMM1	1.76	0.20	2003/10000	+0.24
LPMM6	$\sim$ genotype x sex $+$ LPMM1 variables	LPMM1	5.64	0.02	233/10000	-3.64
LPMM6	*as above*	Null model	5.85	0.07	711/10000	-1.85
LPMM7	$\sim$ genotype x juv. pop. size $+$ genotype x juv. pop. size^2 $+$ LPMM6 variables	LPMM6	9.82	0.02	175/10000	-5.82
LPMM8	$\sim$ genotype x l. ad. pop. size $+$ genotype x l. ad. pop. size^2 $+$ LPMM6 variables	LPMM6	7.87	0.03	316/10000	-3.87
LPMM8	*as above*	Null model	13.71	0.02	158/10000	-5.71
LPMM9	$\sim$ genotype x juv. pop. size $+$ genotype x juv. pop. size^2 $+$ LPMM7 variables	LPMM7	7.86	0.07	740/9881	-3.86

Table 4: Full model outputs of the juvenile within-population migration models using local adult population size. The parameter coefficient is provided followed by the standard error in brackets. Interactions are indicated with an 'x' between model terms. Superscripted '2' indicate quadratic terms.

	Null	LPMM1	LPMM2	LPMM3	LPMM4	LPMM5	LPMM6	LPMM7	LPMM8	LPMM9
Genotype $+/t$		0.199 (0.429)	−1.721 (2.841)	−1.930 (1.556)	−4.213 (5.643)	−0.523 (0.738)	0.832 (0.485)	−0.753 (2.541)	−1.366 (1.651)	−2.996 (4.636)
Juv. Pop. Size at Age 30 Days	0.479 (0.225)	0.495 (0.228)	0.585 (0.234)	0.519 (0.237)	0.583 (0.241)	0.528 (0.229)	0.464 (0.228)	0.580 (0.237)	0.513 (0.237)	0.592 (0.241)
Juv. Pop. Size at Age 30 Days^2	0.220 (0.148)	0.210 (0.150)	0.222 (0.154)	0.183 (0.153)	0.227 (0.154)	0.235 (0.150)	0.226 (0.151)	0.221 (0.155)	0.184 (0.153)	0.220 (0.155)
Local. Adu. Pop. Size at Age 13 Days	−0.599 (0.138)	−0.585 (0.142)	−0.598 (0.144)	−0.484 (0.151)	−0.507 (0.152)	−0.604 (0.143)	−0.580 (0.143)	−0.596 (0.146)	−0.492 (0.151)	−0.519 (0.152)
Local. Adu. Pop. Size at Age 13 Days^2	0.283 (0.100)	0.274 (0.103)	0.253 (0.105)	0.144 (0.118)	0.141 (0.118)	0.285 (0.102)	0.259 (0.105)	0.235 (0.108)	0.147 (0.118)	0.146 (0.118)
Season at 30 Days (Breeding Season)	−0.228 (0.480)	−0.248 (0.482)	−0.403 (0.487)	−0.273 (0.500)	−0.488 (0.508)	−0.430 (0.499)	−0.220 (0.485)	−0.393 (0.493)	−0.279 (0.503)	−0.501 (0.508)
Sex (Female)	0.164 (0.242)	0.165 (0.242)	0.140 (0.243)	0.182 (0.244)	0.168 (0.246)	0.176 (0.242)	0.341 (0.254)	0.339 (0.255)	0.315 (0.253)	0.312 (0.254)
Age When Sampled	−0.076 (0.121)	−0.072 (0.121)	−0.092 (0.124)	−0.043 (0.123)	−0.077 (0.126)	−0.090 (0.122)	−0.051 (0.122)	−0.071 (0.125)	−0.025 (0.124)	−0.067 (0.127)
$+/t$ x Juv. Pop. Size			−6.134 (5.111)		−7.514 (9.550)			−5.932 (4.480)		−7.025 (7.687)
$+/t$ x Juv. Pop. Size^2			−3.306 (2.269)		−4.398 (4.122)			−3.231 (2.020)		−4.412 (3.412)
$+/t$ x Loc. Adu. Pop. Size				0.150 (2.088)	0.038 (1.681)				−0.209 (2.231)	−0.318 (1.687)
$+/t$ x Loc. Adu. Pop. Size^2				1.090 (0.905)	1.048 (0.787)				0.916 (0.945)	0.900 (0.803)
$+/t$ x Breeding Season						1.104 (0.855)				
$+/t$ x Female							−2.251 (1.137)	−2.623 (1.164)	−2.249 (1.233)	−2.835 (1.394)
Intercept	−2.860 (0.434)	−2.843 (0.435)	−2.731 (0.430)	−2.653 (0.447)	−2.554 (0.443)	−2.766 (0.433)	−2.944 (0.441)	−2.812 (0.438)	−2.719 (0.452)	−2.616 (0.447)
Observations	873	873	873	873	873	873	873	873	873	873
Log Likelihood	−255.899	−255.794	−251.746	−251.203	−247.982	−254.912	−252.976	−248.068	−249.041	−245.110
Akaike Inf. Crit.	527.798	529.588	525.493	524.407	521.965	529.824	525.952	520.135	522.083	518.219

