

Title: Advanced parentage simulations: the statistical power to measure relative reproductive success

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Authors: K. Shedd, T. H. Dann, C. Habicht, J. Jasper, and W. D. Templin

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Abstract

1
2 The proportion of fish within each population sampled in the field for the Alaska Hatchery
3 Research Program will affect the power of statistical tests of differences in fitness between
4 hatchery- and natural-origin fish. These tests are based upon data from parentage analyses and
5 quantify the relative reproductive success (RRS) of hatchery- to natural-origin fish. We
6 simulated populations of hatchery- and natural-origin individuals with known fitness differences
7 (i.e., effect sizes) to evaluate the power of these statistical tests under different sampling and
8 straying rates. Here we present results from modeling 36 potential sampling scenarios of parents
9 and offspring for 2 stray rates and 4 effect sizes in order evaluate the power to detect differences
10 in RRS. These simulations suggest limited statistical power to detect RRS of 0.5 with the current
11 field sampling program as stated in the request for proposals (RFP). Sampling scenarios where
12 high proportions of parents and adult offspring (>50%) were sampled had more power to detect
13 RRS < 1. Large effect sizes (greater difference in reproductive success between hatchery- and
14 natural-origin fish) were easier to detect. True differences in RRS were easier to detect under a
15 high stray rate scenario. Lastly, there was greater statistical power to detect RRS < 1 when RRS
16 was determined for single parent-offspring pairs by sex rather than for parent pair-offspring trios
17 by cross type. We recommend that a high proportion of parents and adult offspring (>50%) be
18 sampled in order to have adequate statistical power (>80%) to detect potential fitness differences
19 (0.5-0.8) between hatchery- and natural-origin fish.

Background of AHRP

20
21 Extensive ocean-ranching salmon aquaculture is practiced in Alaska by private non-profit
22 corporations (PNP) to enhance common property fisheries. Most of the approximately 1.7B
23 juvenile salmon that PNP hatcheries release annually are pink salmon in Prince William Sound
24 (PWS) and chum salmon in Southeast Alaska (SEAK; Vercesi 2014). The large scale of these
25 hatchery programs has raised concerns among some that hatchery fish may have a detrimental
26 impact on the productivity and sustainability of natural stocks. Others maintain that the potential
27 for positive effects exists. To address these concerns ADF&G convened a Science Panel for the

ⁱ This document serves as a record of communication between the Alaska Department of Fish and Game Commercial Fisheries Division and other members of the Science Panel of the Alaska Hatchery Research Program. As such, these documents serve diverse ad hoc information purposes and may contain basic, uninterpreted data. The contents of this document have not been subjected to review and should not be cited or distributed without the permission of the authors or the Commercial Fisheries Division

28 Alaska Hatchery Research Program (AHRP) whose members have broad experience in salmon
29 enhancement, management, and natural and hatchery fish interactions. The AHRP was tasked
30 with answering three priority questions:

- 31 I. *What is the genetic stock structure of pink and chum salmon in each region (PWS and*
32 *SEAK)?;*
- 33 II. *What is the extent and annual variability in straying of hatchery pink salmon in PWS and*
34 *chum salmon in PWS and SEAK?;* and
- 35 III. *What is the impact on fitness (productivity) of natural pink and chum salmon stocks due*
36 *to straying of hatchery pink and chum salmon?*

37 **Introduction**

38 *Measuring the Impact on Fitness*

39 To answer the third question, we need to know the origin and pedigree of each fish captured in
40 select streams across multiple generations. **Origin** refers to the type of early life-history habitat
41 (hatchery or natural) that a fish experienced. **Pedigree** refers to the family relationship among
42 parents and offspring. ‘**Ancestral origin**’ refers to the origin of an individual’s ancestors (e.g.,
43 two parents of a single origin [hatchery/hatchery or natural/natural] or two parents of mixed
44 origin [hatchery/natural]). These ancestral origins can be determined by combining information
45 from three sources: identification of hatchery origin from otolith marks, pedigree from genetic
46 data, and age from scales (for chum salmon from SEAK). By pairing these data within fish and
47 across generations, we can estimate **reproductive success (RS)** among cross types (i.e. hatchery-
48 hatchery, hatchery-natural, and natural-natural origin crosses). The AHRP is using the **relative**
49 **reproductive success (RRS)** of hatchery-origin fish to natural-origin fish as the measure of
50 *fitness in this study* (Tech Doc 1 – Shedd et al. 2014).

51 *Problem: Will this Study Accurately Measure Relative Reproductive Success?*

52 Technological advances in high throughput genotyping methods have allowed molecular
53 parentage analysis to become a widespread and cost-effective tool to address conservation
54 questions (Jones and Ardren 2003; Jones et al. 2010). Along with these advances, much work
55 has been done to characterize experimental designs capable of providing high statistical power to
56 address questions of interest. Chief among these biological questions has been research testing
57 for differences in reproductive success between different groups, such as hatchery- and natural-
58 origin salmon (Araki et al. 2008; Christie et al. 2014).

59 Technical Document 3 demonstrated that the number of offspring assigned to parent pairs via
60 parentage analysis increases exponentially with the proportion of parents sampled (Tech Doc 3 –
61 Dann et al. 2014). When broken out by cross type, Dann et al. (2014) found that the number of
62 offspring assigned to the hatchery-hatchery cross type was very small for the low stray-rate
63 scenario (15% hatchery-origin fish). These findings raised concerns that the sampling proportion
64 of adults proposed in the request for proposals (RFP) will result in low effective sample sizes for

65 parent pair assignments. It is uncertain how sampling different proportions of parents and
66 offspring will affect the statistical power of tests for differences in fitness between hatchery- and
67 natural-origin stocks (Araki and Blouin 2005).

68 While many aspects of RRS studies have been evaluated as the field has developed, no study has
69 included all parameters of interest to the AHRP. Other researchers have modeled parentage
70 analysis and fitness studies in order to determine the effect of the number and polymorphism of
71 loci used (Bernatchez and Duchesne 2000; Anderson and Garza 2006; Matson et al. 2008), the
72 type of marker used (SNPs vs. microsatellites; Anderson and Garza 2006; Hauser et al. 2011),
73 genotyping error rate (Christie 2013; Harrison et al. 2013b, 2013a), productivity of systems
74 (Hinrichsen 2003), differences in reproductive success between groups (Aykanat et al. 2014), the
75 fraction of group membership (Hinrichsen 2003; Aykanat et al. 2014), and the proportion of
76 adults and offspring sampled (Hinrichsen 2003; Araki and Blouin 2005; Anderson et al. 2011).
77 However, none have simultaneously modeled the parameters of interest for the AHRP given the
78 broad scope and large scale of this project. The primary concern with regard to the third
79 objective of the AHRP is the statistical power to detect differences in RRS between hatchery-
80 and natural-origin stocks as only a fraction of adults and offspring will be sampled. How will
81 power be affected by low stray rates, and thus lower sample sizes of hatchery-origin fish? How
82 small of a RRS can be reasonably expected (power > 0.8; beta < 0.2) to be detected
83 (significance; alpha < 0.05)? Is there a difference in the power of tests for single parent-
84 offspring assignments by sex and parent pair-offspring assignments by cross type? What
85 sampling design will achieve desired statistical power?

86 *Goals of Technical Document*

87 Five goals of this technical document are to:

- 88 1) Explain methods used to simulate data for hypothetical pink salmon populations.
- 89 2) Using simulated data, determine the statistical power of parentage analysis to find
90 modeled differences in RRS between 0.500 and 0.875 for varying stray rates when not all
91 parents/offspring are sampled.
- 92 3) Compare the power of tests for RRS of single parent-offspring assignments by sex and
93 parent pair-offspring assignments by cross type.
- 94 4) Review the expected power for the AHRP, given the field sampling design outlined in the
95 RFP.
- 96 5) Request a decision by the Science Panel on the field sampling design for upcoming field
97 seasons.

98

Methods

99

Simulated Data Sets

100

CREATION OF F₀ PARENTS

101 One parental data set (F₀) was generated in *EasyPop* 2.0.1 (Balloux 2001) in order to create
102 initial genotypes. The parental data set was created from one population of constant size (3,000
103 reproductive individuals) and equal sex ratio that simulated random mating for 1,000 generations
104 to create diploid genotypes for 96 independent, biallelic loci. All loci had the same mutation
105 dynamics according to K-allele model with a mutation rate of 1×10^{-8} (Brumfield et al. 2003) for
106 two possible allelic states (to create biallelic SNPs) starting with maximum variability. The
107 parental data set created in *EasyPop* 2.0.1 was imported in *R* version 3.1.0 (R Core Team 2014),
108 where all subsequent analyses took place.

Assumption 1. The population has a constant number of individuals (N=3,000) in every generation.

Assumption 2. There are equal numbers of males and females contributing in every generation.

Assumption 3. All loci have a mutation rate of 1×10^{-8} .

109

110 Parental genotypes were first examined for basic population genetic parameters (i.e. minor allele
111 frequency of SNPs, deviations from Hardy-Weinberg equilibrium, etc.) to verify that they were
112 representative of the SNP markers expected for this project. Subsequently, the parental data set
113 was duplicated and individuals were randomly assigned hatchery- (H) or natural-origin (N) in
114 proportions representing *two stray rates* as defined in the RFP. In the High Stray rate set, the
115 relative assignment of individuals was 50% H and 50% N. In the Low Stray rate set, the relative
116 assignment of individuals was 15% H and 85% N.

117

CREATION OF MATING PAIRS

118 For each of these two parental data sets (High Stray and Low Stray), males and females were
119 randomly paired into monogamous pairings. An assigned number of F₁ offspring were generated
120 for each pairing. Other studies have shown that the distribution of salmonid adult offspring can
121 be accurately represented by a negative binomial distribution with a mode of 0, so we used this
122 distribution to generate the number of F₁ offspring assigned to each mating pair (Geiger et al.
123 1997; Gilk et al. 2004; Geiger et al. 2007; Anderson et al. 2011; Anderson et al. 2013; Aykanat
124 et al. 2014; Christie et al. 2014). It was our goal to manipulate the effect size (the RRS of a HxH
125 cross to a NxN cross, both sexes treated equally) while parameterizing the number of offspring at
126 two life stages (alevin and adult offspring) based on survival values for pink salmon found in the
127 literature (Quinn 2011; Table 15.1).

Assumption 4. Random mating between ancestral groups (hatchery vs. natural-origin)

Assumption 5. Monogamous mating.

Assumption 6. Distribution of the number of offspring per mating pair is negative binomial.

Assumption 7. Survival values for pink salmon in PWS are consistent with literature averages.

128

129 In order to capture the variation in family size for matings in our simulation, we began by
 130 assigning each female a number of eggs (N_{eggs}) drawn randomly from a negative binomial
 131 distribution with a mean of 1,648 (Quinn 2011; Table 15.1) and dispersion parameter of 1. The
 132 number of alevin (N_{alevin}) and number of adult offspring (N_{adult}) produced by each pair was
 133 determined by initial N_{eggs} and survivals between life stages ($S_{Stage\ 1-Stage\ 2}$) according to the
 134 following equations:

$$N_{parents} = 3,000$$

$$\mu[N_{eggs}] = 1,648$$

$$S_{egg-alevin} = 0.115$$

$$S_{alevin-adult} = 0.028$$

$$N_{alevin} = N_{eggs} \times S_{egg-alevin}$$

$$N_{adult,initial} = N_{alevin} \times S_{alevin-adult} \times Dem_{adjust}$$

135 where $Dem_{adjust} = \frac{\sum N_{adult,initial}}{N_{parents}}$, in order to model a demographically stable

136 population (i.e. make it such that, on average, each pair produces 2 returning adult offspring
 137 [replacement]). The N_{adult} was further reduced to: 1) keep the number of offspring equal to the
 138 number of natural-origin spawners (demographically stable population over time given that there
 139 will be new strays in subsequent years); and 2) to incorporate the desired effect size [reduction in
 140 fitness of hatchery-origin offspring]. The RRS of hybrids (HxN or NxH pairs) was a linear
 141 interpolation between the modeled effect and 1 (i.e. if the modeled RRS of HxH crosses was 0.5,
 142 then the RRS of HxN and NxH crosses was 0.75). The number of returning adult offspring per
 143 pair was determined by the following equations:

Assumption 8. Stray rate is consistent over years.

Assumption 9. Given assumption 1 and 8 the average RS of natural-spawning salmon (natural origin + hatchery-origin strays) varies based on stray rate in order to keep a stable population of 3,000 adults/stream given that there will be a consistent number of new hatchery-origin strays in subsequent years.

Assumption 10. The RRS of a HxN hybrid cross is identical and indistinguishable from its reciprocal NxH cross.

144

145 Stray = stray rate of hatchery-origin fish into the stream

146 Effect = RRS of HxH cross to NxN cross

147 $RRS_{cross} = 1$ for NxN, $\frac{1+Effect}{2}$ for HxN/NxH, and Effect for HxH

148 Given the assumption that fish mate randomly with respect to origin, the proportion of the
149 mating pairs that consist of the different cross types is:

150 $p_{\text{ExpectedPairs}_{\text{cross}}} = (1 - \text{Stray})^2$ for NxN, $2(\text{Stray})(1 - \text{Stray})$ for HxN/NxH, and $(\text{Stray})^2$ for
151 HxH

152 Thus, given the stray rate and the effect size, the average RS of the population is equal to:

$$\text{avgRS}_{\text{POP}} = \frac{(1 - \text{Stray})}{(\sum p_{\text{ExpectedPairs}_{\text{cross}}} \times \text{RRS}_{\text{cross}})}$$

153 And the proportion of returning adult offspring that will survive for each cross type is equal to:

$$\text{cull}_{\text{cross}} = \text{avgRS}_{\text{POP}} \times \text{RRS}_{\text{cross}}$$

154 So that the final

$$N_{\text{pair},\text{final}}^{\text{adult}} = N_{\text{pair},\text{initial}}^{\text{adult}} \times \text{cull}_{\text{cross}}$$

Assumption 11. There is no difference in RS between males and females.

Assumption 12. There is no difference in straying of natural-origin fish due to the ancestral-origin of their parents (i.e. F₁s with H/H parents are just as likely to naturally stray as F₁s with NxN parents).

Assumption 13. There is no difference in fishing pressure/harvest rate of natural-origin fish due to the ancestral-origin of their parents (i.e. F₁s with H/H parents are just as likely to be caught as F₁s with NxN parents).

155

156 GENERATION OF OFFSPRING

157 For all parent pairs, offspring were generated (according the $N_{\text{pair},\text{final}}^{\text{adult}}$) following Mendelian
158 inheritance (all markers are independent and offspring inherit one allele from each parent).

159 Offspring genotypes were first examined for basic population genetic parameters (i.e. minor
160 allele frequency of SNPs, deviations from Hardy-Weinberg equilibrium) in order to verify that
161 they were realistic given parental genotypes.

162 SUB-SAMPLING OF PARENTS AND OFFSPRING

163 Both parental and adult offspring generations of both stray rates were sampled in $1/6$ proportions
164 from $1/6$ to 1. This allowed for parentage analysis that varied both the proportion of parents (*6*
165 *samples*) and offspring (*6 samples*) sampled and resulted in 36 sampling scenarios. Parental and
166 adult offspring genotypes were also subject to a 0.5% genotyping error rate, which is high for the
167 genotyping of SNP loci by the GCL.

Assumption 14. F_0 and F_1 populations were sampled once for each sampling proportion (i.e. the same 1/6 sample of F_0 is used as the parental sample for all samples of F_1 s).

Assumption 15. Genotyping error rate of 0.5% is random among SNP loci.

168

169

MODELING EFFECT SIZE

170 Utilizing the same F_0 parental population created in *EasyPop* 2.0.1, all above steps were repeated
171 for both stray rates for the following four effect sizes of RRS of a HxH cross to a NxN cross:

172 $\frac{4}{8}$, $\frac{5}{8}$, $\frac{6}{8}$, and $\frac{7}{8}$ (RRS = 0.500, 0.625, 0.750, and 0.875).

173

Parentage Analysis

174 Each of the 288 *data sets* (6 parental sub-samples, 6 offspring sub-samples, 2 stray rates, and 4
175 effect sizes) was analyzed using *SOLOMON* (Christie et al. 2013). *SOLOMON* is an exclusion-
176 Bayesian parentage analysis program that runs in *R*. We used the “Bayes” method for “No
177 Known Parents”, which first makes single parent-offspring pairs based on exclusion. The
178 method then calculates the probability of observing shared alleles between unrelated individuals
179 by chance, given the allele frequencies of shared alleles. For each of our 288 data sets,
180 *SOLOMON* generated 100 simulated data sets with 500,000 simulated genotypes (as
181 recommended by Christie et al. 2013 for SNP data) to determine the posterior probability of each
182 parent-offspring pair assignment. This method does not explicitly account for genotyping error,
183 but does allow for mismatches between parent-offspring pairs if the posterior probability of the
184 parent-offspring pair sharing alleles by chance is less than 1. Assignments are made to single
185 parent-offspring pairs only, however, we made parent pair-offspring trio assignments by
186 assigning the most likely female (dam) and male parent (sire) if the *SOLOMON* posterior was
187 less than a critical level (α). We visualized parentage assignment errors at multiple α levels to
188 determine the level that minimized type I and II errors was 0.5 for this marker set..

Assumption 16. Parent pair assignments were created from single parent-offspring relationships.

189

190

ASSIGNMENT ERRORS

191 For each offspring sampled, the assigned parent or parent pairs were compared to the known true
192 parents sampled. Our definition of assignment errors follows that used in Box 1 of Harrison et
193 al. (2013b). Briefly, there are two decisions to be made for each offspring sampled; 1) was a dam
194 assigned? and 2) was a sire assigned? For each of these decisions, there is one of 5 possible
195 outcomes:

196

- True assignment – assigned to true parent

197

- True exclusion – not assigned to any parent, true parent not in sample

198

- Type Ia error – assigned to a false parent, true parent present in sample

199

- Type Ib error – assigned to a false parent, true parent not in sample

200

- Type II error – not assigned to any parent, true parent present in sample

201 Assignment errors were useful to illustrate how much parentage information could be obtained
202 from different sampling rates of parents.

203 *Relative Reproductive Success*

204 DETERMINATION OF RRS

205 We calculated the RRS of hatchery-origin fish to natural-origin fish in two ways: by sex (H_{Female}
206 to N_{Female} and H_{Male} to N_{Male}) and by cross type (HxH cross to NxN cross and HxN/NxH cross to
207 NxN cross). These two approaches differ in their parentage assignment requirements; RRS by
208 sex only requires single parent assignments while RRS by cross type requires parent pair
209 assignments. While determining RRS for single parents by sex *does not* account for the origin of
210 the other parent (could have been H or N), it *does* account for individuals that produce no
211 returning offspring. Determining RRS for parent pairs by cross type *does* account for both
212 parents (and thus all genetic material of the offspring), but will always have lower sample sizes
213 (as fewer offspring are assigned to parent pairs than to single parents) and also *does not* account
214 for pairs that produce no returning offspring. This is because the only evidence of mating
215 between a pair is returning offspring with this approach (Blouin 2003; Christie et al. 2014). As a
216 result, parent pair RRS by cross type can have markedly lower statistical power than single
217 parent RRS by sex (Box 1 in Christie et al. 2014), even though the true RRS by sex will be
218 greater than the true RRS for a HxH to a NxN cross. Given our previous assumptions the true
219 RRS by sex is a function of the stray rate and the true RRS of a HxH to a NxN cross (RRS_{HH})
220 such that:

$$RRS_{\text{Sex}} = \frac{(\text{Stray} * RRS_{\text{HH}}) + \left((1 - \text{Stray}) * \frac{RRS_{\text{HH}} + 1}{2} \right)}{\left((1 - \text{Stray}) * RRS_{\text{HH}} \right) + \left(\text{Stray} * \frac{RRS_{\text{HH}} + 1}{2} \right)}$$

221 To compare these approaches we present RRS for:

- 222 • Single parent-offspring pairs by sex
 - 223 ○ H_{Females} to N_{Females}
 - 224 ○ H_{Males} to N_{Males}
- 225 • Parent pair-offspring trios by cross type
 - 226 ○ HxH to NxN
 - 227 ○ HxN/NxH to NxN

228 However, note that since there is no parameterized difference in RRS between males and females
229 (sexes are treated equally), any differences between males and females in subsequent analyses
230 are due to chance.

231 We used two formulas for calculating RRS,

232 $RRS_{simple} = \frac{\widehat{W}_x}{\widehat{W}_y}$ and

233 $RRS_{unbiased} = \frac{\widehat{W}_x - \left(\frac{N_{offspring} - N_{assigned}}{N_{parent}}\right) \left(\frac{\widehat{b}}{1-\widehat{b}}\right)}{\widehat{W}_y - \left(\frac{N_{offspring} - N_{assigned}}{N_{parent}}\right) \left(\frac{\widehat{b}}{1-\widehat{b}}\right)}$ (Eq. 14; Araki and Blouin 2005)

234 where

235 \widehat{W}_x = observed mean (absolute) fitness of individuals in group x;

236 \widehat{W}_y = observed mean (absolute) fitness of individuals in group y;

237 $N_{offspring}$ = number of offspring sampled;

238 $N_{assigned}$ = number of offspring assigned to a parent;

239 N_{parent} = number of potential parents sampled from groups x and y; and

240 b = rate of Type Ib parentage assignment errors.

241 The rate of type Ib errors is estimated as

242 $\widehat{b} = \frac{\alpha P_{assigned}}{1 - (1-\alpha)P_{assigned}}$ (Eq. 31; Araki & Blouin 2005)

243 where

244 α = threshold probability of incorrect assignments (i.e. *assignment* to an *untrue* parent) used in
 245 likelihood-based or Bayesian-based parentage assignment to accept/reject a parent-offspring
 246 pairing

247 x = number of potential parents from group x

248 y = number of potential parents from group y

249 $P_{assigned} = \frac{N_{assigned}}{N_{offspring}}$ (Appendix I; Araki & Blouin 2005)

250 $P_{offspring} = \frac{xW_x + yW_y}{N_{offspring}}$ (Eq. 23; Araki & Blouin 2005)

251 Both simple and unbiased RRS (Araki and Blouin 2005) were calculated for all of the 1,152
 252 determinations of RRS (4 RRS values [HxH to NxN, HxN/NxH to NxN, H Dam to N Dam, and
 253 H Sire to N Sire] calculated for 288 datasets [2 stray rates, 4 effect sizes, 6 levels of F₀ sampling,
 254 6 levels of F₁ sampling]). Differences were calculated as:

$$Difference = RRS_{Simple} - RRS_{Unbiased}$$

255 We report results from both formulas, despite minimal differences. The unbiased estimation of
256 RRS from Araki & Blouin (2005; see Tech Doc 1 – Shedd et al. 2014) corrects for biases when
257 only a fraction of the parents are sampled and when offspring are assigned to an untrue parent
258 (Type Ib error). Given that the *SOLOMON* produced very few Type Ib errors, the differences
259 between the RRS_{simple} and $RRS_{unbiased}$ estimates were minimal. Type Ib error was empirically
260 determined from the parentage data, given that all simulated matings were known.