S3: Supplementary concerning relatedness as a controlling variable

Overview

7 Theory predicts that inbreeding avoidance is a major component of an individual's migra-

8 tion propensity. Consequently, we decided to test whether adding an individual's average

9 relatedness to other mice to our best-fitting models from the paper would change our con-

10 clusions. This could be the case if t-carrying individuals were on average differently related

11 to other mice in the population. Under such circumstances, the effect that we ascribed to

12 the genotype would actually be explained by relatedness. In that case, we would expect the

13 genotype in the models with relatedness to have very different coefficients from the models

14 shown in the paper. As can be seen from the following results, this is not the case. While

15 relatedness is an informative negative predictor (i.e. the more a mouse is related to other

16 mice, the less likely it is to migrate or disappear), it does not alter the results presented

17 in the paper. Furthermore, $+/t$ and $+/+$ could be differently affected by the average re-

18 latedness and we tested whether an interaction between genotype and relatedness would be

19 informative, which was not the case.

Methods

Relatedness estimation

Following previous work from our lab on relatedness (Harrison *et al.*, 2018), we used 25 microsatellite markers for the analysis. We estimated relatedness using the Wang estimator (Wang, 2002), as it was found to be highly correlated with pedigree relatedness in our study population (Harrison *et al.*, 2018).

We made use of the R package *related* 1.0 (Pew *et al.*, 2015), which implements the software COANCESTRY (Wang, 2011) into R, to estimate relatedness.

Selection of individuals to use for each focal's relatedness

Due to differences in available information for the disappearances and within-population migration, we used a different selection criteria for the subset of individuals to which we compared the focal individual in regards to relatedness. Because we generally ignored the sectors of the barn in the disappearances models (with the exception of local population sizes in S2), we also estimated the respective focal's relatedness to all mice alive at the focal's age of 30 days (these models are called RDM). In contrast, for the within-population migration models (RMM), we chose to use a similar approach to the local adult population sizes. Thus, we estimated the relatedness of the focal to all adults present in the same sector as the focal at an age of 13 days. We only knew the location of adults and 13 day old pups for certain, which is why we chose this restriction, similarly to the local adult population sizes (S2).

Finally, the variable relatedness in the model is the average of each pairwise relatedness between the focal and the respective subset of individuals alive when the focal was 30 or 13 days of age as described above.

Table 1: Overview of model comparisons of juvenile disappearances with relatedness. The star indicates that this model from the paper (see S1) has been restricted to individuals with known relatedness. Quadratic terms are indicated with a superscripted '2'. Interactions are indicated with an 'x' between terms.

Models	Formula	Comparison	LRT	p	Runs	ΔAIC
DM2*	$\sim$ genotype + genotype x juv. pop. size + genotype x juv. pop. size^2 + adu. pop. size + adu. pop. size^2 + season + sex + age when sampled	NA	NA	NA	NA	NA
RDM1	$\sim$ mean relatedness at age 30 + DM2* variables	DM2*	6.30	0.02	144/7277	-4.30
RDM2	$\sim$ genotype x m. relatedn. age 30 + RDM1 variables	RDM1	0.42	0.70	5472/7773	+1.58

Disappearances model with relatedness

In Table 1, we show that adding relatedness to the best-fitting disappearances model does improve it (RDM1). However, an interaction with the genotype does not improve it further (RDM2) and the coefficients relevant for the main paper's question remain almost unchanged (see Table 2).

Within-population migration models with relatedness

In Table 3, we show that adding relatedness to the best-fitting within-population migration model also improves it. However, similarly to disappearance models (RDM1-2), an interaction with the genotype does not improve the model further and the coefficients relevant for the main paper's question remain almost unchanged (see Table 4).

Table 2: Full model outputs of the juvenile disappearances models with relatedness (RDM). The parameter coefficient is provided followed by the standard error in brackets. All numerical predictors are scaled and centred. The star indicates that this model from the paper has been restricted to individuals with known relatedness (see S1). Quadratic terms are indicated with a superscripted '2'. The 'x' indicates interactions between model terms.

	DM2*	RDM1	RDM2
Genotype $+/t$	0.955	0.958	0.966
	(0.247)	(0.247)	(0.248)
Juv. Pop. Size at Age 30 Days	0.307	0.298	0.299
	(0.066)	(0.066)	(0.066)
Juv. Pop. Size at Age 30 Days^2	-0.261	-0.259	-0.259
	(0.052)	(0.052)	(0.052)
Adu. Pop. Size at Age 30 Days	-0.576	-0.570	-0.575
	(0.104)	(0.104)	(0.106)
Adu. Pop. Size at Age 30 Days^2	0.163	0.157	0.161
	(0.066)	(0.065)	(0.066)
Season at Age 30 Days (Off-Season)	-0.423	-0.438	-0.435
	(0.176)	(0.177)	(0.177)
Sex (Male)	-0.313	-0.313	-0.312
	(0.083)	(0.083)	(0.083)
Age When Sampled	0.602	0.609	0.610
	(0.046)	(0.046)	(0.047)
Relatedness at Age 30 Days		-0.109	-0.101
		(0.043)	(0.045)
$+/t$ x Juv. Pop. Size	0.673	0.671	0.675
	(0.264)	(0.262)	(0.258)
$+/t$ x Juv. Pop. Size^2	0.028	0.022	0.012
	(0.198)	(0.196)	(0.194)
$+/t$ x Relatedness			-0.111
			(0.171)
Intercept	0.479	0.487	0.482
	(0.171)	(0.169)	(0.171)
Observations	2,937	2,937	2,937
Log Likelihood	-1,719.626	-1,716.477	-1,716.267
Akaike Inf. Crit.	3,463.252	3,458.954	3,460.534
Bayesian Inf. Crit.	3,535.074	3,536.760	3,544.326

Table 3: Overview of model comparisons of juvenile within-population migration with relatedness (RMM). The star indicates that this model from the main paper (see S5) has been restricted to individuals with known relatedness. A superscripted '2' indicates a quadratic term while an 'x' indicates an interaction between model terms.

Models	Formula	Comparison	LRT	p	Runs	ΔAIC
MM7*	$\sim$ genotype $+$ genotype x juv. pop. size $+$ genotype x juv. pop. size^2 $+$ adu. pop. size $+$ adu. pop. size^2 $+$ season $+$ genotype * sex $+$ age when sampled	NA	NA	NA	NA	NA
RMM1	$\sim$ mean relatedness at age 13 $+$ MM7* variables	MM7*	4.13	0.04	431/9998	-2.13
RMM2	$\sim$ genotype x m. relatedn. age 13 $+$ RMM1 variables	RMM1	0.38	0.62	6167/9947	+1.62

⁵² # References

⁵³ Harrison, Lindholm, Dobay, Halloran, Manser & König, 2018. Female nursing partner choice

⁵⁴ in a population of wild house mice (*Mus musculus domesticus*). *Frontiers in Zoology* **15**.

⁵⁵ Wang, 2002. An estimator for pairwise relatedness using molecular markers. *Genetics* **160**.

⁵⁶ Pew, Muir, Wang & Frasier, 2015. related: an R package for analysing pairwise relatedness

⁵⁷ from codominant molecular markers. *Molecular Ecology Resources* **15**.

⁵⁸ Wang, 2011. COANCESTRY: a program for simulating, estimating and analysing related-

⁵⁹ ness and inbreeding coefficients. *Molecular Ecology Resources* **11**.

Table 4: Full model outputs of the juvenile within-population migration models with relatedness. The star indicates that this model from the paper (see S5) has been restricted to individuals with known relatedness. The parameter coefficient is provided followed by the standard error in brackets. All numerical predictors are scaled and centred. Quadratic terms are indicated with a superscripted '2'. Interactions are indicated with an 'x' between model terms.