261 TEST FOR RS DIFFERENCES

262 Two types of statistical tests were done to test the null hypothesis that RS is not different for fish
263 of hatchery- and natural-origin (by cross type for parent pairs and by sex for single parent
264 pairings). Both tests were one-tailed tests (testing whether $RRS < 1$) and used an α -level of 0.05
265 as the cutoff for significance.

266 NON-PARAMETRIC

267 The first approach was to implement a nonparametric permutation test as described in Araki and
268 Blouin (2005) to compare the absolute fitness (number of offspring per family) of two groups.
269 This approach was used because it makes no assumption about the distribution of the RS data
270 and empirically quantifies a probability that the estimated RRS is less than 1. One-sided
271 permutation tests to compare absolute fitness between hatchery- and natural-origin groups were
272 calculated with 100,000 permutations by a custom R function. Probabilities were compared to
273 and did not differ from those reported by the “oneway_test” function with 100,000 permutations
274 in the “coin” package in R and the program PERM 1.0 (Duchesne et al. 2006) with 10,000
275 permutations as used by Hess et al. (2012) and Thériault et al. (2011).

276 PARAMETRIC

277 The second approach was to use a parametric generalized linear model (GLM). The GLM used a
278 negative binomial error structure and a log link function that was fit separately for each cross
279 type or sex using the package “MASS” as done by Anderson et al. (2013). The form of the
280 model was $RS = origin + \epsilon$, with origin referring to H or N origin. The significance of origin
281 was evaluated via analysis of deviance. RRS was determined by exponentiation of the origin
282 parameter via the log link in the model. The SE of the origin parameter was also back
283 transformed and multiplied by ± 1.645 in order to give a 90% confidence interval on RRS.

284 POWER OF SAMPLING LEVEL

285 To evaluate the power of tests using the permutation (nonparametric) approach, we used the
286 distribution of RS differences and calculated the minimum difference in RS we could have
287 detected with 80% and 95% probability (Thériault et al. 2011; Hess et al. 2012). These
288 minimum detectable differences in RS are displayed as RRS.

289 We used two methods to evaluate the power of our test for the negative binomial GLM approach.
290 We report the width of the 90% CI for our estimate of RRS and the probability that our estimate
291 of RRS is < 1 (i.e. % of distribution for mean RRS that is less than 1). We report the width of

292 the 90% CI rather than the standard error of the estimate as the CI is asymmetric due to the back
293 transformation of the logit link function.

294 *Model Assumptions*

295 Any simulation work attempting to reliably portray nature comes with assumptions. The
296 assumptions that we made are listed above in the order that they were made in. It is important to
297 consider both the likelihood of such assumptions being true and how robust simulation results
298 are to violations of those assumptions (i.e. sensitivity). While it is unlikely that all the
299 assumptions for these simulations are perfectly met, many of these were “simplifying”
300 assumptions to allow us to get an approximation of the data we may expect from this project
301 given different scenarios. These were necessary to arrive at results and we feel confident they
302 are likely to be true in the AHRP.

303 **Results**

304 *Population Genetics of Simulated Data Sets*

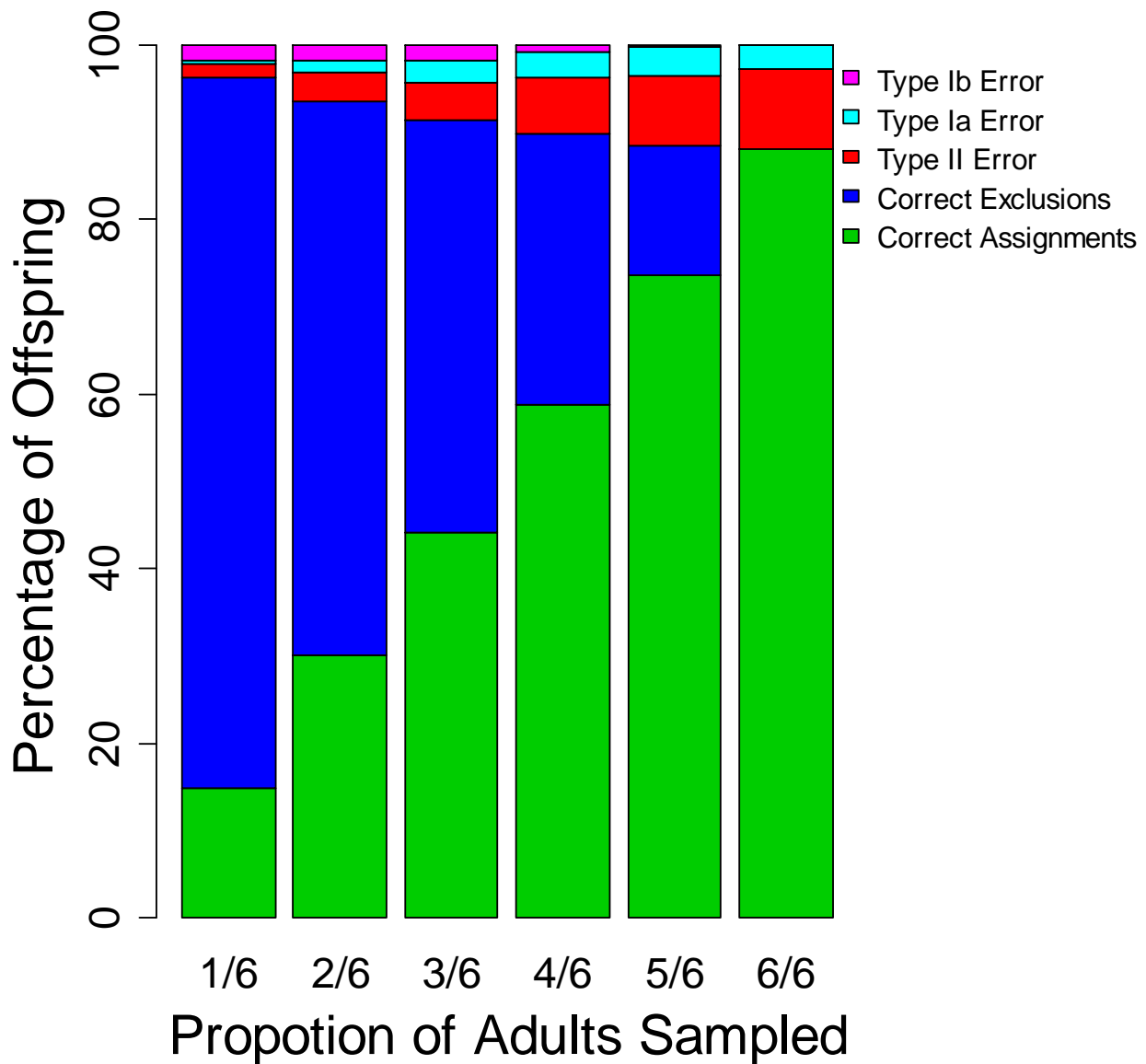
305 The parental data set generated in *EasyPop* 2.0.1 had an average minor allele frequency (MAF)
306 of 0.338 across all 96 loci. Observed and expected heterozygosity was 0.422 and 0.424,
307 respectively for an F_{IS} of 0.003. Fisher’s exact test for deviations from Hardy-Weinberg
308 equilibrium (HWE) across all loci was not significant ($\chi^2=204.04$, $df=192$, $p=0.26$).

309 *Distribution of RS of Simulated Data Sets*

310 The distribution of adult offspring per family (RS) was different between high and low stray rate
311 streams (Figure 1) due to the assumption that 3,000 modeled spawners will produce a fixed
312 number of returning adults such that these recruits + new strays = 3,000 spawners. Thus, the
313 overall RS of spawners in a high stray rate stream was modeled to be lower than in a low stray
314 rate stream ($\mu = 1$ vs. $\mu = 1.7$). Reproductive success is shown for cross types (matings), dams,
315 and sires for both the proportion of crosses/dams/sires that produced a given number of offspring
316 (Figure 1, 2, and 3) and the frequency (number of occurrences) of crosses/dams/sires that produce
317 a given number of offspring (Figure 4, 5, and 6), respectively.

318 *Parentage Analysis Assignment Errors*

319 The rates of parentage assignment outcomes (Box 1 of Harrison et al. 2013b) were consistent
320 across stray rates, effect sizes, and the proportion of F_1 sampling, but varied among different
321 proportions of F_0 sampling (



322
 323 Figure 7). The percentage of F_1 individuals that were correctly assigned to a parent-offspring
 324 pair increased nearly linearly with the increasing proportion of adults sampled, corresponding to
 325 a decrease in the number of F_1 's correctly excluded from a relationship. Type I error rates (both
 326 Type Ia and Ib) in which *incorrect parent-offspring pairings* were made, averaged 3.3% of all
 327 parent-offspring determinations. Type II error rates in which offspring *fail to be assigned* to a
 328 parent when that *parent was sampled*, increased from 1.5% of F_1 determinations for a sampling
 329 of 1/6 of the F_0 's to 9.2% of F_1 determination when all F_0 potential parents were sampled.

330

Determination of RRS

331

UNBIASED VS. SIMPLE

332 Differences between the simple and unbiased calculations of RRS (Araki and Blouin 2005) were
333 minimal for all simulated datasets (median \pm SD = 0.0006 \pm 0.012), as the level of Type Ib error
334 was minimal for the parentage assignment methods that we used (Eq. 14; Araki and Blouin
335 2005). Differences were greater for single parent RRS than for cross type RRS. Of the 73
336 instances where | difference | was $>$ 0.02, 69 were for single parent RRS. Unbiased RRS was
337 closer to the true RRS than simple RRS in 57% of the total determinations of RRS, 72% of the
338 determinations of cross type RRS, and 42% of the determinations of single parent RRS.

339

Significance of RRS

NONPARAMETRIC PERMUTATION TEST VS. PARAMETRIC NEGATIVE BINOMIAL GLM

341 Nonparametric (permutation test) and parametric (negative binomial GLM) approaches testing
342 for significant differences in fitness between hatchery- and natural-origin dams and sires
343 produced qualitatively similar results (Table 1-8). Of the 576 tests performed for each statistical
344 approach, 240 of the parametric tests (42%) and 252 of the nonparametric tests (44%) were
345 significant ($p <$ 0.05). However, the parametric approach was more powerful for detecting
346 known differences in fitness for RRS by cross type, with 68 significant tests out of 576 tests
347 (12%) compared to 36 significant tests out of 576 tests (6%) for the nonparametric approach.

348

SINGLE PARENT

349 As intuitively expected, tests for differences in fitness between hatchery- and natural-origin dams
350 and sires were statistically significant ($p <$ 0.05) more often for *higher sample proportions* of
351 F_0 's and F_1 's, *larger effect sizes* (i.e. smaller modeled RRS of a HxH to a NxN cross), and a
352 *higher stray rate* (50% hatchery-origin F_0 's vs. 15% hatchery-origin F_0 's; Table 1-8). When the
353 modeled RRS of a HxH to a NxN cross was 0.50, most sampling schemes of F_0 's and F_1 's
354 resulted in findings of significance. As effect size decreased (an increase in the modeled RRS of
355 a HxH to a NxN cross), more sampling of both F_0 and F_1 was required to detect the effect. For
356 each effect size, more sampling of both F_0 and F_1 was required to detect the effect for the low
357 stray rate scenario (15% hatchery-origin) than the high stray rate scenario (50% hatchery-origin).
358 Only one simulation found a significant difference in fitness between hatchery- and natural-
359 origin fish when only 1/6 of the F_0 parents (500 out of 3,000 adults) and 1/6 of the F_1 offspring
360 (500 out of 3,000 adults) were sampled.

361

CROSS TYPE

362 Similar to tests of single parent RRS, tests for differences in fitness between HxH cross type and
363 NxN cross type were statistically significant ($p <$ 0.05) more often for *higher sample*
364 *proportions* of F_0 's and F_1 's, *larger effect sizes* (i.e. smaller modeled RRS of a HxH to a NxN
365 cross), and a *higher stray rate* (Table 9-12). However, tests for differences in fitness between
366 hatchery/natural hybrid cross type and natural/natural cross type were statistically significant

367 ($p < 0.05$) more often for *higher sample proportions* of F_0 's and F_1 's, *larger effect sizes* (i.e.
368 smaller modeled RRS of a HxH to a NxN cross), and the *lower stray rate* (Table 13-16).

369 Overwhelmingly, for a given stray rate and effect size, it took a larger sampling proportion of
370 F_0 's and F_1 's to find statistically significant differences in fitness between hatchery- and natural-
371 origin fish when considering RRS by cross type than RRS for single parents. This is due to the
372 smaller number of families detected (i.e. lower numbers of offspring assigned to parent pairs
373 than single parents) and the fact that families producing 0 offspring are not considered when
374 estimating RRS by cross type. Simulations were unable to detect a significant fitness difference
375 ($p < 0.05$) between HxH and NxN cross types in a high stray rate scenario when less than half
376 of the F_0 parents were sampled, and only once detected a significant fitness difference in a low
377 stray rate scenario (Table 9-12). Simulations found significant fitness differences ($p < 0.05$)
378 between HxN/NxH hybrid cross type and NxN cross type in a high stray rate scenario only when
379 greater than half of the F_0 parents were sampled, and in a low stray rate scenario when at least a
380 third of F_0 parents and half of F_1 offspring were sampled (Table 13-16).

381 *Power to Detect RRS < 1*

382 "POWER" FROM PERMUTATION TEST

383 We used the distribution of RS differences from the permutation tests to evaluate the power of
384 tests by calculating the minimum difference in RS we could have detected with 80% and 95%
385 probability (Thériault et al. 2011; Hess et al. 2012). The maximum RRS value that could be
386 detected with 80% and 95% probability increased for all stray rates and effect sizes with
387 increasing sampling proportions of F_0 's and F_1 's (Figure 8-11). The rate of increase was faster
388 with increases in F_0 sampling proportions than with F_1 sampling proportions. For the largest
389 modeled effect size (a modeled RRS of HxH cross to NxN cross of 0.50), a sampling scheme of
390 at least a third of the F_0 adults and a third of the F_1 offspring would have shown a significant
391 difference in RS ($p < 0.05$) for a high stray rate scenario, while a sampling scheme of 1/6 of the
392 F_0 parents (500 out of 3,000 adults) and 1/6 of the F_1 offspring (500 out of 3,000 adults) would
393 only have power to detect a single parent RRS of 0.50. In a low stray rate scenario, at least half
394 of the F_0 adults and half of the F_1 offspring would have shown a significant difference in RS
395 ($p < 0.05$). As the effect size decreases (i.e. increasing RRS of HxH cross to a NxN cross), the
396 sampling proportion of F_0 's and F_1 's must increase to be able to statistically detect a true
397 difference in single parent RRS.

398 CONFIDENCE INTERVAL WIDTH FOR RRS ESTIMATE FROM NEGATIVE BINOMIAL GLM

399 The 90% CI width for single parent RRS decreased with increasing sampling proportions of F_0 's
400 and F_1 's. However, this decrease occurs more rapidly for increases in F_0 sampling than for
401 increases in F_1 sampling (Figure 12). Sampling less than half of F_0 's and half of F_1 's resulted in
402 a 90% CI width for the single parent RRS estimate of less than 0.3 and 0.4 for high and low stray
403 rate scenarios, respectively.

404 Similarly, the 90% CI width for HxH cross type RRS decreases with increasing sampling rates.
405 However, even with full sampling of all F_0 's and all F_1 's it remains as high as 0.3 for a high stray
406 rate stream and 0.5 for a low stray rate stream (Figure 13). Over two-thirds of F_0 's and F_1 's
407 needed to be sampled for the 90% CI width of the single parent RRS estimate to be less than 1.0
408 in a low stray rate stream.

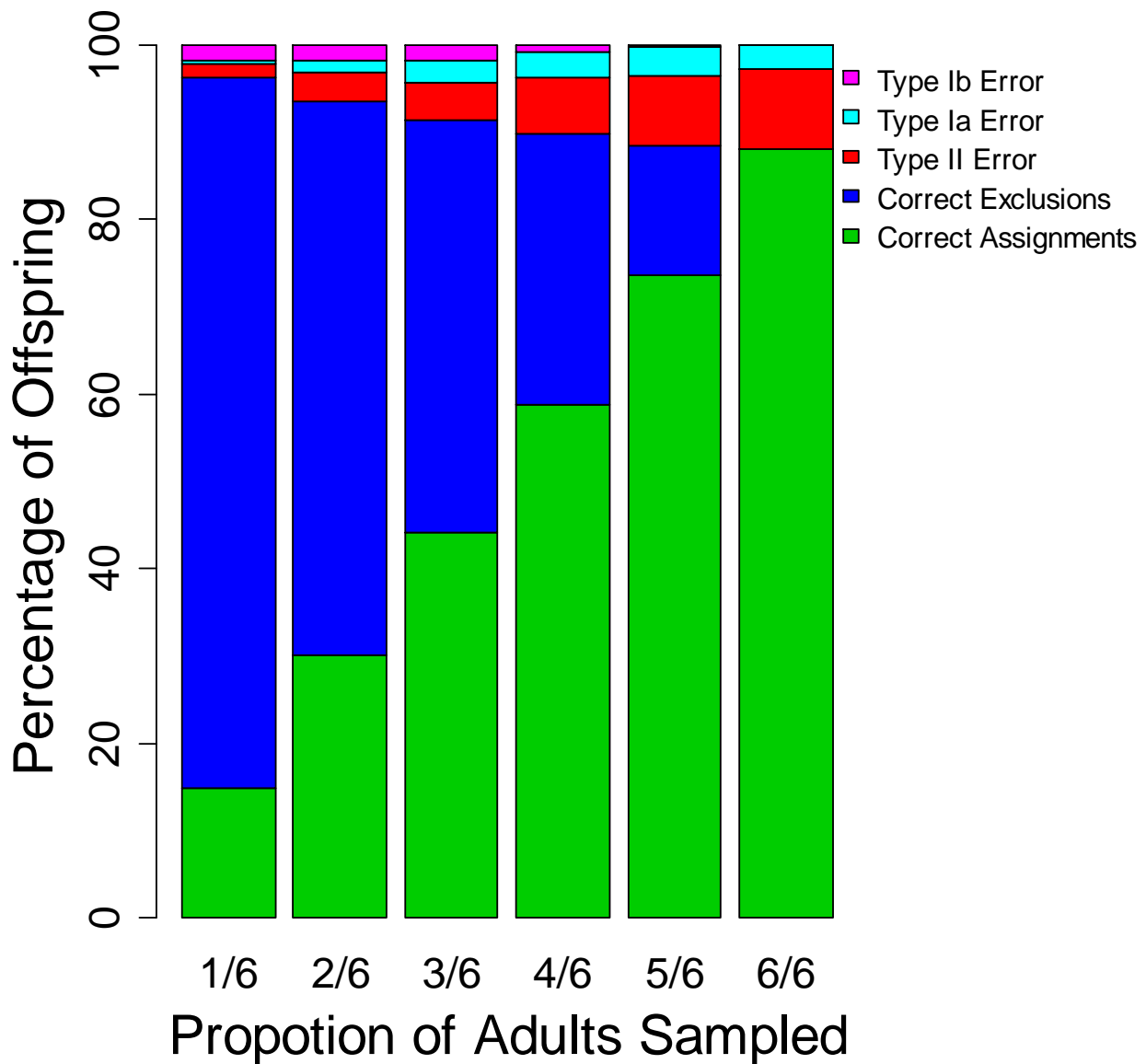
409 The 90% CI width for HxN cross type RRS is similar to that of the HxH cross type for the high
410 stray rate scenario (Figure 14). For the low stray rate scenario, the 90% CI width for HxN cross
411 type RRS is lower than that of the HxH cross type for a given level of F_0 and F_1 sampling.
412 Nonetheless, a sampling scheme of half of the F_0 's and half of the F_1 's would result in a 90% CI
413 width of 0.5 RRS.

414 Discussion

415 *Simulation Parameters*

416 Parameters were chosen for both the demographic and genetic characteristics of our simulated
417 populations. Demographic parameters were largely constrained by assumptions of constant
418 escapement size, constant stray rate, and the modeled differences in RRS between hatchery- and
419 natural-origin fish. With regard to the sampling distribution of family size, it is important to note
420 that this study only samples escapement, not the total run (catch + escapement). Mean returns
421 per spawner for broodyears 1960-2011 for PWS pink salmon is 5.39 (Fair et al. 2011) and other
422 studies have shown a wide range of family sizes for pink salmon from year to year (Geiger et al.
423 1997). However, we constrained the mean family size for our escapement populations to $\mu < 2$
424 for consistent escapement across years given a constant stray rate into the populations (Figure 1-
425 6). This reduction in mean family size between the total return and the escapement may not
426 affect the point estimate of RRS of hatchery- to natural-origin fish (the ratio of mean family sizes
427 between groups), but likely reduces the difference in mean family sizes between groups, thus
428 reducing the power to detect an effect (see Table 4 in Araki and Blouin 2005). Other simulation
429 work has shown that power to detect differential RS increases with increasing productivity of a
430 system (i.e. when mean family size is large; Hinrichsen 2003).