	MM7*	RMM1	RMM2
Genotype $+/t$	-0.920	-0.980	-0.818
	(2.981)	(3.046)	(2.881)
Juv. Pop. Size at Age 30 Days	0.585	0.542	0.551
	(0.254)	(0.257)	(0.258)
Juv. Pop. Size at Age 30 Days^2	0.220	0.231	0.232
	(0.141)	(0.144)	(0.144)
Adu. Pop. Size at Age 30 Days	-0.268	-0.224	-0.237
	(0.143)	(0.146)	(0.147)
Adu. Pop. Size at Age 30 Days^2	0.452	0.376	0.396
	(0.163)	(0.168)	(0.170)
Season at Age 30 Days (Breeding Season)	-0.557	-0.452	-0.456
	(0.534)	(0.543)	(0.543)
Sex (Female)	0.229	0.211	0.212
	(0.251)	(0.251)	(0.252)
Age When Sampled	-0.072	-0.078	-0.066
	(0.122)	(0.125)	(0.127)
Relatedness at Age 13 Days		-0.251	-0.267
		(0.122)	(0.125)
$+/t$ x Juv. Pop. Size	-5.557	-5.340	-5.623
	(5.750)	(5.825)	(5.619)
$+/t$ x Juv. Pop. Size^2	-3.078	-2.941	-3.119
	(3.057)	(3.079)	(3.040)
$+/t$ x Female	-2.152	-2.202	-2.112
	(1.258)	(1.272)	(1.248)
$+/t$ x Relatedness			0.299
			(0.487)
Intercept	-2.814	-2.827	-2.852
	(0.423)	(0.432)	(0.434)
Observations	861	861	861
Log Likelihood	-247.721	-245.657	-245.469
Akaike Inf. Crit.	519.443	517.313	518.937

S4: Pup body mass models

Full model outputs and comparison between the pup body mass models.

Details on the linear mixed models explaining the pup body mass can be found in Table 1. Similar to the disappearance models, these models include year of birth as a random effect. Pup body mass model 1 (PBM1) includes the genotype as a predictor. The comparison between the null model without the genotype and PBM1 can be found in Table 2. All numerical independent variables are scaled and centred as described in the manuscript. The dependent variable pup body mass remains in grams to help with the interpretation.

Table 1: Full model outputs of the pup body mass models (PBM). Quadratic terms are indicated with a superscripted '2'. All numerical variables are scaled and centred. The parameter coefficient is provided followed by the standard error in brackets.

	Null	PBM1
Genotype $+/t$		0.174
		(0.081)
Juv. Pop. Size at Age 30 Days	0.119	0.121
	(0.033)	(0.033)
Juv. Pop. Size at Age 30 Days^2	0.042	0.044
	(0.027)	(0.027)
Adu. Pop. Size at Age 30 Days	0.057	0.079
	(0.065)	(0.066)
Adu. Pop. Size at Age 30 Days^2	0.179	0.171
	(0.038)	(0.038)
Season at 30 Days (Off-Season)	-0.185	-0.183
	(0.094)	(0.094)
Sex (Male)	0.009	0.011
	(0.042)	(0.042)
Age When Sampled	0.143	0.144
	(0.021)	(0.021)
Intercept	6.469	6.459
	(0.158)	(0.160)
Observations	2,898	2,898
Log Likelihood	$-4,480.535$	$-4,478.234$
Akaike Inf. Crit.	8,981.071	8,978.468
Bayesian Inf. Crit.	9,040.789	9,044.158

Table 2: Comparison between pup body mass models (PBM). Quadratic terms are indicated with a superscripted '2'. Comparison shows against which other model the model in the row was evaluated. LRT indicates the likelihood ratio test statistic of the observed dataset. The p-value is the fraction of simulated datasets with LRT larger than the observed LRT (see Methods). Runs indicate the absolute values on which the p is based. The ΔAIC is given for comparison with other statistical approaches.

Models	Formula	Comparison	LRT	p	Runs	ΔAIC
Null model with covariates	$\sim$ juvenile population size $+$ juvenile population size^2 $+$ adult population size $+$ adult population size^2 $+$ season $+$ sex $+$ age when sampled	NA	NA	NA	NA	NA
PBM1	$\sim$ genotype $+$ null model variables	Null model	4.61	0.03	311/10000	-2.60