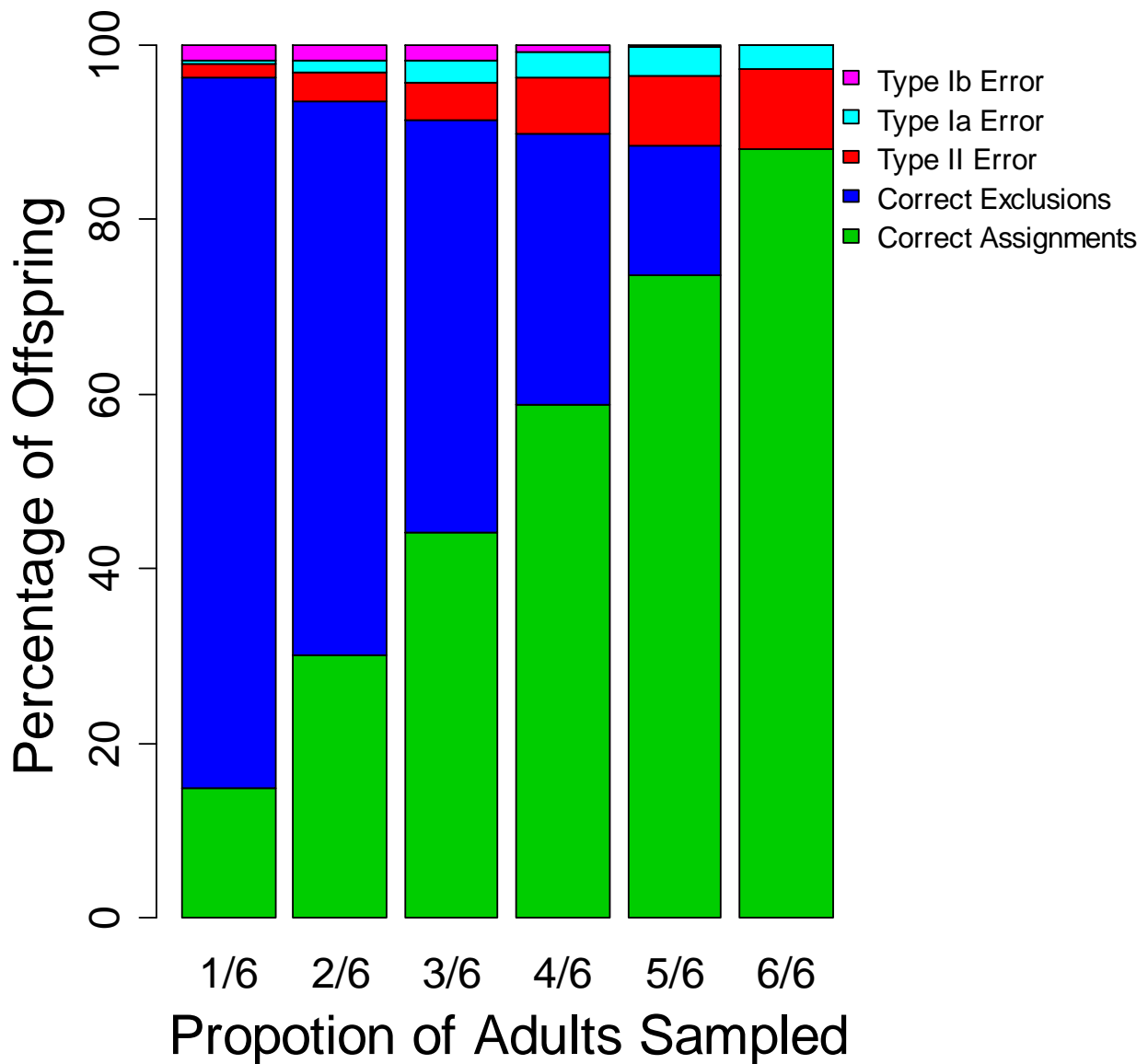
431 The main genetic parameter of interest for parentage analysis with SNP markers is the MAF of
432 the markers. Higher MAF results in increased power for parentage inference and decreased
433 false-positive rates (Anderson and Garza 2006). Our simulated genetic dataset had a MAF of
434 0.338 for the 96 SNPs used, allowing for high power for parentage inference with minimal
435 parentage assignment errors (



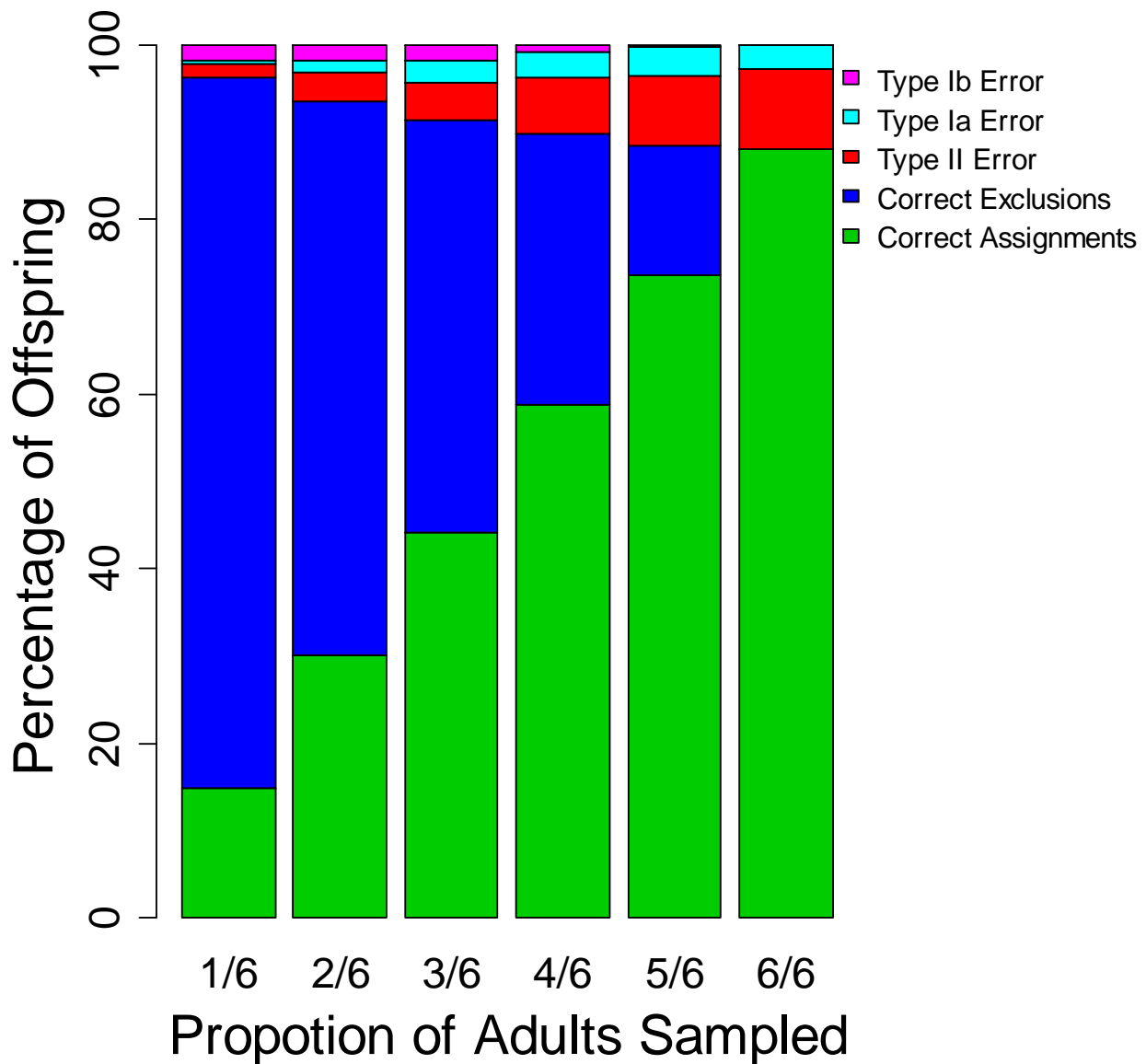
436
 437 Figure 7). While SNP markers for pink salmon for parentage analyses are still in development,
 438 we are confident that we will be able to use a set of 96 SNPs with a mean MAF of > 0.3, which
 439 will provide sufficient power for parentage analyses (Anderson and Garza 2006; Hauser et al.
 440 2011; Steele et al. 2013). Preliminary marker selection for the 188 chum SNPs available have
 441 indicated a mean MAF of 0.24 for the four chum streams in the fitness study. It is likely that the
 442 final 96 SNP marker panel will have a mean MAF > 0.3. As a result, the key limiting factor to
 443 power in this study will be the level of sampling, not the genetic markers or the specific
 444 parentage analysis software used.

445 *Parentage Analysis Assignment Errors*

446 The simulated genotype data provided sufficiently high power for parentage inference with
 447 minimal type I error, or false assignments of offspring to incorrect parents (



448
 449 Figure 7). Nevertheless, there is a tradeoff in parentage analysis between type I error (false
 450 assignments) and type II error (failing to make correct assignments). While increased sampling
 451 of F_0 's resulted in a higher proportion of F_1 's being correctly assigned to a parent-offspring
 452 relationship, it also resulted in an increase in type II error (



453 Figure 7). Similar issues with high levels of type II error with the parentage analysis package
 454 *SOLOMON* (Christie 2010; Christie et al. 2013) have been noted in the literature (Christie 2013;
 455 Harrison et al. 2013b, 2013a). High type II error is akin to failing to sample offspring (i.e.
 456 effectively decreasing the proportion of offspring sampled) and may contribute to a reduction in
 457 power to detect differences in RRS (Araki and Blouin 2005).
 458

459 These simulations were designed to determine the power to detect differences in the RRS of two
 460 groups via parentage analysis according to stray rate, effect size, and the sampling proportions of
 461 F_0 's and F_1 's. There are many software packages available for parentage analysis (Jones et al.
 462 2010), however, with informative genotypic data any differences among approaches should be
 463 minimal. Nevertheless, it is likely that the GCL will pursue methods other than *SOLOMON* in

464 the future due to the undesirably high levels of type II error, the lack of parent pair-offspring trio
465 assignments, and the relatively slow computational speed.

466 *Determination of RRS*

467 We found small differences between RRS_{Simple} and the $RRS_{Unbiased}$ (Araki and Blouin 2005) for
468 most of the simulated data sets. Differences will be minimized at high sampling proportions of
469 F_0 and F_1 's and low Type Ib errors. Thresholds of likelihood/probability measures for parentage
470 assignment can be maintained to keep type b error low and avoid differences between simple and
471 unbiased estimates of RRS.

472 *Nonparametric vs. Parametric Statistical Tests*

473 There are many statistical tests that can be used to detect differences in reproductive success.
474 The two most common methods that we have seen used in the literature are parametric negative
475 binomial GLMs (Anderson et al. 2013) and nonparametric permutation tests (Araki and Blouin
476 2005; Thériault et al. 2011; Hess et al. 2012). We found that a parametric approach utilizing a
477 negative binomial GLM had higher power to detect a known difference in RRS than a
478 nonparametric permutation test for our simulated data. However, this comes with the
479 assumption that family size is characterized by a negative binomial distribution. This
480 assumption was certainly valid for our simulations, as family size data was generated from a
481 negative binomial distribution, but may not be valid for future data. Family size in salmonids is
482 non-normally distributed for natural populations, and often appears well described by the
483 negative binomial distribution (Geiger et al. 1997; Geiger et al. 2007; Anderson et al. 2011;
484 Anderson et al. 2013; Aykanat et al. 2014; Christie et al. 2014). If our sample data appear to fit a
485 negative binomial distribution, then a parametric approach may have more power. Otherwise a
486 permutation test may be more appropriate with real data if it does not appear to fit a given
487 distribution.

488 *Single Parent vs. Cross Type RRS*

489 These simulations showed much more power to detect differential RS for single parent-offspring
490 pairs by sex than for parent pair-offspring trios by cross type. There are two main reasons for
491 this: 1) difference in sample sizes and 2) the accounting for matings that produce 0 offspring.
492 Sample size is the number of families for which family size (RS) is being compared. The number
493 of F_0 's sampled relates to the potential number of families sampled (sample size for describing
494 family size distribution), while the number of F_1 's sampled will determine how well those family
495 size distributions are characterized. We know from previous research on individual RS in
496 salmonids that family size is often highly skewed (negative binomial) with most families
497 contributing very little to production (0, 1, or 2 offspring) and few families contributing much
498 more (10+ offspring; Geiger et al. 1997; Anderson et al. 2013). Thus, sampling a small
499 proportion of the returning adult offspring will result in truncated distributions (i.e. cut off the
500 tails) in which fewer large families (those that contribute the most to production) are represented
501 in the sample.

502 The number of F_1 offspring that are assigned to single parent-offspring pairs is proportional to
 503 the fraction of F_0 parents that are sampled. However, the number of F_1 offspring that are
 504 assigned to a parent pair-offspring trio is proportional to the square of the fraction of F_0 parents
 505 that are sampled (assuming equal sex ratio).

$$n. families_{RRS \text{ by Sex}} = n. F_0. sampled \times \left(n. F_0. sampled / n. F_0. total \right)$$

$$n. families_{RRS \text{ by Cross Type}} = n. F_0. sampled \times \left(n. F_0. sampled / n. F_0. total \right)^2$$

506 Thus, the number of families available for determination of the single parent RRS by sex will
 507 always be larger than the number of families available for determination of parent pair RRS by
 508 cross type (Appendices). This smaller number of cross type families is then further reduced by
 509 being broken out into the three cross types (HxH, HxN/NxH, and NxN), rather than two origin
 510 groups (H and N), especially if the stray rate is low and few HxH matings occur.

511 In addition to the larger sample size of families for single parent RRS by sex than for parent pair
 512 RRS by cross type there is the issue of being unable to represent parent pairs that produce 0
 513 offspring, because the only way parent pair matings are known to have taken place is the
 514 presence of at least 1 adult offspring that is assigned to that parent pair (Blouin 2003). Unless
 515 assumptions are made about the number of matings that occurred based on the stray rate, it is not
 516 possible to disentangle non-random mating from differences in parental fecundity or offspring
 517 survival (Blouin 2003).

518 *Power to Detect $RRS < 1$*

519 These simulations show that the power to detect an effect ($RRS < 1$) increases with: increasing
 520 sample proportion of F_0 's, increasing sample proportion of F_1 's, a higher stray rate (50% vs.
 521 15%), a larger effect size (i.e. smaller true RRS), and determining RRS for single parent-
 522 offspring pairs by sex rather than parent pair-offspring trios by cross type. Power to detect an
 523 effect increased and the 90% CI surrounding RRS estimates decreased faster for increasing
 524 sample proportions of F_0 's than for F_1 's. This suggests that while it is important to increase both
 525 the number of families sampled (by increasing the proportion of F_0 's sampled) and better
 526 characterize the distribution of family size for each group (by increasing the proportion of F_1 's
 527 sampled), it may be more important to focus limited resources on sampling a large proportion of
 528 F_0 's. However, this will be confounded by the fact that as this study continues, each sampling
 529 year will be collecting the offspring for the previous generation and the parents for the next (for
 530 pink salmon; F_1 's are offspring of F_0 's, but parents for F_2 's). Nonetheless, it is important to
 531 sample a high proportion of both F_0 's and F_1 's, as power increases the fastest per unit effort if the
 532 sampling proportions are roughly equal.

533 Both single parent and cross type RRS can be estimated from future data. However, there will
534 be less power to detect an effect for a given level of sampling for cross type RRS, especially for
535 detecting an effect for HxH to NxN matings, due to the lower expected number of HxH matings
536 relative to HxN matings (Figure 13-14). There will have to be fairly large effect ($RRS < 0.5$) for
537 the current study plan to detect a difference in the RRS of HxH to NxN or HxN to NxN cross
538 types.

539 On the other hand, we demonstrate that it should be possible to detect a significant difference in
540 the RS of hatchery- and natural-origin fish (single parent by sex) if the true RRS of a HxH to
541 NxN cross is 0.5, the stray rate is 50%, and at least 1/3 of the F_0 parents and 1/3 of the F_1
542 offspring are sampled. Increases in F_0 and F_1 offspring continue to offer improved power,
543 however the marginal improvement appears to slow down and begin to asymptote past a
544 sampling proportion of 1/2 of the F_0 parents and 1/2 of the F_1 offspring. This may be the point of
545 diminishing marginal returns for increasing power to find $RRS < 1$. The Science Panel will
546 ultimately determine what level of power, in terms of the maximum RRS that will likely be
547 detectable, is appropriate for this study.

548 *Comparisons with other Power Analyses in the Literature*

549 Given the increased recent interest in genetic parentage analysis (Jones et al. 2010) and the
550 growing number of studies on the relative reproductive success of hatchery- to natural-origin
551 salmonids (see Naish et al. 2007; Araki et al. 2008; and Christie et al. 2014 for recent reviews),
552 there has been previous research done to assess the power of studies of RRS. None of the
553 previous studies were completely suited to the needs of the AHRP due to the scope of the
554 parameters that were modeled, but each provides support for different conclusions of these
555 simulations.

556 These simulations and other work have confirmed that a set of 96 SNPs is both sufficient and
557 powerful for genetic parentage analysis on a broad scale (Anderson and Garza 2006; Hauser et
558 al. 2011; Steele et al. 2013). Similar to both Hinrichsen (2003) and Aykanat et al. (2014), we
559 found more power when the stray rate was closer to 50%. We also demonstrated that it is
560 possible to detect significant differences in RS when only a fraction of F_0 parents and F_1
561 offspring are sampled, if the effect is sufficiently large (Hinrichsen 2003; Anderson et al. 2011;
562 Aykanat et al. 2014), but that power increases dramatically when multiple brood years are
563 considered (Hinrichsen 2003; Aykanat et al. 2014). For example, simulations performed by
564 Aykanat et al (2014) based on field data with average sampling proportions of 0.32 found that
565 when only a single sex and cohort was considered, there was greater than 0.8 power to detect a
566 RRS less than 0.35ⁱⁱ. However, when data was combined across 10 cohorts (brood years), they
567 had greater than 0.8 power to detect a RRS (single parent by sex) less than 0.7, so long as the

ⁱⁱ Note: Aykanat et al. 2014 present RRS as the ratio of the high RS group to that of the low RS group, which is the inverse of how RRS has been reported throughout this document. Thus an RRS of 2.9 corresponds to an RRS of 0.35 here.

568 stray rate was between 15-85% (Aykanat et al. 2014). Qualitatively similar results were
569 described by Hinrichsen (2003), who found that increasing the number of brood years being
570 sampled from 1 to 5 resulted in an increase in power from 0.14 to 0.79 when true RRS was 0.8
571 (single parent by sex), the stray rate was 50%, and a sampling proportion of 0.5 for both
572 spawners (F_0 's) and recruits (F_1 's). Hinrichsen (2003) also found that the power for RRS studies
573 increases with higher productivity (i.e. high recruits per spawner or higher mean family size) and
574 lower variance in family size.

575 With regard to these simulations, power was determined for the single brood year being
576 measured, so power should increase when data from multiple brood years are combined
577 (Hinrichsen 2003; Aykanat et al. 2014).

578 *Potential Risks in Sampling Design*

579 These simulations focused on pink salmon due to their simpler life history without overlapping
580 generations. It will be important to consider that each year will need a consistently high
581 sampling effort for the chum fitness study ongoing in SEAK, as adult offspring return 2-5 years
582 later. This will be especially critical if there are differences in the age at return between
583 offspring from the different origin groups. For example, if hatchery-origin offspring return more
584 often at age 3 and natural-origin offspring return more often at age 4, what would be the effect
585 on the estimate of RRS if the sampling proportion of offspring is relatively high in the 3rd year,
586 but low in the 4th year? While estimates of the proportion of adults sampled in a given year are
587 currently unavailable, the numbers of adults sampled per stream can vary wildly from one year to
588 the next, based on samples collected in 2013 and 2014. This high variability in the proportion of
589 returning adults sampled with current field methods may represent an additional source of
590 vulnerability in the current study design. Each sampling year for chum is highly interdependent
591 with other years due to the overlapping generations, as opposed to pinks for which a year of low
592 sampling will affect fewer other years of sampling.

593 *Future Directions*

594 While we believe that these simulations have provided valuable insight into the potential
595 statistical power of this fitness study, any simulation work comes with assumptions and caveats.
596 With these assumptions and caveats in mind, we see two primary directions for future work.

597 A recent review paper by Christie et al. (2014) included a section (Box 2) with a brief
598 explanation of how statistical power relates to studies of RRS. Christie et al. (2014) describe the
599 relationship between statistical power, true RRS (effect size), and the sample size of F_0 parents.
600 It would be useful for the AHRP to replicate those simulations with a larger range of F_0 parental
601 sample sizes (Christie et al. 2014 chose 10-400), variable stray rate (Christie et al. 2014 only
602 modeled 50% stray rate), variable proportion of offspring sampled (Christie et al. 2014 assumed
603 that all offspring are sampled), and variable distribution of family size (Christie et al. 2014 used
604 a negative binomial distribution with $\mu = 8$, which is unlikely for our scenario given that we are
605 sampling escapement). These simulations would be relatively simple and much faster as they do

606 not involve the creation of genotypes to perform genetic parentage analysis, as the parentage
607 analysis is assumed to be nearly perfect. These simulations would provide better resolution as
608 power is calculated as the proportion of tests that are found significant, as opposed to these
609 simulations which relied on one dataset for each set of parameters (no replicates). These new
610 simulations based on the Christie et al. (2014) could further be extended to include power over
611 multiple brood years (cohorts).

612 Another important line of future effort is to explore other programs to perform genetic parentage
613 analysis. At the time these simulations were initiated, *SOLOMON* (Christie 2010) was chosen
614 for its Bayesian approach and lack of assumptions required. Most other parentage analysis
615 approaches assume that all possible parents have been sampled or that the sampling fraction of
616 true parents is known (Anderson 2013). However, there are a large and growing number of
617 parentage analysis programs available (Jones et al. 2010) and *SOLOMON* has been shown to
618 have a higher than desirable type II error rate (Harrison et al. 2013b, 2013a), is relatively slow,
619 and only makes single parent-offspring pairings. Anderson and Ng (2014) have recently
620 published an update to *SOLOMON* that they have dubbed *SOLIDMON*, which is more accurate
621 and two orders of magnitude faster than *SOLOMON*. Other potential approaches include
622 utilizing *MYKISS* (Kalinowski 2008) or *SNPPIT* (Anderson 2010), which are both very fast, but
623 only assign offspring to parent pair-offspring trios, or *FRANz* (Riester et al. 2009) which is able
624 to perform both single parent-offspring pairs and parent pair-offspring trios and utilize additional
625 data such as age and sex. However, some of these other programs have additional assumptions,
626 such as accurately knowing the proportion of parents sampled. Nevertheless, methods continue
627 to improve and future work promises to solve these technical problems (Anderson 2013).

628

Summary

629 We performed a series of analyses on simulated genetic data to determine the power of parentage
630 analysis to detect differential RS between hatchery- and natural-origin fish with respect to stray
631 rate, effect size, and the proportion of F_0 parents and F_1 offspring. Genotypes were created for
632 hypothetical pink salmon populations based on demographic parameters from the literature and
633 the study RFP. We found that this study will have sufficient power to perform parentage
634 analysis with minimal assignment errors with a set of 96 SNPs. The power to detect $RRS < 1$
635 increases with a higher stray rate, larger effect size (lower true RRS), and increased proportions
636 of adults and offspring sampled. There is higher power to detect $RRS < 1$ when RRS is
637 calculated for single parent-offspring pairs by sex, rather than for parent pair-offspring trios by
638 cross type. While power increases for both increases in the sampling proportion of F_0 parents
639 and F_1 offspring, it increases faster for the proportion of F_0 parents. Increases in power begin to
640 reach diminishing marginal returns once greater than half of F_0 parents and F_1 offspring are
641 sampled. The current study design, as listed in the RFP likely does not have sufficient power to
642 detect a significant effect, even if true RRS is as low as 0.5. Future work will focus on more

643 robust estimates of power in order to inform sampling design, and improvements in the
644 computational speed, accuracy, and robustness of parentage analysis.

645 **Questions for the AHRP**

- 646 1. What level of power, in terms of the maximum RRS that would likely be detectable, is
647 appropriate for this study?
- 648 2. What are alternative study designs that could increase the proportion of adults and
649 offspring sampled?

650 **AHRP Review and Comments**

651 *This technical document was discussed at the December 12, 2014 meeting of the AHRG. In*
652 *addition it was reviewed by email exchange prior to the meeting.*

653 This document raised several important considerations for the research related to reproductive
654 success of hatchery and natural origin parents. The panel recommended increased effort to
655 collect more samples in response to the document findings. However it was noted that in the
656 pedigree study streams there are finite populations and thus the minimum numbers offered in this
657 document would not apply.

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Tables

786 **Table 1: The estimated RRS of a hatchery-origin dam to a natural-origin dam for a modeled RRS of 0.5 for a HxH cross**
 787 **to a NxN cross for different sampling proportions of parents (F_0) and offspring (F_1) ranging from 1/6 to 6/6. Results are**
 788 **shown for high and low stray rates (top and bottom) and two statistical tests for significance (left and right). Note that**
 789 **cells are colored light gray for a p-value < 0.2, gray for a p-value < 0.05, and dark gray for a p-value < 0.01.**

		Negative Binomial GLM						Permutation Test							
		F_0 Sample Proportion						F_0 Sample Proportion							
		1/6	2/6	3/6	4/6	5/6	6/6	1/6	2/6	3/6	4/6	5/6	6/6		
High Stray (50%)	F_1 Sample Proportion	1/6	0.91	0.51	0.92	0.71	0.63	0.76	1/6	0.91	0.51	0.92	0.71	0.63	0.76
		2/6	0.76	0.51	0.57	0.66	0.68	0.67	2/6	0.76	0.51	0.57	0.66	0.68	0.67
		3/6	0.76	0.58	0.66	0.77	0.75	0.70	3/6	0.76	0.58	0.66	0.77	0.75	0.70
		4/6	0.84	0.61	0.66	0.76	0.71	0.71	4/6	0.84	0.61	0.66	0.76	0.71	0.71
		5/6	0.75	0.64	0.64	0.71	0.69	0.69	5/6	0.75	0.64	0.64	0.71	0.69	0.69
		6/6	0.71	0.62	0.66	0.71	0.68	0.66	6/6	0.71	0.62	0.66	0.71	0.68	0.66
Low Stray (15%)	F_1 Sample Proportion	1/6	0.73	0.74	0.69	0.65	0.85	0.82	1/6	0.73	0.74	0.69	0.65	0.85	0.82
		2/6	0.87	0.74	0.64	0.65	0.76	0.72	2/6	0.87	0.74	0.64	0.65	0.76	0.72
		3/6	0.79	0.60	0.61	0.66	0.70	0.66	3/6	0.79	0.60	0.61	0.66	0.70	0.66
		4/6	0.76	0.85	0.75	0.75	0.73	0.76	4/6	0.76	0.85	0.75	0.75	0.73	0.76
		5/6	0.89	0.78	0.75	0.76	0.78	0.78	5/6	0.89	0.78	0.75	0.76	0.78	0.78
		6/6	0.87	0.73	0.74	0.71	0.75	0.73	6/6	0.87	0.73	0.74	0.71	0.75	0.73

Note: F_0 parental and F_1 offspring were generated and sampled once for a given stray rate and effect size.

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Table 2: The estimated RRS of a hatchery-origin dam to a natural-origin dam for a modeled RRS of 0.625 for a HxH cross to a NxN cross for different sampling proportions of parents (F_0) and offspring (F_1) ranging from 1/6 to 6/6. Results are shown for high and low stray rates (top and bottom) and two statistical tests for significance (left and right). Note that cells are colored light gray for a p-value < 0.2, gray for a p-value < 0.05, and dark gray for a p-value < 0.01.

		Negative Binomial GLM						Permutation Test							
		F ₀ Sample Proportion						F ₀ Sample Proportion							
		1/6	2/6	3/6	4/6	5/6	6/6	1/6	2/6	3/6	4/6	5/6	6/6		
High Stray (50%)	F ₁ Sample Proportion	1/6	1.23	0.85	1.03	0.96	1.03	0.94	1/6	1.23	0.85	1.03	0.96	1.03	0.94
		2/6	0.65	1.03	0.88	0.84	0.86	0.81	2/6	0.65	1.03	0.88	0.84	0.86	0.81
		3/6	0.67	0.87	0.95	0.90	0.88	0.84	3/6	0.67	0.87	0.95	0.90	0.88	0.84
		4/6	0.74	0.94	0.89	0.94	0.89	0.82	4/6	0.74	0.94	0.89	0.94	0.89	0.82
		5/6	0.73	0.95	0.90	0.88	0.87	0.78	5/6	0.73	0.95	0.90	0.88	0.87	0.78
		6/6	0.84	1.00	0.83	0.91	0.88	0.84	6/6	0.84	1.00	0.83	0.91	0.88	0.84
Low Stray (15%)	F ₁ Sample Proportion	1/6	0.41	0.76	0.42	0.52	0.57	0.59	1/6	0.41	0.76	0.42	0.52	0.57	0.59
		2/6	0.94	0.84	0.78	0.85	0.82	0.90	2/6	0.94	0.84	0.78	0.85	0.82	0.90
		3/6	0.97	0.93	0.78	0.92	0.82	0.83	3/6	0.97	0.93	0.78	0.92	0.82	0.83
		4/6	0.70	0.78	0.70	0.70	0.73	0.72	4/6	0.70	0.78	0.70	0.70	0.73	0.72
		5/6	0.92	0.82	0.70	0.79	0.75	0.78	5/6	0.92	0.82	0.70	0.79	0.75	0.78
		6/6	0.84	0.75	0.68	0.80	0.72	0.74	6/6	0.84	0.75	0.68	0.80	0.72	0.74

Note: F_0 parental and F_1 offspring were generated and sampled once for a given stray rate and effect size.

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Table 3: The estimated RRS of a hatchery-origin dam to a natural-origin dam for a modeled RRS of 0.75 for a HxH cross to a NxN cross for different sampling proportions of parents (F_0) and offspring (F_1) ranging from 1/6 to 6/6. Results are shown for high and low stray rates (top and bottom) and two statistical tests for significance (left and right). Note that cells are colored light gray for a p-value < 0.2, gray for a p-value < 0.05, and dark gray for a p-value < 0.01.

		Negative Binomial GLM						Permutation Test							
		F ₀ Sample Proportion						F ₀ Sample Proportion							
		1/6	2/6	3/6	4/6	5/6	6/6	1/6	2/6	3/6	4/6	5/6	6/6		
High Stray (50%)	F ₁ Sample Proportion	1/6	0.99	0.89	0.66	0.88	0.86	0.90	1/6	0.99	0.89	0.66	0.88	0.86	0.90
		2/6	0.86	0.84	0.68	0.81	0.79	0.83	2/6	0.86	0.84	0.68	0.81	0.79	0.83
		3/6	0.94	0.83	0.74	0.87	0.79	0.83	3/6	0.94	0.83	0.74	0.87	0.79	0.83
		4/6	0.88	0.74	0.73	0.85	0.80	0.80	4/6	0.88	0.74	0.73	0.85	0.80	0.80
		5/6	0.95	0.93	0.77	0.86	0.81	0.88	5/6	0.95	0.93	0.77	0.86	0.81	0.88
		6/6	0.95	0.86	0.75	0.90	0.84	0.86	6/6	0.95	0.86	0.75	0.90	0.84	0.86
Low Stray (15%)	F ₁ Sample Proportion	1/6	0.87	0.88	1.02	0.69	0.90	0.80	1/6	0.87	0.88	1.02	0.69	0.90	0.80
		2/6	0.58	0.88	0.80	0.79	0.85	0.82	2/6	0.58	0.88	0.80	0.79	0.85	0.82
		3/6	0.71	0.83	0.81	0.78	0.83	0.85	3/6	0.71	0.83	0.81	0.78	0.83	0.85
		4/6	0.60	0.86	0.87	0.83	0.78	0.82	4/6	0.60	0.86	0.87	0.83	0.78	0.82
		5/6	0.69	0.82	0.88	0.79	0.83	0.84	5/6	0.69	0.82	0.88	0.79	0.83	0.84
		6/6	0.65	0.81	0.82	0.80	0.82	0.84	6/6	0.65	0.81	0.82	0.80	0.82	0.84

Note: F_0 parental and F_1 offspring were generated and sampled once for a given stray rate and effect size.

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Table 4: The estimated RRS of a hatchery-origin dam to a natural-origin dam for a modeled RRS of 0.875 for a HxH cross to a NxN cross for different sampling proportions of parents (F_0) and offspring (F_1) ranging from 1/6 to 6/6. Results are shown for high and low stray rates (top and bottom) and two statistical tests for significance (left and right). Note that cells are colored light gray for a p-value < 0.2, gray for a p-value < 0.05, and dark gray for a p-value < 0.01.

		Negative Binomial GLM						Permutation Test							
		F ₀ Sample Proportion						F ₀ Sample Proportion							
		1/6	2/6	3/6	4/6	5/6	6/6	1/6	2/6	3/6	4/6	5/6	6/6		
High Stray (50%)	F ₁ Sample Proportion	1/6	1.20	1.46	1.17	1.26	1.28	1.19	1/6	1.20	1.46	1.17	1.26	1.28	1.19
		2/6	1.04	1.07	1.12	1.31	1.26	1.09	2/6	1.04	1.07	1.12	1.31	1.26	1.09
		3/6	0.63	0.99	0.87	0.91	0.91	0.85	3/6	0.63	0.99	0.87	0.91	0.91	0.85
		4/6	0.81	1.00	1.08	1.01	1.06	0.96	4/6	0.81	1.00	1.08	1.01	1.06	0.96
		5/6	0.83	1.05	1.01	1.11	1.06	1.00	5/6	0.83	1.05	1.01	1.11	1.06	1.00
		6/6	0.85	1.08	1.02	1.09	1.06	1.01	6/6	0.85	1.08	1.02	1.09	1.06	1.01
Low Stray (15%)	F ₁ Sample Proportion	1/6	0.73	1.23	1.03	0.87	0.92	0.89	1/6	0.73	1.23	1.03	0.87	0.92	0.89
		2/6	0.88	0.88	1.30	1.02	1.05	1.08	2/6	0.88	0.88	1.30	1.02	1.05	1.08
		3/6	0.97	1.06	0.95	1.01	1.02	1.01	3/6	0.97	1.06	0.95	1.01	1.02	1.01
		4/6	0.90	0.88	1.03	0.89	0.95	0.94	4/6	0.90	0.88	1.03	0.89	0.95	0.94
		5/6	1.03	0.89	0.99	0.90	0.91	0.93	5/6	1.03	0.89	0.99	0.90	0.91	0.93
		6/6	1.02	0.99	1.07	1.02	1.04	1.03	6/6	1.02	0.99	1.07	1.02	1.04	1.03

Note: F_0 parental and F_1 offspring were generated and sampled once for a given stray rate and effect size.

802 Table 5: The estimated RRS of a hatchery-origin sire to a natural-origin sire for a modeled RRS of 0.5 for a HxH cross to
 803 a NxN cross for different sampling proportions of parents (F_0) and offspring (F_1) ranging from 1/6 to 6/6. Results are
 804 shown for high and low stray rates (top and bottom) and two statistical tests for significance (left and right). Note that
 805 cells are colored light gray for a p-value < 0.2, gray for a p-value < 0.05, and dark gray for a p-value < 0.01.

		Negative Binomial GLM						Permutation Test							
		F ₀ Sample Proportion						F ₀ Sample Proportion							
		1/6	2/6	3/6	4/6	5/6	6/6	1/6	2/6	3/6	4/6	5/6	6/6		
High Stray (50%)	F ₁ Sample Proportion	1/6	0.60	0.76	0.77	0.79	0.84	0.80	1/6	0.60	0.76	0.77	0.79	0.84	0.80
		2/6	0.66	0.57	0.67	0.65	0.67	0.67	2/6	0.66	0.57	0.67	0.65	0.67	0.67
		3/6	0.67	0.81	0.67	0.79	0.75	0.75	3/6	0.67	0.81	0.67	0.79	0.75	0.75
		4/6	0.65	0.75	0.67	0.79	0.74	0.72	4/6	0.65	0.75	0.67	0.79	0.74	0.72
		5/6	0.66	0.73	0.68	0.75	0.74	0.75	5/6	0.66	0.73	0.68	0.75	0.74	0.75
		6/6	0.65	0.69	0.65	0.72	0.71	0.71	6/6	0.65	0.69	0.65	0.72	0.71	0.71
Low Stray (15%)	F ₁ Sample Proportion	1/6	0.77	0.96	0.88	0.69	0.74	0.83	1/6	0.77	0.96	0.88	0.69	0.74	0.83
		2/6	0.84	0.80	0.68	0.73	0.84	0.79	2/6	0.84	0.80	0.68	0.73	0.84	0.79
		3/6	0.68	0.75	0.67	0.61	0.66	0.69	3/6	0.68	0.75	0.67	0.61	0.66	0.69
		4/6	0.69	0.83	0.67	0.74	0.79	0.77	4/6	0.69	0.83	0.67	0.74	0.79	0.77
		5/6	0.56	0.72	0.68	0.69	0.77	0.75	5/6	0.56	0.72	0.68	0.69	0.77	0.75
		6/6	0.63	0.77	0.67	0.70	0.73	0.74	6/6	0.63	0.77	0.67	0.70	0.73	0.74

Note: F_0 parental and F_1 offspring were generated and sampled once for a given stray rate and effect size.

806 **Table 6: The estimated RRS of a hatchery-origin sire to a natural-origin sire for a modeled RRS of 0.625 for a HxH cross**
 807 **to a NxN cross for different sampling proportions of parents (F_0) and offspring (F_1) ranging from 1/6 to 6/6. Results are**
 808 **shown for high and low stray rates (top and bottom) and two statistical tests for significance (left and right). Note that**
 809 **cells are colored light gray for a p-value < 0.2, gray for a p-value < 0.05, and dark gray for a p-value < 0.01.**

		Negative Binomial GLM						Permutation Test							
		F ₀ Sample Proportion						F ₀ Sample Proportion							
		1/6	2/6	3/6	4/6	5/6	6/6	1/6	2/6	3/6	4/6	5/6	6/6		
High Stray (50%)	F ₁ Sample Proportion	1/6	1.03	0.90	0.67	0.76	0.83	0.81	1/6	1.03	0.90	0.67	0.76	0.83	0.81
		2/6	1.13	0.79	0.91	0.89	0.90	0.83	2/6	1.13	0.79	0.91	0.89	0.90	0.83
		3/6	0.84	0.79	0.80	0.80	0.89	0.80	3/6	0.84	0.79	0.80	0.80	0.89	0.80
		4/6	0.81	0.89	0.90	0.79	0.88	0.81	4/6	0.81	0.89	0.90	0.79	0.88	0.81
		5/6	0.77	0.75	0.78	0.75	0.80	0.77	5/6	0.77	0.75	0.78	0.75	0.80	0.77
		6/6	0.81	0.74	0.81	0.77	0.83	0.77	6/6	0.81	0.74	0.81	0.77	0.83	0.77
Low Stray (15%)	F ₁ Sample Proportion	1/6	0.91	0.76	0.96	0.89	0.88	0.90	1/6	0.91	0.76	0.96	0.89	0.88	0.90
		2/6	0.83	0.83	0.84	0.66	0.69	0.73	2/6	0.83	0.83	0.84	0.66	0.69	0.73
		3/6	0.79	0.72	0.82	0.70	0.79	0.80	3/6	0.79	0.72	0.82	0.70	0.79	0.80
		4/6	0.92	0.79	0.85	0.79	0.83	0.86	4/6	0.92	0.79	0.85	0.79	0.83	0.86
		5/6	0.99	0.76	0.91	0.82	0.81	0.84	5/6	0.99	0.76	0.91	0.82	0.81	0.84
		6/6	0.83	0.76	0.84	0.81	0.81	0.82	6/6	0.83	0.76	0.84	0.81	0.81	0.82

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

810 Table 7: The estimated RRS of a hatchery-origin sire to a natural-origin sire for a modeled RRS of 0.75 for a HxH cross
 811 to a NxN cross for different sampling proportions of parents (F_0) and offspring (F_1) ranging from 1/6 to 6/6. Results are
 812 shown for high and low stray rates (top and bottom) and two statistical tests for significance (left and right). Note that
 813 cells are colored light gray for a p-value < 0.2, gray for a p-value < 0.05, and dark gray for a p-value < 0.01.

		Negative Binomial GLM						Permutation Test							
		F ₀ Sample Proportion						F ₀ Sample Proportion							
		1/6	2/6	3/6	4/6	5/6	6/6	1/6	2/6	3/6	4/6	5/6	6/6		
High Stray (50%)	F ₁ Sample Proportion	1/6	0.92	1.03	0.85	1.02	0.99	1.02	1/6	0.92	1.03	0.85	1.02	0.99	1.02
		2/6	0.95	1.07	0.81	0.89	0.87	0.88	2/6	0.95	1.07	0.81	0.89	0.87	0.88
		3/6	1.02	0.92	0.93	0.93	0.95	0.93	3/6	1.02	0.92	0.93	0.93	0.95	0.93
		4/6	1.18	1.06	0.91	0.87	0.91	0.91	4/6	1.18	1.06	0.91	0.87	0.91	0.91
		5/6	0.96	0.89	0.80	0.79	0.78	0.81	5/6	0.96	0.89	0.80	0.79	0.78	0.81
		6/6	1.05	0.93	0.85	0.86	0.86	0.89	6/6	1.05	0.93	0.85	0.86	0.86	0.89
Low Stray (15%)	F ₁ Sample Proportion	1/6	0.45	0.54	0.70	0.79	0.65	0.64	1/6	0.45	0.54	0.70	0.79	0.65	0.64
		2/6	0.87	0.94	0.91	1.06	0.89	0.98	2/6	0.87	0.94	0.91	1.06	0.89	0.98
		3/6	1.07	0.95	0.98	1.04	0.95	0.97	3/6	1.07	0.95	0.98	1.04	0.95	0.97
		4/6	0.87	0.98	0.95	0.99	0.94	0.94	4/6	0.87	0.98	0.95	0.99	0.94	0.94
		5/6	0.86	0.89	0.96	0.94	0.84	0.87	5/6	0.86	0.89	0.96	0.94	0.84	0.87
		6/6	0.82	0.92	0.93	0.95	0.85	0.87	6/6	0.82	0.92	0.93	0.95	0.85	0.87

Note: F_0 parental and F_1 offspring were generated and sampled once for a given stray rate and effect size.

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Table 8: The estimated RRS of a hatchery-origin sire to a natural-origin sire for a modeled RRS of 0.875 for a HxH cross to a NxN cross for different sampling proportions of parents (F₀) and offspring (F₁) ranging from 1/6 to 6/6. Results are shown for high and low stray rates (top and bottom) and two statistical tests for significance (left and right). Note that cells are colored light gray for a p-value < 0.2, gray for a p-value < 0.05, and dark gray for a p-value < 0.01.

		Negative Binomial GLM						Permutation Test							
		F ₀ Sample Proportion						F ₀ Sample Proportion							
		1/6	2/6	3/6	4/6	5/6	6/6	1/6	2/6	3/6	4/6	5/6	6/6		
High Stray (50%)	F ₁ Sample Proportion	1/6	0.43	0.73	0.76	1.03	0.90	0.90	1/6	0.43	0.73	0.76	1.03	0.90	0.90
		2/6	0.91	0.81	0.81	0.87	0.86	0.84	2/6	0.91	0.81	0.81	0.87	0.86	0.84
		3/6	0.77	0.76	0.82	0.86	0.90	0.84	3/6	0.77	0.76	0.82	0.86	0.90	0.84
		4/6	0.87	0.76	0.87	0.89	0.91	0.87	4/6	0.87	0.76	0.87	0.89	0.91	0.87
		5/6	0.87	0.75	0.82	0.88	0.88	0.89	5/6	0.87	0.75	0.82	0.88	0.88	0.89
		6/6	0.89	0.76	0.84	0.89	0.91	0.88	6/6	0.89	0.76	0.84	0.89	0.91	0.88
Low Stray (15%)	F ₁ Sample Proportion	1/6	0.54	0.50	0.59	0.53	0.69	0.66	1/6	0.54	0.50	0.59	0.53	0.69	0.66
		2/6	1.01	0.95	1.05	0.90	1.02	0.95	2/6	1.01	0.95	1.05	0.90	1.02	0.95
		3/6	1.02	0.94	1.01	0.93	0.97	0.95	3/6	1.02	0.94	1.01	0.93	0.97	0.95
		4/6	0.84	0.83	0.97	0.92	0.95	0.91	4/6	0.84	0.83	0.97	0.92	0.95	0.91
		5/6	1.06	0.85	0.89	0.86	0.90	0.89	5/6	1.06	0.85	0.89	0.86	0.90	0.89
		6/6	0.97	0.87	0.97	0.90	0.97	0.94	6/6	0.97	0.87	0.97	0.90	0.97	0.94

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

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Table 9: The estimated RRS of a HxH cross to a NxN cross for a modeled RRS of 0.5 for a HxH cross to a NxN cross for different sampling proportions of parents (F_0) and offspring (F_1) ranging from 1/6 to 6/6. Results are shown for high and low stray rates (top and bottom) and two statistical tests for significance (left and right). Note that cells are colored light gray for a p-value < 0.2, gray for a p-value < 0.05, and dark gray for a p-value < 0.01.

		Negative Binomial GLM						Permutation Test							
		F ₀ Sample Proportion						F ₀ Sample Proportion							
		1/6	2/6	3/6	4/6	5/6	6/6	1/6	2/6	3/6	4/6	5/6	6/6		
High Stray (50%)	F ₁ Sample Proportion	1/6	NA	1.00	1.00	1.14	1.00	1.11	1/6	NA	NA	NA	1.14	NA	1.11
		2/6	0.88	0.88	0.68	0.81	0.77	0.77	2/6	0.88	0.88	0.68	0.81	0.77	0.77
		3/6	0.95	0.85	0.95	0.85	0.87	0.80	3/6	0.95	0.85	0.95	0.85	0.87	0.80
		4/6	0.94	0.91	0.82	0.85	0.80	0.79	4/6	0.94	0.91	0.82	0.85	0.80	0.79
		5/6	1.02	0.94	0.95	0.83	0.85	0.80	5/6	1.02	0.94	0.95	0.83	0.85	0.80
		6/6	0.93	0.91	0.86	0.82	0.79	0.75	6/6	0.93	0.91	0.86	0.82	0.79	0.75
Low Stray (15%)	F ₁ Sample Proportion	1/6	NA	NA	0.59	1.13	1.06	0.90	1/6	NA	NA	0.59	NA	NA	NA
		2/6	0.82	1.69	0.69	0.63	0.89	0.54	2/6	0.82	NA	0.69	0.63	0.89	0.54
		3/6	0.85	0.79	0.85	1.32	1.00	1.00	3/6	0.85	0.79	0.85	1.32	1.00	1.00
		4/6	0.77	0.75	1.10	0.96	0.62	0.78	4/6	0.77	0.75	1.10	0.96	0.62	0.78
		5/6	0.82	0.74	0.87	0.75	0.88	0.76	5/6	0.82	0.74	0.87	0.75	0.88	0.76
		6/6	0.82	0.82	0.90	0.96	0.80	0.75	6/6	0.82	0.82	0.90	0.96	0.80	0.75

Note: F_0 parental and F_1 offspring were generated and sampled once for a given stray rate and effect size.