S5: Supplementary for within-population migration models

Using a simple comparison test, we found that the genotypes were not similarly represented in the migrants (see paper). However, when controlling for other variables in a generalized linear model, the results were less clear (Table 1). Adding the genotype to a null model with control variables did not improve the model, while a model that contained two genotype interactions, one with juvenile population size and one with sex, was found to be significantly more informative than the null model. We used this model to visualise and estimate effect sizes. The predictor estimates of this model had large confidence intervals. The estimate for $+/t$ became negative when the interaction with juvenile population size was added to the model. The reason for that was that $+/t$ juveniles were more likely to migrate within the population than $+/+$ only when the juvenile population size was small (see Figure 2). The probability to migrate increased with juvenile population size for $+/+$ mice. A model with an interaction of genotype with adult population size instead of genotype with juvenile population size revealed similar (negative) interaction coefficients and adding both interactions (genotype with adult population size and genotype with juvenile population size) did not improve the model any further compared to keeping only one of these interactions, suggesting that population size in general is the relevant metric. Furthermore, male $+/t$ were more likely to migrate than female $+/t$. Importantly, only few individuals were $+/t$, which decreased our power to detect and describe effects accurately. Mice born in the main breeding season were less likely to migrate within the population, but there was no difference

between the genotypes (i.e. no informative interaction between genotype and season). Pup body mass was had no effect on migration, and its effect did not differ between the genotypes or change the genotype's effect (see within-population migration models 10-12) in Table 3.

Full model comparisons

Table 1 presents the comparisons between different within-population juvenile migration models ("MM").

Effect estimates

We used the *confint* function of R package *MASS* 7.3-50 to estimate the confidence intervals in Figure 1 using a 95% confidence interval.

Full model outputs and additional comparisons of the juvenile within-population migration models.

The full model outputs of the juvenile within-population migration models ("MM") can be found in Tables 2 and 3. The best-fitting within-population migration model was determined to be MM7, which is thus also used to visualise the results in Figures 1-2. All numerical variables are scaled and centred as described in the paper.

Table 1: Overview of models of juvenile within-population migration (MM). The 'x' in model terms indicates interactions. Quadratic terms are indicated with a superscripted '2'. Comparison shows against which other model the model in the row was evaluated. *LRT* indicates the likelihood ratio test statistic of the observed dataset. The *p*-value is the fraction of simulated datasets with *LRT* larger than the observed *LRT* (see Methods). Runs indicate the absolute values on which the *p* is based. The ΔAIC is given for comparison with other statistical approaches.