822 **Table 10: The estimated RRS of a HxH cross to a NxN cross for a modeled RRS of 0.625 for a HxH cross to a NxN cross**
 823 **for different sampling proportions of parents (F₀) and offspring (F₁) ranging from 1/6 to 6/6. Results are shown for high**
 824 **and low stray rates (top and bottom) and two statistical tests for significance (left and right). Note that cells are colored**
 825 **light gray for a p-value < 0.2, gray for a p-value < 0.05, and dark gray for a p-value < 0.01.**

		Negative Binomial GLM						Permutation Test							
		F ₀ Sample Proportion						F ₀ Sample Proportion							
		1/6	2/6	3/6	4/6	5/6	6/6	1/6	2/6	3/6	4/6	5/6	6/6		
High Stray (50%)	F ₁ Sample Proportion	1/6	1.00	1.00	0.86	0.87	0.82	0.73	1/6	NA	NA	0.86	0.87	0.82	0.73
		2/6	1.00	1.20	0.92	0.85	0.79	0.80	2/6	NA	1.20	0.92	0.85	0.79	0.80
		3/6	0.86	0.97	0.96	0.83	0.92	0.86	3/6	0.86	0.97	0.96	0.83	0.92	0.86
		4/6	1.00	0.88	0.88	0.84	0.84	0.81	4/6	NA	0.88	0.88	0.84	0.84	0.81
		5/6	0.97	0.95	0.92	0.87	0.89	0.79	5/6	0.97	0.95	0.92	0.87	0.89	0.79
		6/6	0.96	0.91	0.93	0.88	0.89	0.81	6/6	0.96	0.91	0.93	0.88	0.89	0.81
Low Stray (15%)	F ₁ Sample Proportion	1/6	NA	NA	NA	NA	NA	NA	1/6	NA	NA	NA	NA	NA	NA
		2/6	NA	0.99	0.89	0.78	0.74	0.82	2/6	NA	0.99	0.89	0.78	0.74	0.82
		3/6	0.88	0.97	0.87	0.82	0.91	0.84	3/6	0.88	0.97	0.87	0.82	0.91	0.84
		4/6	1.11	1.07	0.78	0.71	0.74	0.93	4/6	1.11	1.07	0.78	0.71	0.74	0.93
		5/6	0.87	0.83	0.89	0.91	0.77	0.81	5/6	0.87	0.83	0.89	0.91	0.77	0.81
		6/6	0.96	0.97	0.86	0.85	0.78	0.79	6/6	0.96	0.97	0.86	0.85	0.78	0.79

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

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Table 11: The estimated RRS of a HxH cross to a NxN cross for a modeled RRS of 0.75 for a HxH cross to a NxN cross for different sampling proportions of parents (F₀) and offspring (F₁) ranging from 1/6 to 6/6. Results are shown for high and low stray rates (top and bottom) and two statistical tests for significance (left and right). Note that cells are colored light gray for a p-value < 0.2, gray for a p-value < 0.05, and dark gray for a p-value < 0.01.

		Negative Binomial GLM						Permutation Test							
		F ₀ Sample Proportion						F ₀ Sample Proportion							
		1/6	2/6	3/6	4/6	5/6	6/6	1/6	2/6	3/6	4/6	5/6	6/6		
High Stray (50%)	F ₁ Sample Proportion	1/6	1.00	2.00	1.00	0.67	0.33	0.90	1/6	NA	NA	NA	0.67	NA	0.90
		2/6	0.88	0.91	0.69	0.67	0.73	0.60	2/6	0.88	0.91	0.69	0.67	0.73	0.60
		3/6	1.00	0.97	0.96	0.84	0.97	0.87	3/6	NA	0.97	0.96	0.84	0.97	0.87
		4/6	0.96	0.93	0.80	0.83	0.89	0.82	4/6	0.96	0.93	0.80	0.83	0.89	0.82
		5/6	0.96	0.96	0.89	1.01	0.91	0.92	5/6	0.96	0.96	0.89	1.01	0.91	0.92
		6/6	1.02	0.93	0.95	0.97	0.89	0.92	6/6	1.02	0.93	0.95	0.97	0.89	0.92
Low Stray (15%)	F ₁ Sample Proportion	1/6	0.82	0.79	0.65	0.73	1.02	0.95	1/6	0.82	0.79	0.65	0.73	1.02	0.95
		2/6	0.86	1.83	0.74	1.03	0.83	0.96	2/6	0.86	NA	0.74	1.03	0.83	0.96
		3/6	0.91	0.97	0.78	0.97	0.90	1.05	3/6	0.91	0.97	0.78	0.97	0.90	1.05
		4/6	0.85	1.10	0.81	0.84	0.83	0.73	4/6	0.85	1.10	0.81	0.84	0.83	0.73
		5/6	0.90	1.01	0.94	0.84	0.68	0.79	5/6	0.90	1.01	0.94	0.84	0.68	0.79
		6/6	0.88	1.08	0.86	0.88	0.75	0.78	6/6	0.88	1.08	0.86	0.88	0.75	0.78

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

830 Table 12: The estimated RRS of a HxH cross to a NxN cross for a modeled RRS of 0.875 for a HxH cross to a NxN cross
 831 for different sampling proportions of parents (F₀) and offspring (F₁) ranging from 1/6 to 6/6. Results are shown for high
 832 and low stray rates (top and bottom) and two statistical tests for significance (left and right). Note that cells are colored
 833 light gray for a p-value < 0.2, gray for a p-value < 0.05, and dark gray for a p-value < 0.01.

		Negative Binomial GLM						Permutation Test							
		F ₀ Sample Proportion						F ₀ Sample Proportion							
		1/6	2/6	3/6	4/6	5/6	6/6	1/6	2/6	3/6	4/6	5/6	6/6		
High Stray (50%)	F ₁ Sample Proportion	1/6	NA	1.20	1.00	1.25	1.40	1.25	1/6	NA	1.20	NA	1.25	1.40	1.25
		2/6	0.78	1.06	1.14	0.89	0.95	1.01	2/6	0.78	1.06	1.14	0.89	0.95	1.01
		3/6	0.88	1.01	0.91	0.87	0.87	0.91	3/6	0.88	1.01	0.91	0.87	0.87	0.91
		4/6	1.01	0.96	1.07	0.98	1.03	1.02	4/6	1.01	0.96	1.07	0.98	1.03	1.02
		5/6	1.01	1.07	0.98	1.08	1.01	1.04	5/6	1.01	1.07	0.98	1.08	1.01	1.04
		6/6	0.94	1.06	1.01	1.01	0.99	0.99	6/6	0.94	1.06	1.01	1.01	0.99	0.99
		6/6	0.94	1.06	1.01	1.01	0.99	0.99	6/6	0.94	1.06	1.01	1.01	0.99	0.99
Low Stray (15%)	F ₁ Sample Proportion	1/6	NA	NA	NA	NA	NA	NA	1/6	NA	NA	NA	NA	NA	NA
		2/6	0.85	1.60	3.58	1.40	3.56	2.75	2/6	0.85	1.60	NA	1.40	NA	2.75
		3/6	0.90	0.69	1.06	1.27	1.27	1.48	3/6	0.90	0.69	1.06	1.27	1.27	1.48
		4/6	1.07	1.01	0.89	0.82	0.96	0.92	4/6	1.07	1.01	0.89	0.82	0.96	0.92
		5/6	0.87	0.88	0.79	0.74	0.82	0.67	5/6	0.87	0.88	0.79	0.74	0.82	0.67
		6/6	1.00	0.82	0.83	0.84	0.90	0.90	6/6	1.00	0.82	0.83	0.84	0.90	0.90
		6/6	1.00	0.82	0.83	0.84	0.90	0.90	6/6	1.00	0.82	0.83	0.84	0.90	0.90

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

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Table 13: The estimated RRS of a HxN cross to a NxN cross for a modeled RRS of 0.5 for a HxH cross to a NxN cross for different sampling proportions of parents (F₀) and offspring (F₁) ranging from 1/6 to 6/6. Results are shown for high and low stray rates (top and bottom) and two statistical tests for significance (left and right). Note that cells are colored light gray for a p-value < 0.2, gray for a p-value < 0.05, and dark gray for a p-value < 0.01.

		Negative Binomial GLM						Permutation Test							
		F ₀ Sample Proportion						F ₀ Sample Proportion							
		1/6	2/6	3/6	4/6	5/6	6/6	1/6	2/6	3/6	4/6	5/6	6/6		
High Stray (50%)	F ₁ Sample Proportion	1/6	NA	1.33	1.00	1.40	1.50	1.62	1/6	NA	1.33	NA	1.40	1.50	1.62
		2/6	0.88	0.85	0.93	0.81	0.90	0.85	2/6	0.88	0.85	0.93	0.81	0.90	0.85
		3/6	0.95	0.95	1.01	0.98	0.92	0.89	3/6	0.95	0.95	1.01	0.98	0.92	0.89
		4/6	1.00	0.93	0.94	0.87	0.85	0.84	4/6	1.00	0.93	0.94	0.87	0.85	0.84
		5/6	1.02	1.09	1.07	0.95	0.97	0.98	5/6	1.02	1.09	1.07	0.95	0.97	0.98
		6/6	1.00	0.99	0.96	0.92	0.88	0.91	6/6	1.00	0.99	0.96	0.92	0.88	0.91
Low Stray (15%)	F ₁ Sample Proportion	1/6	0.62	0.58	0.74	0.89	0.74	0.66	1/6	NA	0.58	0.74	0.89	0.74	0.66
		2/6	0.82	0.92	0.85	0.87	0.82	0.85	2/6	0.82	0.92	0.85	0.87	0.82	0.85
		3/6	0.89	0.83	0.98	0.90	0.82	0.90	3/6	0.89	0.83	0.98	0.90	0.82	0.90
		4/6	0.88	0.91	0.93	0.90	0.85	0.88	4/6	0.88	0.91	0.93	0.90	0.85	0.88
		5/6	0.88	0.88	0.89	0.90	0.85	0.88	5/6	0.88	0.88	0.89	0.90	0.85	0.88
		6/6	0.92	0.86	0.91	0.90	0.87	0.86	6/6	0.92	0.86	0.91	0.90	0.87	0.86

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

838 **Table 14: The estimated RRS of a HxN cross to a NxN cross for a modeled RRS of 0.625 for a HxH cross to a NxN cross**
 839 **for different sampling proportions of parents (F₀) and offspring (F₁) ranging from 1/6 to 6/6. Results are shown for high**
 840 **and low stray rates (top and bottom) and two statistical tests for significance (left and right). Note that cells are colored**
 841 **light gray for a p-value < 0.2, gray for a p-value < 0.05, and dark gray for a p-value < 0.01.**

		Negative Binomial GLM						Permutation Test							
		F ₀ Sample Proportion						F ₀ Sample Proportion							
		1/6	2/6	3/6	4/6	5/6	6/6	1/6	2/6	3/6	4/6	5/6	6/6		
High Stray (50%)	F ₁ Sample Proportion	1/6	1.00	1.25	1.29	1.05	0.94	0.86	1/6	NA	NA	1.29	1.05	0.94	0.86
		2/6	1.00	1.09	1.02	0.92	0.87	0.91	2/6	NA	1.09	1.02	0.92	0.87	0.91
		3/6	0.89	1.01	1.02	1.01	1.11	0.97	3/6	0.89	1.01	1.02	1.01	1.11	0.97
		4/6	1.08	0.92	0.94	1.04	0.96	0.97	4/6	1.08	0.92	0.94	1.04	0.96	0.97
		5/6	0.96	1.08	1.00	1.04	0.95	0.91	5/6	0.96	1.08	1.00	1.04	0.95	0.91
		6/6	0.97	0.98	1.00	1.06	0.96	0.92	6/6	0.97	0.98	1.00	1.06	0.96	0.92
Low Stray (15%)	F ₁ Sample Proportion	1/6	0.91	0.98	0.82	0.96	0.98	1.00	1/6	0.91	0.98	0.82	0.96	0.98	1.00
		2/6	0.92	1.09	0.89	0.92	0.81	0.96	2/6	0.92	1.09	0.89	0.92	0.81	0.96
		3/6	1.03	1.00	1.00	0.97	0.91	0.94	3/6	1.03	1.00	1.00	0.97	0.91	0.94
		4/6	0.99	0.92	0.95	0.84	0.84	0.80	4/6	0.99	0.92	0.95	0.84	0.84	0.80
		5/6	1.02	0.99	1.01	0.95	0.88	0.86	5/6	1.02	0.99	1.01	0.95	0.88	0.86
		6/6	0.93	0.95	0.93	0.92	0.86	0.86	6/6	0.93	0.95	0.93	0.92	0.86	0.86

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

842 **Table 15: The estimated RRS of a HxN cross to a NxN cross for a modeled RRS of 0.75 for a HxH cross to a NxN cross for**
 843 **different sampling proportions of parents (F₀) and offspring (F₁) ranging from 1/6 to 6/6. Results are shown for high and**
 844 **low stray rates (top and bottom) and two statistical tests for significance (left and right). Note that cells are colored light**
 845 **gray for a p-value < 0.2, gray for a p-value < 0.05, and dark gray for a p-value < 0.01.**

		Negative Binomial GLM						Permutation Test							
		F ₀ Sample Proportion						F ₀ Sample Proportion							
		1/6	2/6	3/6	4/6	5/6	6/6	1/6	2/6	3/6	4/6	5/6	6/6		
High Stray (50%)	F ₁ Sample Proportion	1/6	1.00	1.29	1.10	0.67	0.36	0.72	1/6	NA	NA	1.10	0.67	NA	NA
		2/6	0.95	1.04	0.84	0.71	0.92	0.83	2/6	0.95	1.04	0.84	0.71	0.92	0.83
		3/6	1.09	1.15	1.09	1.04	1.11	1.01	3/6	1.09	1.15	1.09	1.04	1.11	1.01
		4/6	1.03	1.11	0.93	0.91	0.94	0.85	4/6	1.03	1.11	0.93	0.91	0.94	0.85
		5/6	1.07	1.08	0.98	1.01	0.95	0.95	5/6	1.07	1.08	0.98	1.01	0.95	0.95
		6/6	1.09	1.05	0.97	0.97	0.94	0.92	6/6	1.09	1.05	0.97	0.97	0.94	0.92
Low Stray (15%)	F ₁ Sample Proportion	1/6	0.82	0.79	0.86	0.93	0.81	0.87	1/6	0.82	0.79	0.86	0.93	0.81	0.87
		2/6	0.91	0.91	0.95	0.88	0.94	0.95	2/6	0.91	0.91	0.95	0.88	0.94	0.95
		3/6	1.04	0.93	1.03	1.03	1.00	1.03	3/6	1.04	0.93	1.03	1.03	1.00	1.03
		4/6	0.95	0.86	0.85	0.92	0.87	0.85	4/6	0.95	0.86	0.85	0.92	0.87	0.85
		5/6	0.97	0.84	0.93	0.92	0.90	0.90	5/6	0.97	0.84	0.93	0.92	0.90	0.90
		6/6	0.99	0.86	0.89	0.92	0.86	0.90	6/6	0.99	0.86	0.89	0.92	0.86	0.90

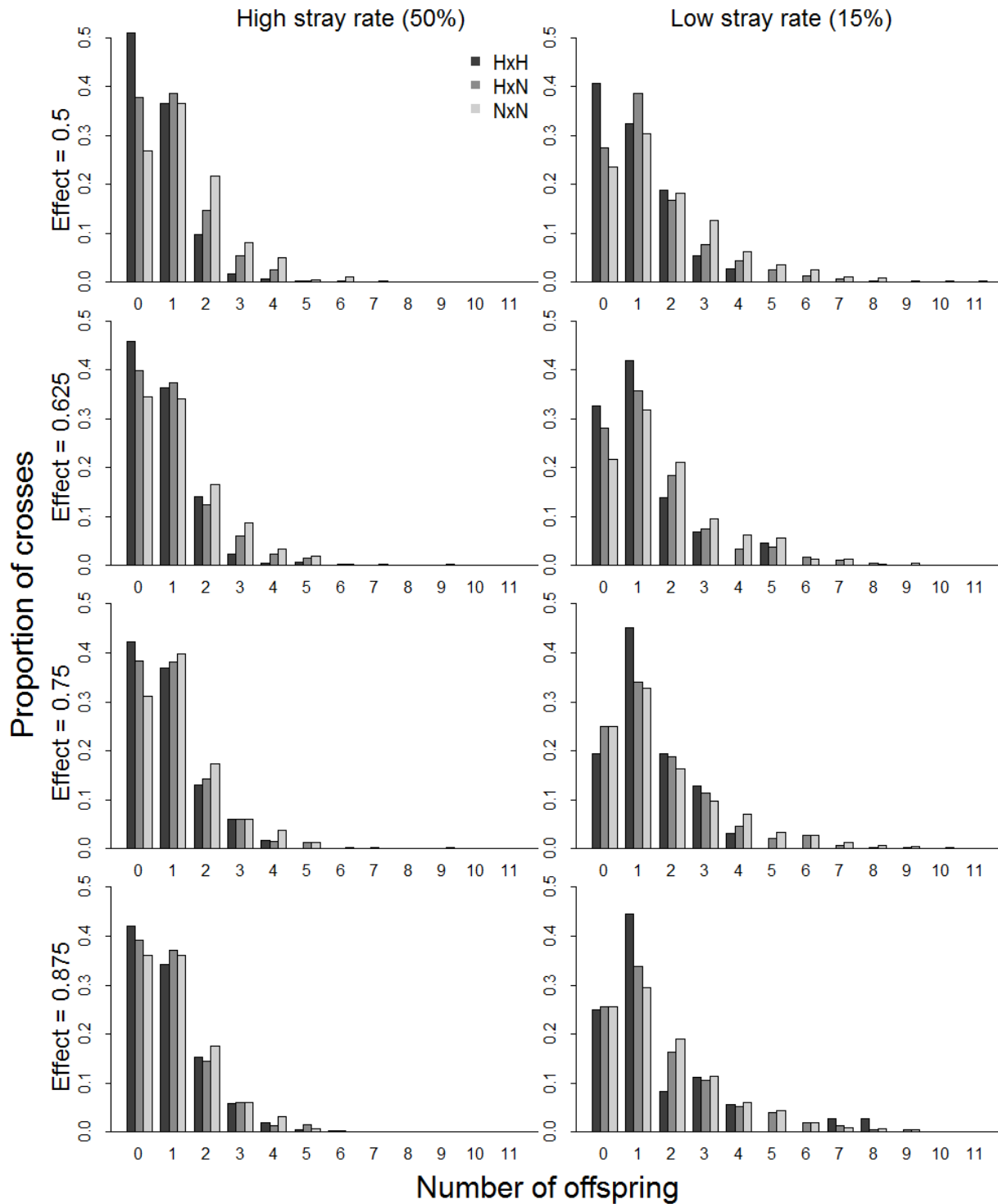
Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

846 **Table 16: The estimated RRS of a HxN cross to a NxN cross for a modeled RRS of 0.875 for a HxH cross to a NxN cross**
 847 **for different sampling proportions of parents (F₀) and offspring (F₁) ranging from 1/6 to 6/6. Results are shown for high**
 848 **and low stray rates (top and bottom) and two statistical tests for significance (left and right). Note that cells are colored**
 849 **light gray for a p-value < 0.2, gray for a p-value < 0.05, and dark gray for a p-value < 0.01.**

		Negative Binomial GLM						Permutation Test							
		F ₀ Sample Proportion						F ₀ Sample Proportion							
		1/6	2/6	3/6	4/6	5/6	6/6	1/6	2/6	3/6	4/6	5/6	6/6		
High Stray (50%)	F ₁ Sample Proportion	1/6	1.00	1.08	1.12	1.15	1.16	1.16	1/6	NA	NA	1.12	NA	1.16	1.16
		2/6	0.82	1.00	1.01	0.88	0.86	1.07	2/6	0.82	1.00	1.01	0.88	0.86	1.07
		3/6	0.94	0.99	0.97	0.92	0.88	0.92	3/6	0.94	0.99	0.97	0.92	0.88	0.92
		4/6	0.99	0.97	1.02	1.02	1.01	1.03	4/6	0.99	0.97	1.02	1.02	1.01	1.03
		5/6	1.02	0.98	0.97	1.12	1.00	1.04	5/6	1.02	0.98	0.97	1.12	1.00	1.04
		6/6	0.97	1.01	0.99	1.01	0.94	0.99	6/6	0.97	1.01	0.99	1.01	0.94	0.99
Low Stray (15%)	F ₁ Sample Proportion	1/6	1.00	0.78	0.67	0.67	0.80	0.69	1/6	NA	0.78	0.67	0.67	0.80	0.69
		2/6	0.91	0.94	0.93	0.92	1.03	0.89	2/6	0.91	0.94	0.93	0.92	1.03	0.89
		3/6	0.94	0.87	0.94	0.97	0.96	0.97	3/6	0.94	0.87	0.94	0.97	0.96	0.97
		4/6	0.99	0.88	0.93	0.93	0.96	0.91	4/6	0.99	0.88	0.93	0.93	0.96	0.91
		5/6	1.01	0.95	0.91	0.93	0.94	0.90	5/6	1.01	0.95	0.91	0.93	0.94	0.90
		6/6	1.05	0.97	0.94	1.02	1.00	0.98	6/6	1.05	0.97	0.94	1.02	1.00	0.98

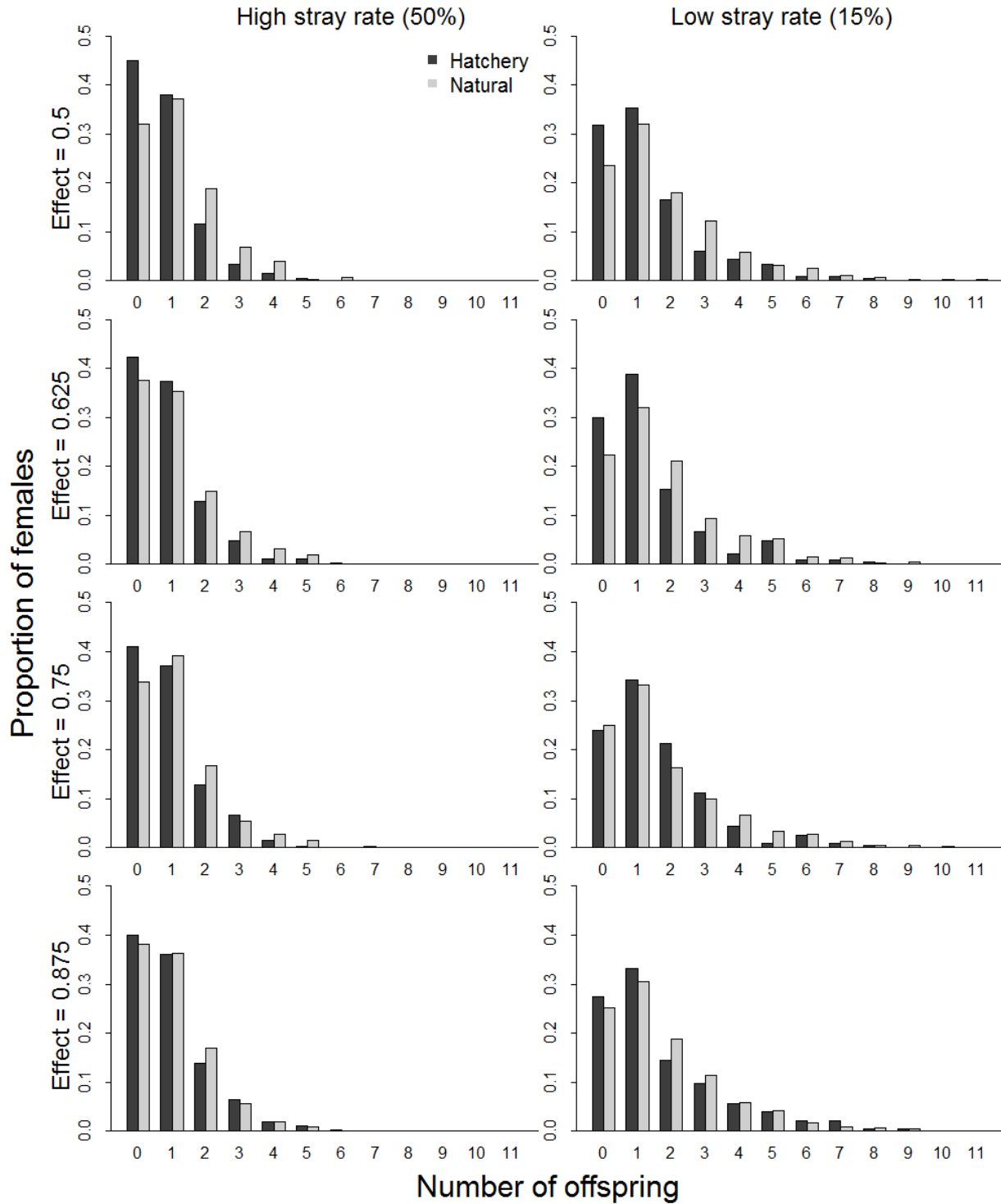
Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

Figures



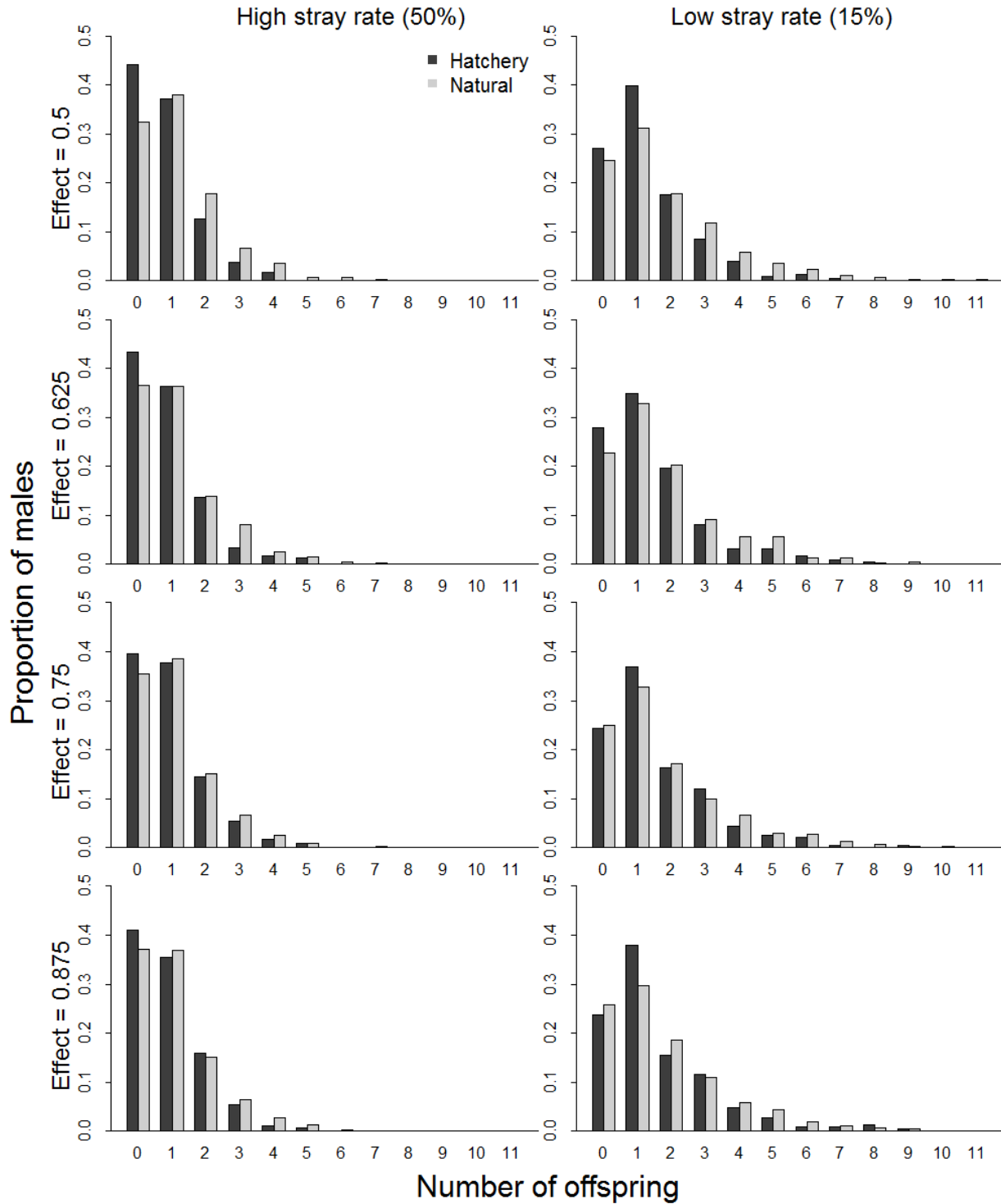
851

852 Figure 1: Histograms showing the proportion of crosses that produce a given number of offspring
 853 for the four different modeled effect sizes (RRS of HxH cross to NxN cross) and two modeled
 854 stray rates (high – 50% strays, low – 15% strays).



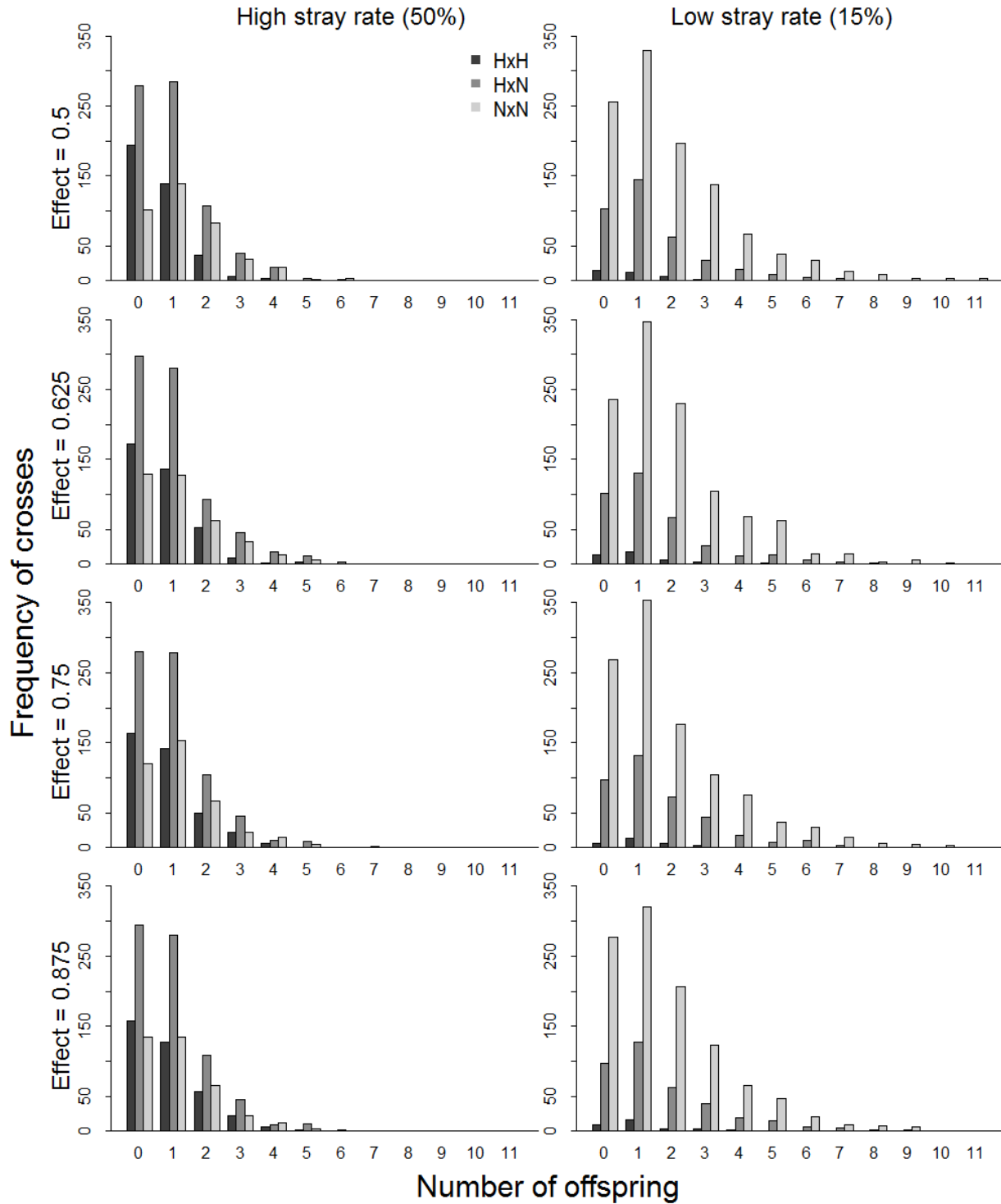
855

856 Figure 2: Histograms showing the proportion of females that produce a given number of
 857 offspring for the four different modeled effect sizes (RRS of HxH cross to NxN cross) and two
 858 modeled stray rates (high – 50% strays, low – 15% strays).



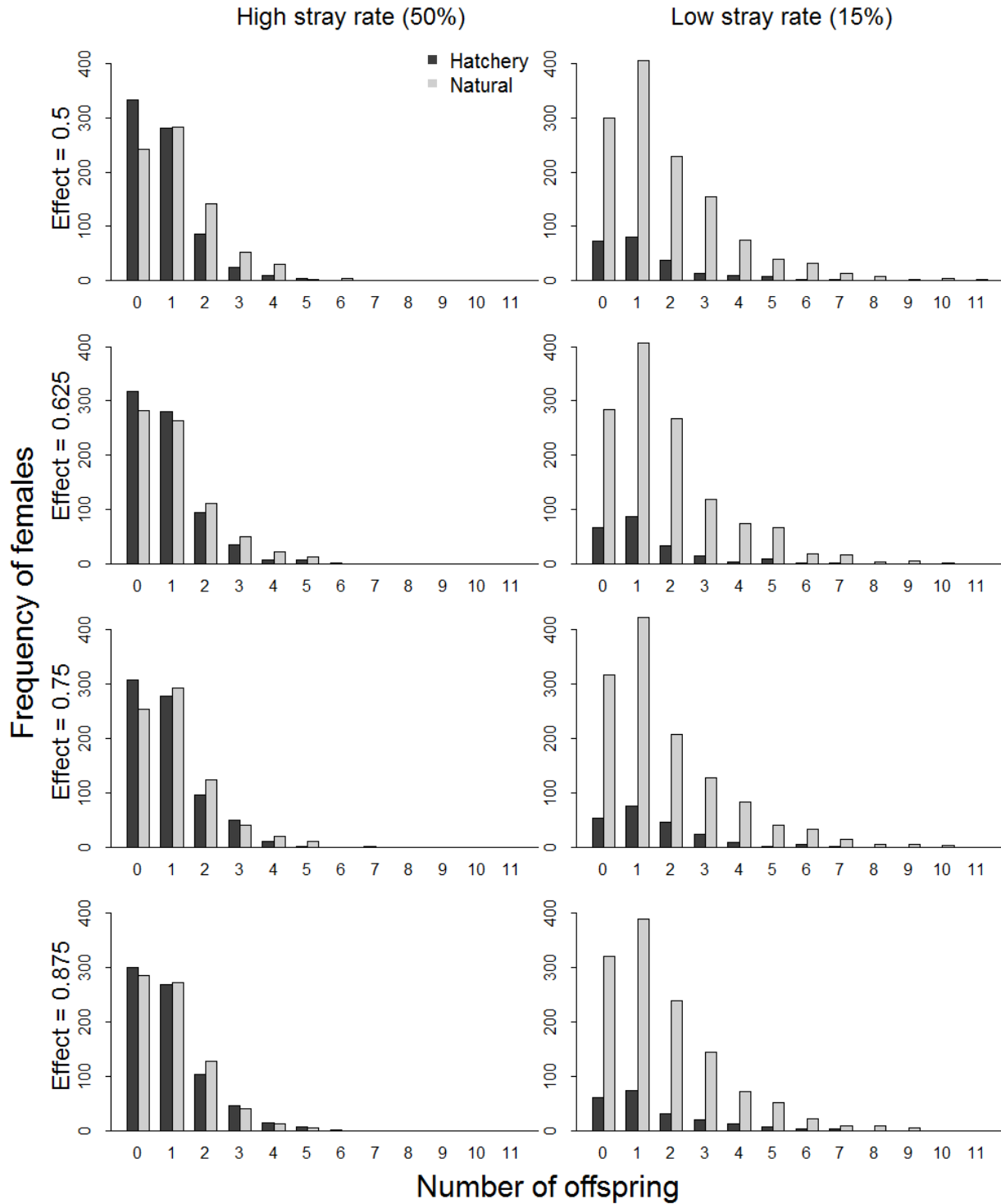
859

860 Figure 3: Histograms showing the proportion of males that produce a given number of offspring
 861 for the four different modeled effect sizes (RRS of HxH cross to NxN cross) and two modeled
 862 stray rates (high – 50% strays, low – 15% strays).



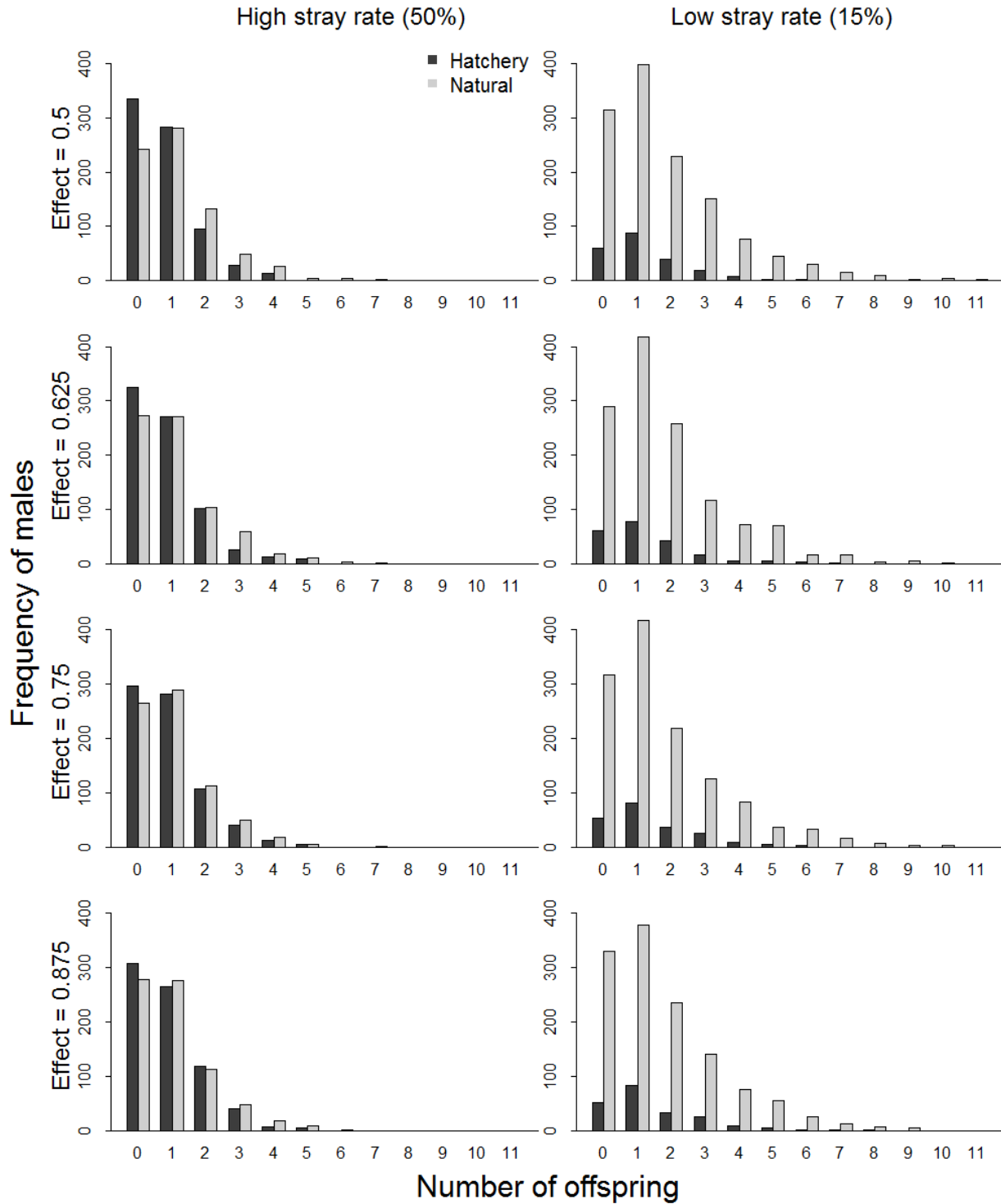
863

864 Figure 4: Histograms showing the frequency of crosses that produce a given number of offspring
 865 for the four different modeled effect sizes (RRS of HxH cross to NxN cross) and two modeled
 866 stray rates (high – 50% strays, low – 15% strays).



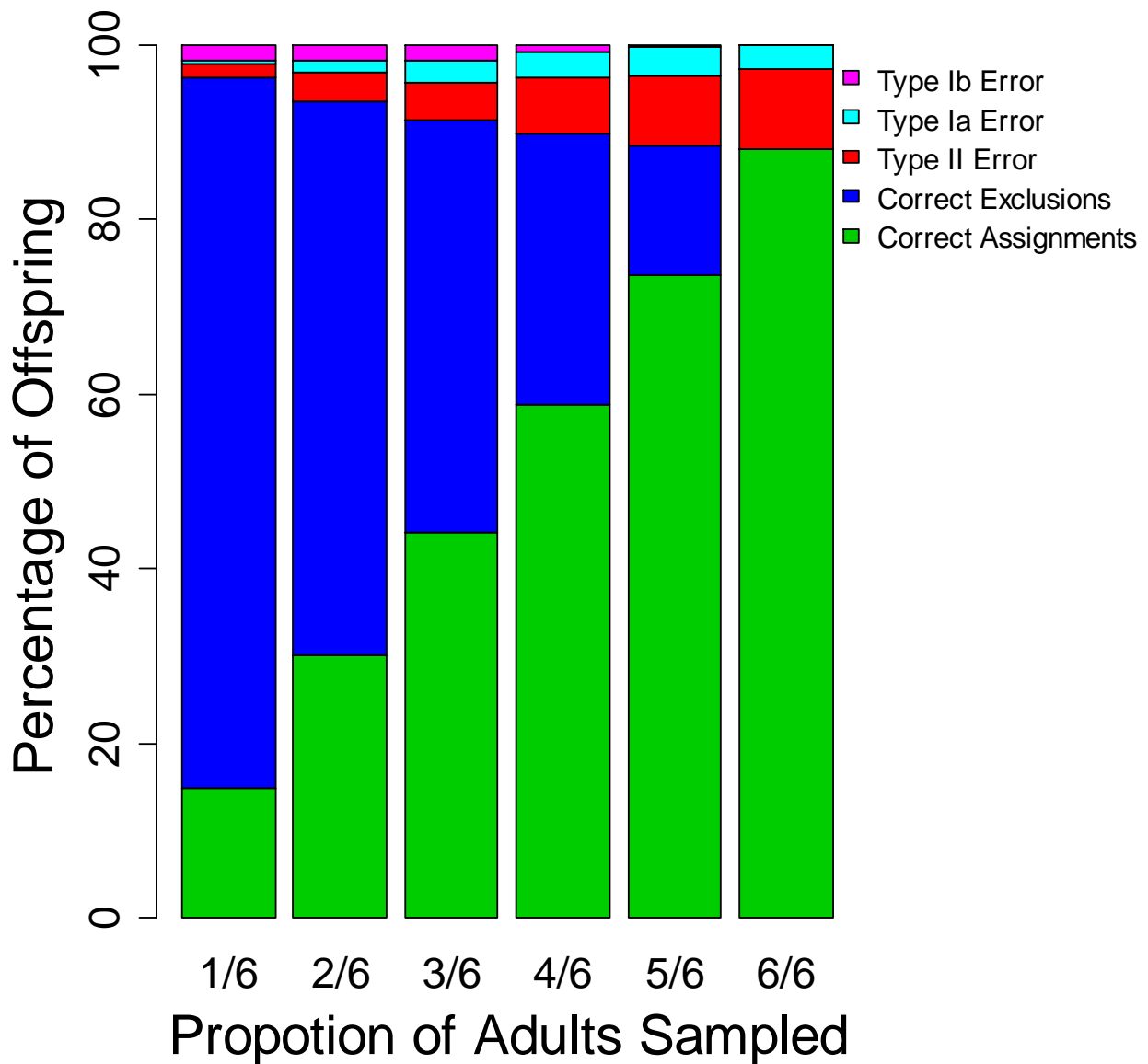
867

868 Figure 5: Histograms showing the frequency of females that produce a given number of offspring
 869 for the four different modeled effect sizes (RRS of HxH cross to NxN cross) and two modeled
 870 stray rates (high – 50% strays, low – 15% strays).