| Models	Formula	Comparison	*LRT*	*p*	Runs	ΔAIC
Null model with covariates	$\sim$ juvenile population size + juvenile population size^2 + adult population size + adult population size^2 + season + sex + age when sampled	NA	NA	NA	NA	NA
MM1	$\sim$ genotype + null model variables	Null model	0.28	0.61	6057/10000	+1.72
MM2	$\sim$ genotype x juv. pop. size + genotype x juv. pop. size^2 + MM1 variables	MM1	7.78	0.04	385/10000	-3.78
MM3	$\sim$ genotype x ad. pop. size + genotype x ad. pop. size^2 + MM1 variables	MM1	4.67	0.13	1330/10000	-0.67
MM4	$\sim$ genotype x ad. pop. size + genotype x ad. pop. size^2 + MM2 variables	MM2	3.01	0.30	3032/9998	+0.99
MM5	$\sim$ genotype x season + MM1 variables	MM1	1.88	0.19	1852/10000	0.12
MM6	$\sim$ genotype x sex + MM1 variables	MM1	5.95	0.02	217/10000	-3.95
MM6	*as above*	Null model	6.22	0.06	564/10000	-2.22
MM7	$\sim$ genotype x juv. pop. size + genotype x juv. pop. size^2 + MM6 variables	MM6	8.99	0.02	242/10000	-4.99
MM7	*as above*	Null model	15.22	0.01	100/10000	-7.22
MM8	$\sim$ genotype x adu. pop. size + genotype x adu. pop. size^2 + MM6 variables	MM6	5.84	0.08	772/10000	-1.84
MM9	$\sim$ genotype x adu. pop. size + genotype x adu. pop. size^2 + MM7 variables	MM7	3.96	0.23	2258/9996	+0.04
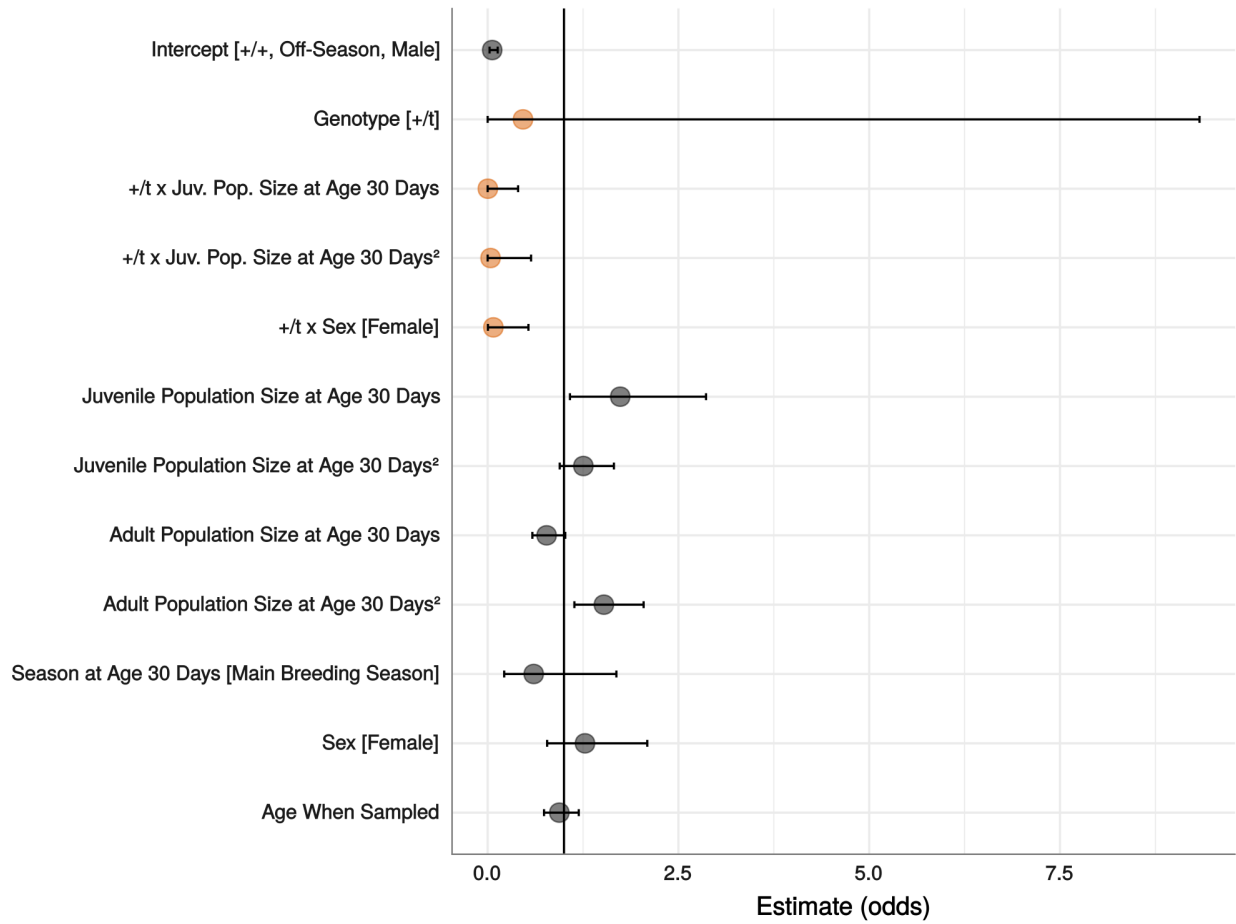
Figure 1: Effect estimates in odds with 95% confidence intervals of the most informative juvenile within-population migration model ($N = 873$). The level of a categorical variable for which the effect is calculated is given in square brackets. Continuous variables are scaled. Interactions are indicated with an 'x' between the variables. A superscripted '2' indicates a quadratic term. t main effect and interactions with t are highlighted in orange.
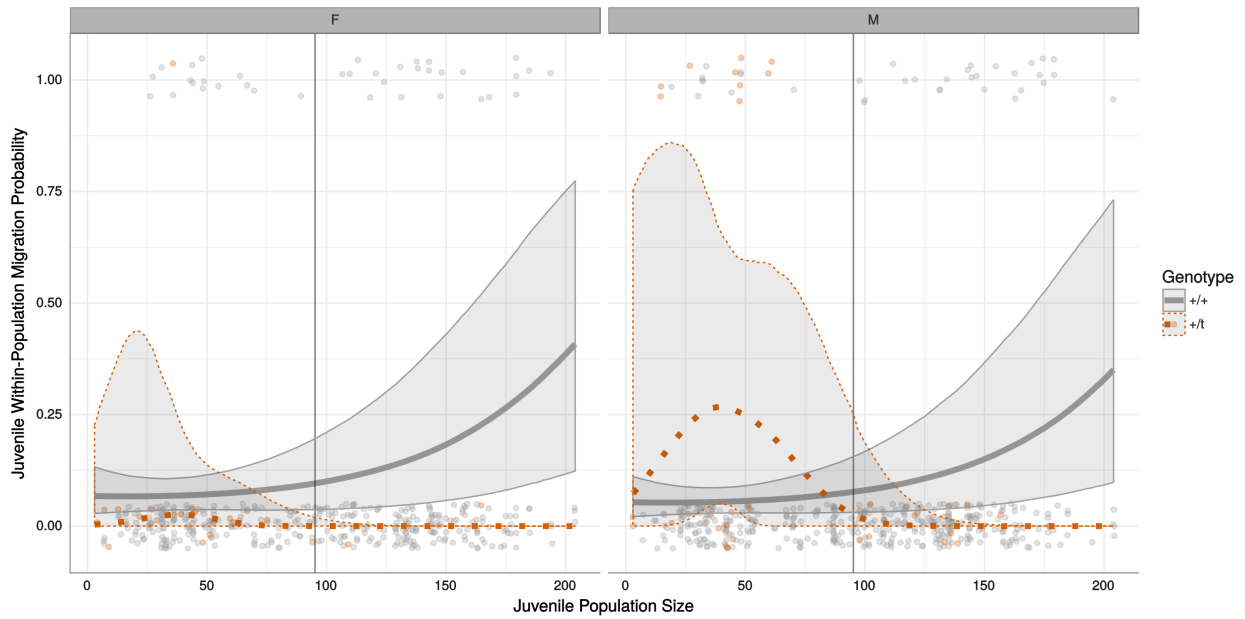
Figure 2: Predicted probabilities of juvenile within-population migration (lines) with 95% confidence intervals and actual data points (top and bottom, jittered) of $+/t$ (orange, dotted line) and $+/+$ (grey, solid line) individuals in varying juvenile population sizes, separated by sex ($N = 873$). These plots are based on predictions from the most informative within-population migration model (migration model 7) for individuals that were born in the off-season in average adult population size. The vertical line indicates the mean juvenile population size.