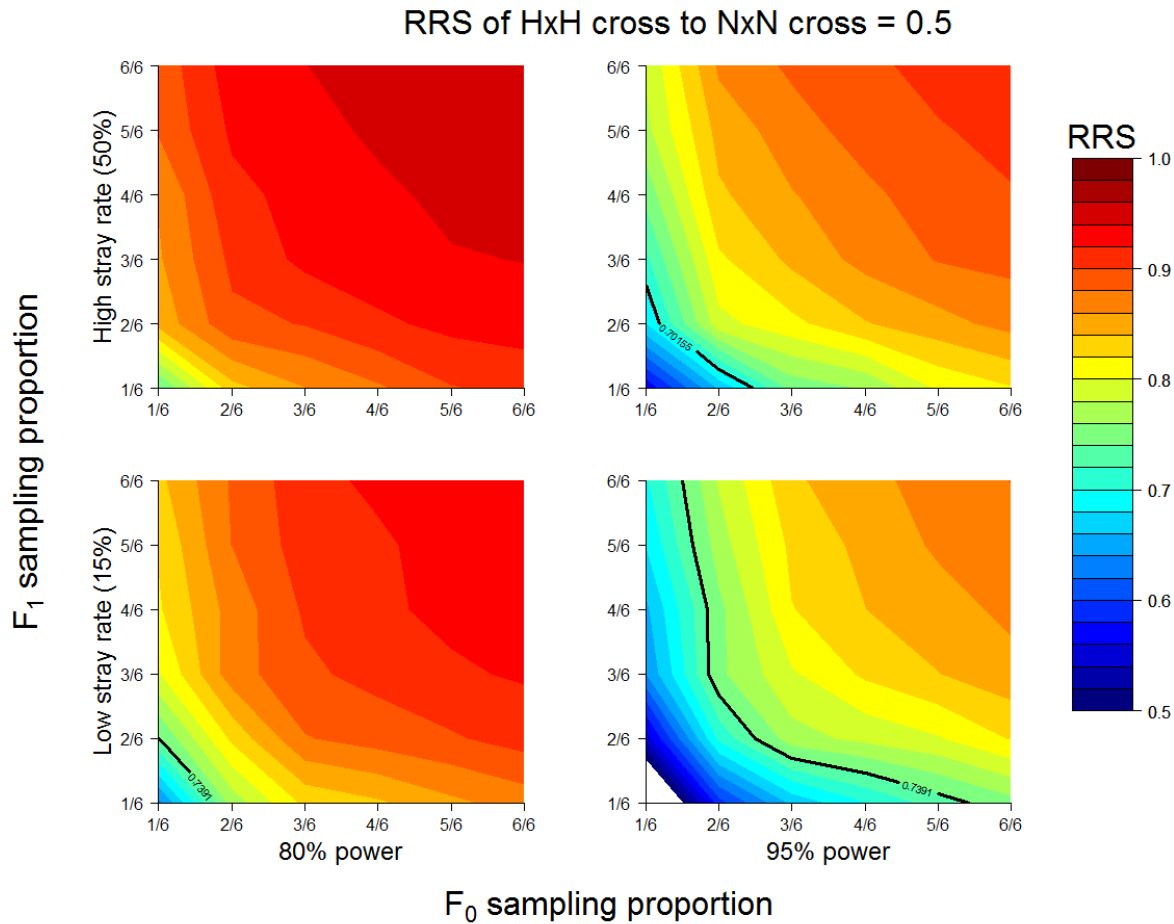


871

872 Figure 6: Histograms showing the frequency of males that produce a given number of offspring
 873 for the four different modeled effect sizes (RRS of HxH cross to NxN cross) and two modeled
 874 stray rates (high – 50% strays, low – 15% strays).

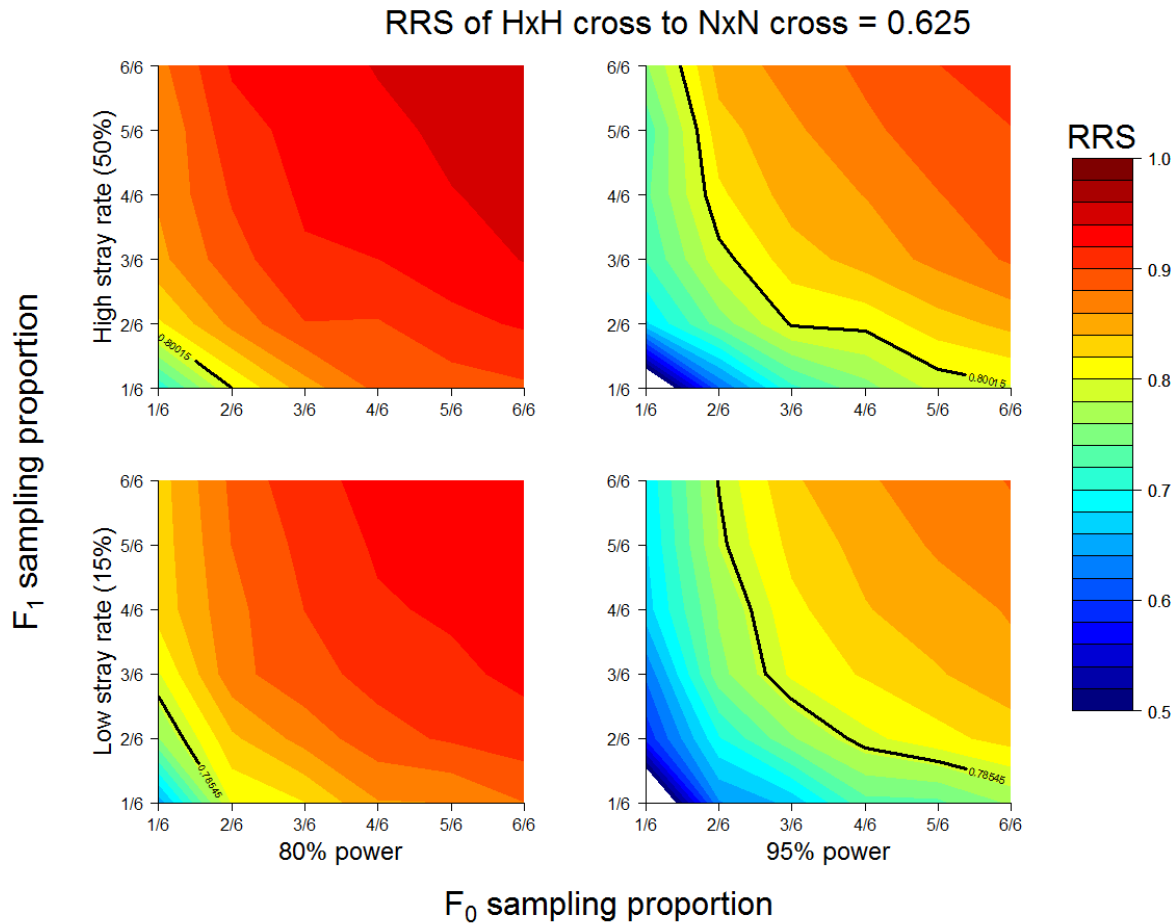


875
 876 Figure 7: Parentage assignment rates for offspring sampled based on the proportion of F_0 adults
 877 sampled averaged over all simulations. Error types: Ib – assigned to a false parent, true parent
 878 not in sample; Ia – assigned to a false parent, true parent present in sample; II – not assigned to
 879 any parent, true parent present in sample.



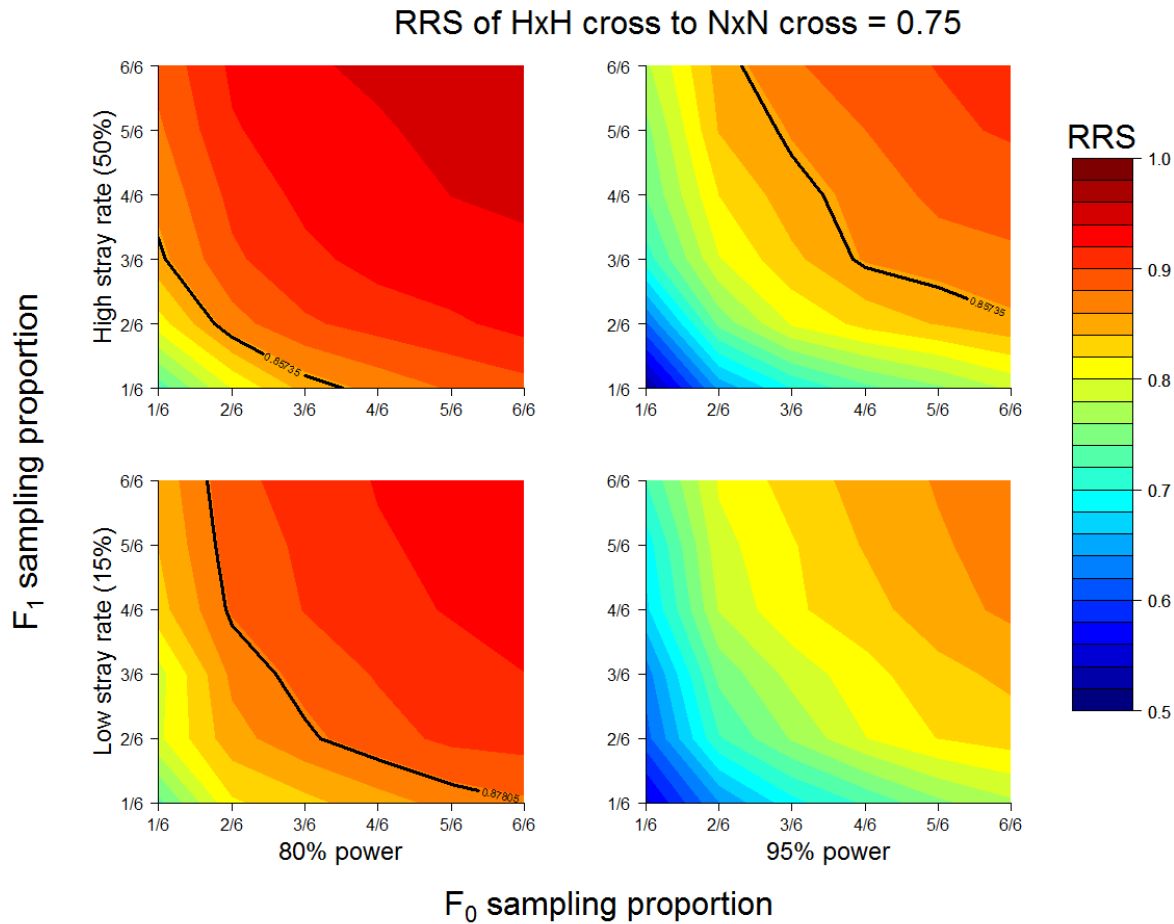
880

881 Figure 8: Color contour plot of the single parent RRS detectable at $\alpha = 0.20$ (80% power) and α
 882 $= 0.05$ (95% power) for an effect size (RRS of HxH cross to a NxN cross) of 0.5 for the two
 883 modeled stray rates (high – 50% strays, low – 15% strays) and 36 combinations of F₀ and F₁
 884 sampling proportion (1/6 to 1 in steps of 1/6). Note that the RRS values for dam and sire were
 885 averaged, as there was no modeled difference in RRS between sexes. The black contour line
 886 shows the true, single parent RRS for the model. Thus, all sampling designs to the lower left of
 887 the contour lines would fail to find a measured RRS significantly different from 1, for the given
 888 α (0.20 or 0.05).



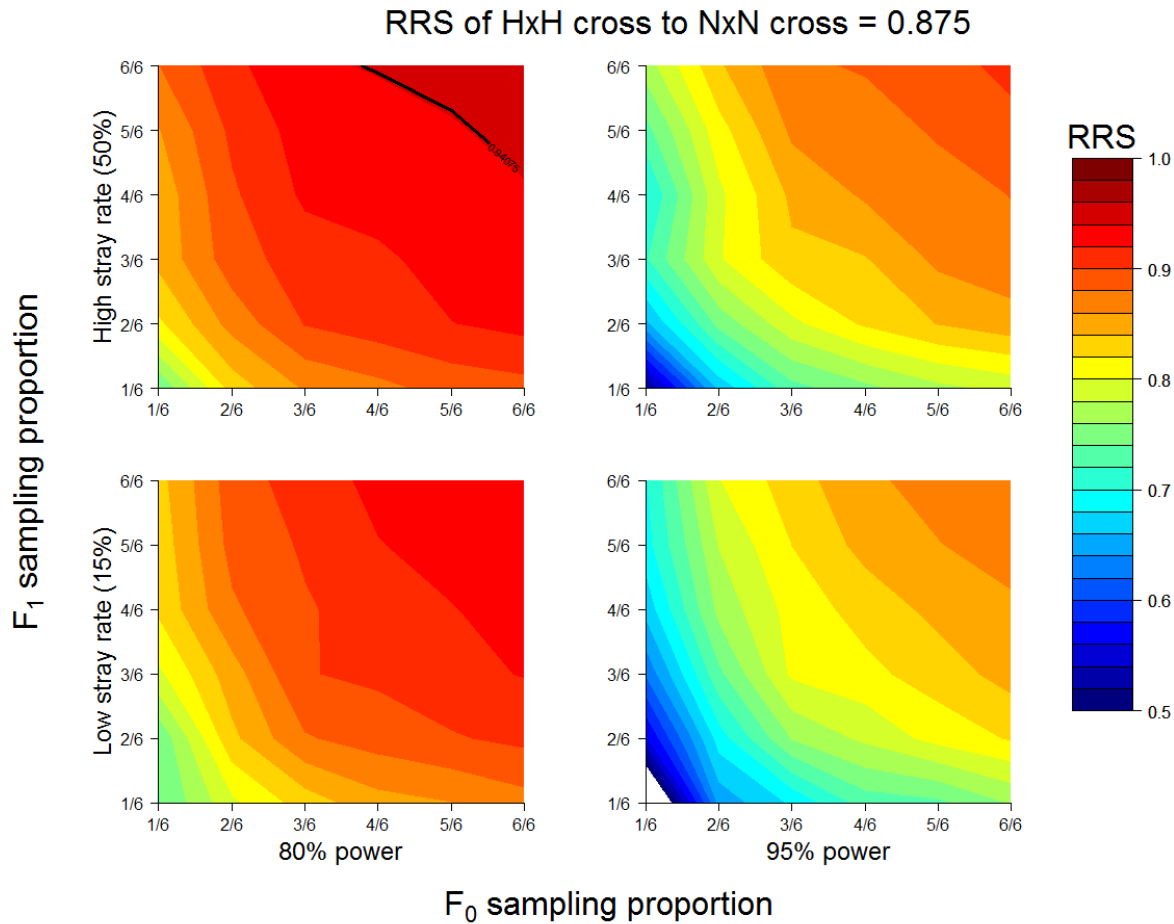
889

890 Figure 9: Color contour plot of the single parent RRS detectable at $\alpha = 0.20$ (80% power) and α
 891 $= 0.05$ (95% power) for an effect size (RRS of HxH cross to a NxN cross) of 0.625 for the two
 892 modeled stray rates (high – 50% strays, low – 15% strays) and 36 combinations of F₀ and F₁
 893 sampling proportion (1/6 to 1 in steps of 1/6). Note that the RRS values for dam and sire were
 894 averaged, as there was no modeled difference in RRS between sexes. The black contour line
 895 shows the true, single parent RRS for the model. Thus, all sampling designs to the lower left of
 896 the contour lines would fail to find a measured RRS significantly different from 1, for the given
 897 α (0.20 or 0.05).



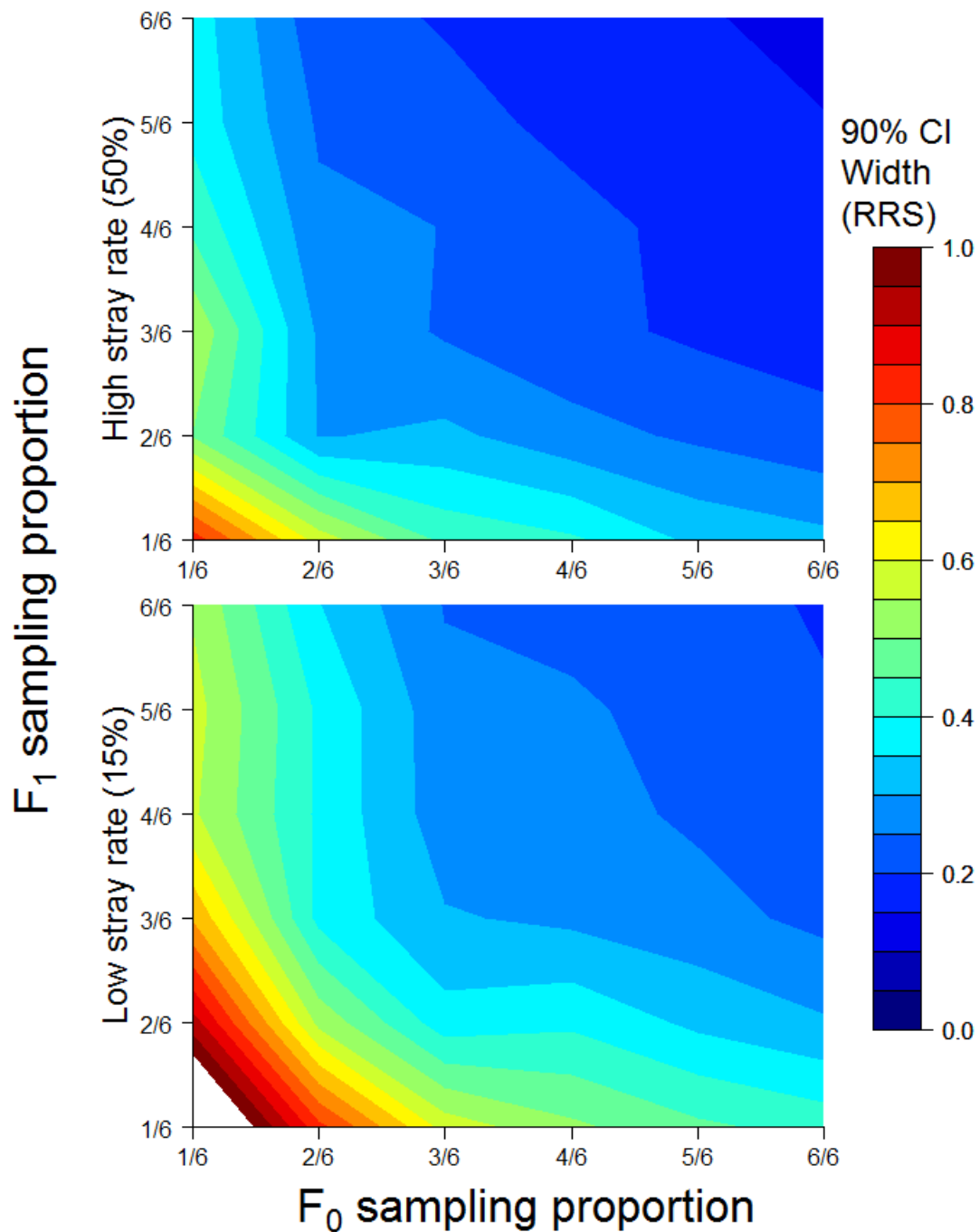
898

899 Figure 10: Color contour plot of the single parent RRS detectable at $\alpha = 0.20$ (80% power) and α
 900 $= 0.05$ (95% power) for an effect size (RRS of HxH cross to a NxN cross) of 0.75 for the two
 901 modeled stray rates (high – 50% strays, low – 15% strays) and 36 combinations of F₀ and F₁
 902 sampling proportion (1/6 to 1 in steps of 1/6). Note that the RRS values for dam and sire were
 903 averaged, as there was no modeled difference in RRS between sexes. The black contour line
 904 shows the true, single parent RRS for the model. Thus, all sampling designs to the lower left of
 905 the contour lines would fail to find a measured RRS significantly different from 1, for the given
 906 α (0.20 or 0.05).