Table 2: Full model outputs of the juvenile within-population migration models. The parameter coefficient is provided followed by the standard error in brackets. An 'x' indicates an interaction term. Quadratic terms are indicated with a superscripted '2'. All numerical predictors are scaled and centred.

	Null	MM1	MM2	MM3	MM4	MM5	MM6	MM7	MM8	MM9
Genotype $+/t$		0.246 (0.459)	−2.039 (3.468)	−6.570 (5.246)	−6.466 (5.152)	−0.544 (0.788)	0.909 (0.509)	−0.770 (2.866)	−8.110 (5.415)	−6.599 (4.884)
Juv. Pop. Size at Age 30 Days	0.493 (0.239)	0.493 (0.240)	0.572 (0.246)	0.501 (0.248)	0.589 (0.254)	0.541 (0.243)	0.462 (0.241)	0.552 (0.249)	0.505 (0.250)	0.606 (0.256)
Juv. Pop. Size at Age 30 Days²	0.230 (0.136)	0.221 (0.138)	0.235 (0.142)	0.164 (0.141)	0.208 (0.142)	0.251 (0.138)	0.231 (0.138)	0.227 (0.143)	0.168 (0.142)	0.197 (0.143)
Adu. Pop. Size at Age 30 Days	−0.285 (0.126)	−0.259 (0.136)	−0.267 (0.138)	−0.186 (0.151)	−0.217 (0.152)	−0.275 (0.137)	−0.254 (0.136)	−0.258 (0.140)	−0.197 (0.151)	−0.230 (0.152)
Adu. Pop. Size at Age 30 Days²	0.468 (0.132)	0.444 (0.138)	0.445 (0.145)	0.336 (0.168)	0.382 (0.170)	0.478 (0.142)	0.431 (0.141)	0.421 (0.149)	0.348 (0.168)	0.394 (0.171)
Season at 30 Days (Breeding Season)	−0.388 (0.500)	−0.375 (0.501)	−0.542 (0.517)	−0.395 (0.508)	−0.659 (0.529)	−0.592 (0.523)	−0.349 (0.505)	−0.505 (0.523)	−0.449 (0.514)	−0.694 (0.534)
Sex (Female)	0.065 (0.238)	0.065 (0.238)	0.050 (0.240)	0.056 (0.240)	0.048 (0.241)	0.074 (0.239)	0.245 (0.251)	0.243 (0.251)	0.241 (0.250)	0.241 (0.251)
Age When Sampled	−0.056 (0.119)	−0.053 (0.119)	−0.081 (0.121)	−0.041 (0.119)	−0.076 (0.121)	−0.073 (0.120)	−0.034 (0.120)	−0.063 (0.122)	−0.019 (0.120)	−0.056 (0.123)
$+/t$ x Juv. Pop. Size				−6.700 (6.124)	−6.136 (6.755)			−5.976 (4.987)		−5.504 (5.032)
$+/t$ x Juv. Pop. Size²				−3.550 (2.630)	−3.476 (2.852)			−3.268 (2.187)		−3.220 (2.202)
$+/t$ x Adu. Pop. Size				−9.337 (7.405)	−6.891 (6.640)				−13.289 (7.906)	−10.027 (6.981)
$+/t$ x Adu. Pop. Size²				−2.766 (2.464)	−2.085 (2.257)				−4.216 (2.674)	−3.367 (2.433)
Model $+/t$ x Breeding Season						1.166 (0.878)				
$+/t$ x Female							−2.312 (1.140)	−2.593 (1.166)	−2.682 (1.196)	−2.938 (1.228)
Intercept	−2.843 (0.418)	−2.837 (0.419)	−2.742 (0.415)	−2.648 (0.427)	−2.568 (0.425)	−2.762 (0.416)	−2.934 (0.425)	−2.825 (0.421)	−2.715 (0.431)	−2.639 (0.430)
Observations	873	873	873	873	873	873	873	873	873	873
Log Likelihood	−260.651	−260.512	−256.619	−258.178	−255.114	−259.572	−257.539	−253.044	−254.618	−251.065
Akaike Inf. Crit.	537.302	539.023	535.238	538.355	536.229	539.145	535.077	530.087	533.236	530.130

Table 3: Full model outputs of the juvenile within-population migration models, continued.

	MM10	MM11	MM12
Genotype $+/t$	−0.543	−0.515	−0.594
	(2.648)	(2.634)	(2.654)
Juv. Pop. Size at Age 30 Days	0.574	0.571	0.553
	(0.253)	(0.253)	(0.253)
Juv. Pop. Size at Age 30 Days^2	0.220	0.238	0.242
	(0.142)	(0.145)	(0.145)
Adu. Pop. Size at Age 30 Days	−0.201	−0.208	−0.205
	(0.141)	(0.142)	(0.142)
Adu. Pop. Size at Age 30 Days^2	0.383	0.381	0.384
	(0.153)	(0.153)	(0.154)
Season at 30 Days (Breeding Season)	−0.488	−0.505	−0.442
	(0.540)	(0.541)	(0.546)
Sex (Female)	0.238	0.240	0.238
	(0.254)	(0.255)	(0.255)
Age When Sampled	−0.089	−0.113	−0.115
	(0.123)	(0.127)	(0.128)
Pup Body Mass		0.106	0.076
		(0.126)	(0.129)
$+/t$ x Juv. Pop. Size	−5.632	−5.533	−5.126
	(5.468)	(5.420)	(5.234)
$+/t$ x Juv. Pop. Size^2	−3.070	−3.000	−2.457
	(3.207)	(3.175)	(3.003)
$+/t$ x Female	−2.471	−2.473	−2.581
	(1.199)	(1.200)	(1.230)
$+/t$ x Body Mass			0.581
			(0.568)
Intercept	−2.835	−2.843	−2.892
	(0.432)	(0.434)	(0.438)
Observations	864	864	864
Log Likelihood	−245.194	−244.834	−244.292
Akaike Inf. Crit.	514.388	515.667	516.584

Table 4: Comparison between within-population migration models including pup body mass as predictor. The star indicates that this model was restricted to only individuals with pup body mass information. Interactions are indicated with a star between terms.

Models	Formula	Comparison	LRT	p	Runs	ΔAIC
MM10 (MM7*)	$\sim$ genotype + genotype x juv. pop. size + genotype x juv. pop. size^2 + juvenile population size + juvenile population size^2 + adult population size + adult population size^2 + season + genotype x sex + sex + age when sampled	NA	NA	NA	NA	NA
MM11	$\sim$ MM10 + pup body mass	MM10	0.72	0.40	4015/9997	+1.28
MM12	$\sim$ genotype x pup body mass + MM10 variables	MM10	1.80	0.45	4501/9992	+2.20