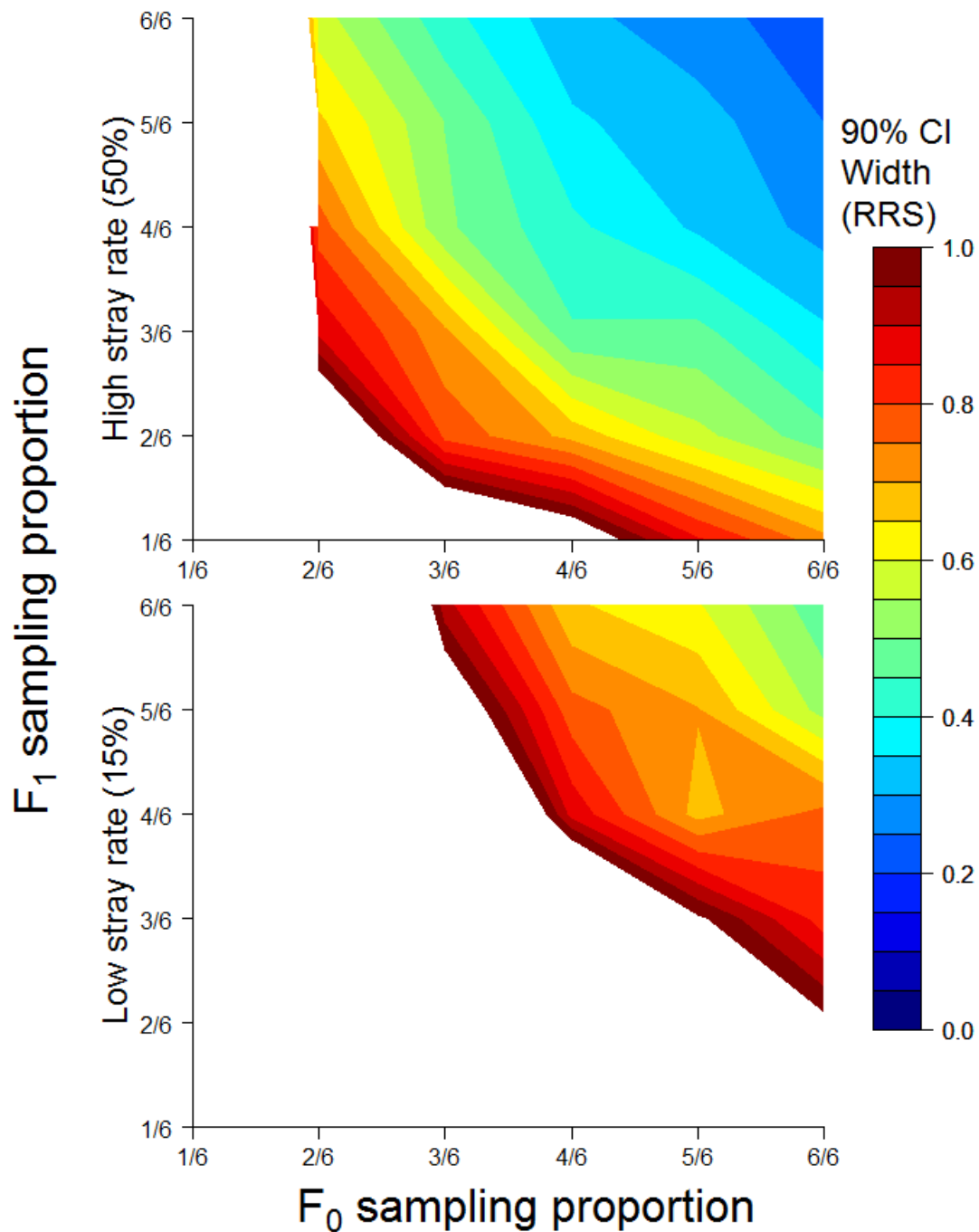
907

908 Figure 11: Color contour plot of the single parent RRS detectable at $\alpha = 0.20$ (80% power) and α
 909 $= 0.05$ (95% power) for an effect size (RRS of HxH cross to a NxN cross) of 0.875 for the two
 910 modeled stray rates (high – 50% strays, low – 15% strays) and 36 combinations of F₀ and F₁
 911 sampling proportion (1/6 to 1 in steps of 1/6). Note that the RRS values for dam and sire were
 912 averaged, as there was no modeled difference in RRS between sexes. The black contour line
 913 shows the true, single parent RRS for the model. Thus, all sampling designs to the lower left of
 914 the contour lines would fail to find a measured RRS significantly different from 1, for the given
 915 α (0.20 or 0.05).



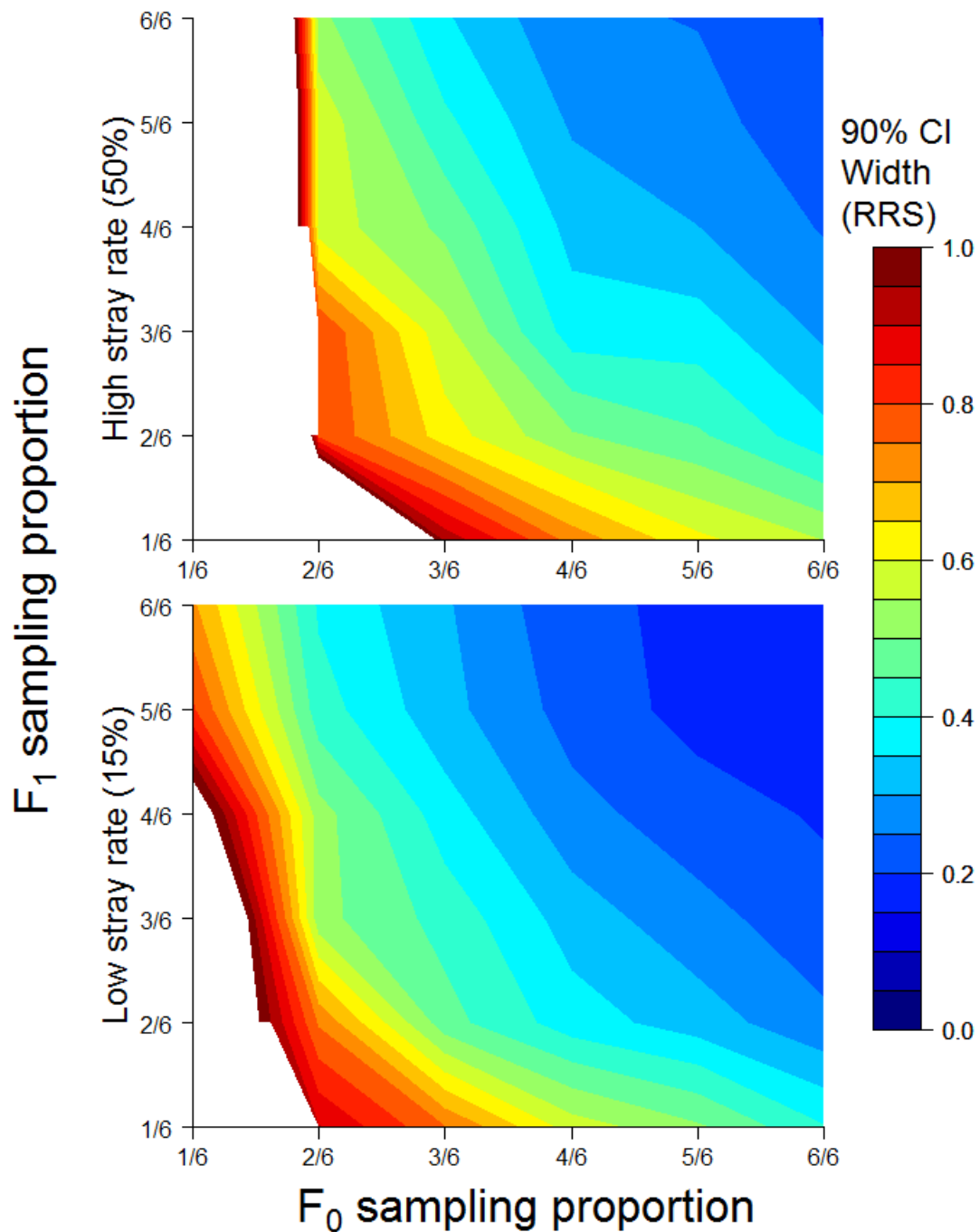
916

917 Figure 12: Color contour plot of the single parent 90% confidence interval (CI) width for the
 918 estimated RRS for an effect size (RRS of HxH cross to a NxN cross) of 0.500 for the two
 919 modeled stray rates (high – 50% strays, low – 15% strays) and 36 combinations of F₀ and F₁
 920 sampling proportions (1/6 to 1 in steps of 1/6). Note that the RRS values for dam and sire were
 921 averaged, as there was no modeled difference in RRS between sexes. Portions of the graphs in
 922 white represent 90% CI intervals that are wider than 1.0.



923

924 Figure 13: Color contour plot of the HxH cross type 90% confidence interval (CI) width for the
 925 estimated RRS for an effect size (RRS of HxH cross to a NxN cross) of 0.500 for the two
 926 modeled stray rates (high – 50% strays, low – 15% strays) and 36 combinations of F₀ and F₁
 927 sampling proportion (1/6 to 1 in steps of 1/6). Portions of the graphs in white represent 90% CI
 928 intervals that are wider than 1.0.



929

930 Figure 14: Color contour plot of the HxN cross type 90% confidence interval (CI) width for the
 931 estimated RRS for an effect size (RRS of HxH cross to a NxN cross) of 0.500 for the two
 932 modeled stray rates (high – 50% strays, low – 15% strays) and 36 combinations of F₀ and F₁
 933 sampling proportion (1/6 to 1 in steps of 1/6). Portions of the graphs in white represent 90% CI
 934 intervals that are wider than 1.0.

935

Appendices

936 Appendix Table 1.-Summary statistics for tests of relative reproductive success (RRS) of a HxH cross to a NxN cross from
 937 simulations of a high stray rate (50% spawners hatchery-origin) stream with a modeled RRS of 0.500 for a HxH cross to a NxN cross
 938 for different sampling proportions of parents (F₀) and offspring (F₁) ranging from 1/6 to 6/6. Statistics include proportion of offspring
 939 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
 940 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, and the RRS values that we could have
 941 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
 942 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, 90% confidence interval, and the one tailed p-value that RRS is <1). See
 943 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM				
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1	
						Simple	Unbiased		α = 0.20	α = 0.05		5%	95%		
1/6	1/6	0.69	0.29	0.02	0.49	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
1/6	2/6	0.70	0.28	0.02	0.49	1.00	1.00	NA	NA	NA	NA	NA	NA	NA	NA
1/6	3/6	0.70	0.29	0.01	0.49	1.00	1.00	NA	NA	NA	NA	NA	NA	NA	NA
1/6	4/6	0.71	0.27	0.02	0.49	1.14	1.15	1.000	0.80	0.80	0.593	0.45	2.92	0.407	
1/6	5/6	0.70	0.28	0.02	0.49	1.00	1.00	NA	NA	NA	NA	NA	NA	NA	
1/6	6/6	0.70	0.28	0.02	0.49	1.11	1.11	1.000	0.83	0.83	0.581	0.48	2.60	0.419	
2/6	1/6	0.51	0.42	0.07	0.49	0.88	0.87	0.638	0.88	0.88	0.414	0.32	2.40	0.586	
2/6	2/6	0.45	0.43	0.12	0.49	0.88	0.88	0.421	0.88	0.75	0.374	0.47	1.66	0.626	
2/6	3/6	0.45	0.45	0.10	0.49	0.68	0.67	0.072	0.89	0.68	0.148	0.37	1.25	0.852	
2/6	4/6	0.47	0.42	0.11	0.49	0.81	0.81	0.125	0.88	0.81	0.226	0.51	1.29	0.774	
2/6	5/6	0.47	0.43	0.10	0.49	0.77	0.77	0.074	0.88	0.77	0.155	0.51	1.17	0.845	
2/6	6/6	0.46	0.44	0.10	0.49	0.77	0.77	0.028	0.89	0.81	0.117	0.53	1.11	0.883	
3/6	1/6	0.27	0.49	0.24	0.49	0.95	0.95	0.654	0.95	0.95	0.450	0.52	1.75	0.550	
3/6	2/6	0.30	0.45	0.25	0.49	0.85	0.85	0.051	0.91	0.85	0.273	0.54	1.33	0.728	
3/6	3/6	0.29	0.48	0.23	0.49	0.95	0.95	0.423	0.91	0.86	0.415	0.66	1.37	0.585	
3/6	4/6	0.29	0.48	0.23	0.49	0.85	0.85	0.030	0.94	0.88	0.179	0.63	1.14	0.821	
3/6	5/6	0.29	0.49	0.22	0.49	0.87	0.87	0.095	0.92	0.84	0.208	0.65	1.15	0.792	
3/6	6/6	0.28	0.49	0.23	0.49	0.80	0.80	0.008	0.93	0.86	0.078	0.62	1.04	0.922	

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		α = 0.20	α = 0.05		5%	95%	
4/6	1/6	0.18	0.42	0.40	0.49	0.94	0.94	0.530	0.94	0.94	0.430	0.54	1.63	0.570
4/6	2/6	0.15	0.49	0.36	0.49	0.91	0.91	0.210	0.91	0.87	0.343	0.63	1.32	0.657
4/6	3/6	0.14	0.43	0.43	0.49	0.82	0.82	0.004	0.94	0.90	0.120	0.63	1.08	0.880
4/6	4/6	0.16	0.46	0.38	0.49	0.85	0.85	0.012	0.94	0.88	0.127	0.67	1.08	0.873
4/6	5/6	0.16	0.47	0.37	0.49	0.80	0.79	0.002	0.94	0.87	0.045	0.64	0.99	0.955
4/6	6/6	0.15	0.47	0.38	0.49	0.79	0.78	0.001	0.94	0.89	0.023	0.64	0.96	0.977
5/6	1/6	0.06	0.32	0.62	0.49	1.02	1.02	0.898	0.96	0.96	0.535	0.68	1.54	0.465
5/6	2/6	0.05	0.33	0.62	0.49	0.94	0.94	0.249	0.94	0.91	0.369	0.70	1.27	0.631
5/6	3/6	0.04	0.37	0.59	0.49	0.95	0.95	0.246	0.95	0.91	0.356	0.74	1.21	0.643
5/6	4/6	0.05	0.39	0.56	0.49	0.83	0.83	0.001	0.96	0.92	0.072	0.68	1.02	0.928
5/6	5/6	0.06	0.37	0.57	0.49	0.85	0.85	0.008	0.95	0.90	0.083	0.71	1.03	0.917
5/6	6/6	0.06	0.36	0.58	0.49	0.80	0.80	0.000	0.95	0.90	0.015	0.68	0.95	0.985
6/6	1/6	0.02	0.26	0.72	0.49	0.93	0.93	0.190	0.98	0.93	0.382	0.64	1.36	0.619
6/6	2/6	0.01	0.21	0.78	0.49	0.91	0.91	0.056	0.96	0.91	0.274	0.71	1.18	0.726
6/6	3/6	0.01	0.21	0.78	0.49	0.86	0.86	0.005	0.96	0.92	0.112	0.70	1.06	0.888
6/6	4/6	0.01	0.22	0.77	0.49	0.82	0.82	0.000	0.96	0.92	0.026	0.69	0.97	0.974
6/6	5/6	0.01	0.21	0.78	0.49	0.79	0.79	0.000	0.95	0.91	0.006	0.67	0.92	0.994
6/6	6/6	0.01	0.23	0.76	0.49	0.75	0.75	0.000	0.96	0.92	0.001	0.65	0.87	0.999

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

944 Appendix Table 2.-Summary statistics for tests of relative reproductive success (RRS) of a HxH cross to a NxN cross from
 945 simulations of a low stray rate (15% spawners hatchery-origin) stream with a modeled RRS of 0.500 for a HxH cross to a NxN cross
 946 for different sampling proportions of parents (F_0) and offspring (F_1) ranging from 1/6 to 6/6. Statistics include proportion of offspring
 947 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
 948 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , and the RRS values that we could have
 949 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
 950 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , 90% confidence interval, and the one tailed p-value that RRS is < 1). See
 951 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM				
F_0	F_1	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1	
					Simple	Unbiased	$\alpha = 0.20$		$\alpha = 0.05$	5%		95%			
1/6	1/6	0.70	0.27	0.03	0.51	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
1/6	2/6	0.72	0.26	0.02	0.51	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
1/6	3/6	0.71	0.27	0.02	0.51	0.59	0.59	0.788	0.59	0.59	0.311	0.10	3.41	0.689	
1/6	4/6	0.71	0.27	0.02	0.51	1.13	1.14	NA	NA	NA	NA	NA	NA	NA	
1/6	5/6	0.70	0.28	0.02	0.51	1.06	1.06	NA	NA	NA	NA	NA	NA	NA	
1/6	6/6	0.70	0.28	0.02	0.51	0.90	0.90	NA	NA	NA	NA	NA	NA	NA	
2/6	1/6	0.47	0.43	0.10	0.51	0.82	0.82	0.876	0.82	0.82	0.423	0.15	4.38	0.577	
2/6	2/6	0.49	0.41	0.10	0.51	1.69	1.70	NA	NA	NA	NA	NA	NA	NA	
2/6	3/6	0.42	0.44	0.14	0.51	0.69	0.69	0.726	0.69	0.69	0.358	0.13	3.62	0.642	
2/6	4/6	0.47	0.43	0.10	0.51	0.63	0.62	0.479	0.63	0.63	0.257	0.19	2.03	0.743	
2/6	5/6	0.47	0.43	0.10	0.51	0.89	0.89	0.669	0.59	0.59	0.424	0.34	2.33	0.576	
2/6	6/6	0.47	0.42	0.11	0.51	0.54	0.54	0.409	0.54	0.54	0.203	0.16	1.81	0.797	
3/6	1/6	0.28	0.52	0.20	0.51	0.85	0.85	0.707	0.85	0.85	0.408	0.26	2.76	0.592	
3/6	2/6	0.25	0.51	0.24	0.51	0.79	0.79	0.481	0.79	0.79	0.343	0.30	2.06	0.657	
3/6	3/6	0.24	0.49	0.27	0.51	0.85	0.85	0.442	0.73	0.73	0.339	0.45	1.60	0.661	
3/6	4/6	0.26	0.48	0.26	0.51	1.32	1.33	0.907	0.78	0.65	0.808	0.78	2.24	0.192	
3/6	5/6	0.29	0.49	0.22	0.51	1.00	1.00	0.622	0.80	0.59	0.505	0.59	1.70	0.494	
3/6	6/6	0.28	0.49	0.23	0.51	1.00	1.00	0.598	0.78	0.63	0.494	0.64	1.56	0.506	

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		α = 0.20	α = 0.05		5%	95%	
4/6	1/6	0.14	0.46	0.40	0.51	0.77	0.77	0.684	0.77	0.77	0.358	0.24	2.49	0.642
4/6	2/6	0.14	0.44	0.42	0.51	0.75	0.75	0.281	0.75	0.75	0.265	0.36	1.58	0.735
4/6	3/6	0.13	0.44	0.43	0.51	1.10	1.10	0.775	0.82	0.68	0.608	0.61	1.98	0.392
4/6	4/6	0.11	0.43	0.46	0.51	0.96	0.96	0.559	0.82	0.68	0.446	0.62	1.50	0.554
4/6	5/6	0.14	0.45	0.41	0.51	0.62	0.62	0.078	0.78	0.62	0.091	0.35	1.12	0.909
4/6	6/6	0.11	0.42	0.47	0.51	0.78	0.78	0.207	0.78	0.65	0.162	0.52	1.18	0.838
5/6	1/6	0.04	0.40	0.56	0.51	0.82	0.82	0.605	0.82	0.82	0.365	0.31	2.13	0.635
5/6	2/6	0.06	0.38	0.56	0.51	0.74	0.74	0.242	0.74	0.74	0.255	0.35	1.56	0.745
5/6	3/6	0.04	0.34	0.62	0.51	0.87	0.87	0.418	0.77	0.67	0.341	0.50	1.51	0.659
5/6	4/6	0.03	0.30	0.67	0.51	0.75	0.75	0.120	0.80	0.69	0.138	0.48	1.16	0.863
5/6	5/6	0.04	0.30	0.66	0.51	0.88	0.88	0.362	0.83	0.68	0.291	0.59	1.30	0.709
5/6	6/6	0.06	0.36	0.58	0.51	0.76	0.76	0.141	0.80	0.68	0.121	0.51	1.12	0.879
6/6	1/6	0.01	0.19	0.80	0.51	0.82	0.82	0.501	0.82	0.82	0.345	0.36	1.87	0.655
6/6	2/6	0.02	0.18	0.80	0.51	0.82	0.82	0.322	0.82	0.72	0.292	0.46	1.48	0.708
6/6	3/6	0.00	0.10	0.90	0.51	0.90	0.90	0.416	0.84	0.70	0.350	0.58	1.40	0.650
6/6	4/6	0.01	0.16	0.83	0.51	0.96	0.96	0.521	0.85	0.69	0.433	0.65	1.42	0.567
6/6	5/6	0.01	0.11	0.88	0.51	0.80	0.80	0.144	0.86	0.73	0.128	0.58	1.11	0.873
6/6	6/6	0.00	0.11	0.89	0.51	0.75	0.75	0.068	0.85	0.75	0.064	0.56	1.02	0.936

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

952 Appendix Table 3.-Summary statistics for tests of relative reproductive success (RRS) of a HxN cross to a NxN cross from
 953 simulations of a high stray rate (50% spawners hatchery-origin) stream with a modeled RRS of 0.500 for a HxH cross to a NxN cross
 954 for different sampling proportions of parents (F_0) and offspring (F_1) ranging from 1/6 to 6/6. Statistics include proportion of offspring
 955 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
 956 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , and the RRS values that we could have
 957 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
 958 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , 90% confidence interval, and the one tailed p-value that RRS is < 1). See
 959 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM				
F_0	F_1	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1	
						Simple	Unbiased		$\alpha = 0.20$	$\alpha = 0.05$		5%	95%		
1/6	1/6	0.69	0.29	0.02	0.74	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
1/6	2/6	0.70	0.28	0.02	0.74	1.33	1.34	1.000	0.67	0.67	0.647	0.38	4.68	0.353	
1/6	3/6	0.70	0.29	0.01	0.74	1.00	1.00	NA	NA	NA	NA	NA	NA	NA	
1/6	4/6	0.71	0.27	0.02	0.74	1.40	1.41	1.000	0.60	0.60	0.717	0.53	3.67	0.283	
1/6	5/6	0.70	0.28	0.02	0.74	1.50	1.51	1.000	0.77	0.40	0.766	0.60	3.75	0.234	
1/6	6/6	0.70	0.28	0.02	0.74	1.62	1.64	1.000	0.46	0.17	0.837	0.72	3.66	0.163	
2/6	1/6	0.51	0.42	0.07	0.74	0.88	0.87	0.542	0.88	0.88	0.402	0.36	2.13	0.598	
2/6	2/6	0.45	0.43	0.12	0.74	0.85	0.85	0.148	0.92	0.85	0.283	0.54	1.34	0.717	
2/6	3/6	0.45	0.45	0.10	0.74	0.93	0.93	0.405	0.87	0.75	0.394	0.62	1.42	0.606	
2/6	4/6	0.47	0.42	0.11	0.74	0.81	0.81	0.060	0.89	0.81	0.165	0.57	1.15	0.835	
2/6	5/6	0.47	0.43	0.10	0.74	0.90	0.90	0.225	0.90	0.82	0.286	0.65	1.23	0.714	
2/6	6/6	0.46	0.44	0.10	0.74	0.85	0.85	0.101	0.91	0.82	0.185	0.63	1.15	0.815	
3/6	1/6	0.27	0.49	0.24	0.74	0.95	0.95	0.437	0.95	0.95	0.436	0.60	1.53	0.564	
3/6	2/6	0.30	0.45	0.25	0.74	0.95	0.95	0.300	0.95	0.87	0.389	0.68	1.31	0.611	
3/6	3/6	0.29	0.48	0.23	0.74	1.01	1.01	0.618	0.95	0.89	0.516	0.76	1.33	0.484	
3/6	4/6	0.29	0.48	0.23	0.74	0.98	0.98	0.476	0.94	0.87	0.458	0.77	1.26	0.542	
3/6	5/6	0.29	0.49	0.22	0.74	0.92	0.92	0.192	0.94	0.87	0.276	0.74	1.15	0.724	
3/6	6/6	0.28	0.49	0.23	0.74	0.89	0.89	0.070	0.94	0.89	0.165	0.73	1.08	0.835	

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		α = 0.20	α = 0.05		5%	95%	
4/6	1/6	0.18	0.42	0.40	0.74	1.00	1.00	0.666	0.95	0.90	0.499	0.70	1.43	0.501
4/6	2/6	0.15	0.49	0.36	0.74	0.93	0.93	0.135	0.95	0.90	0.324	0.71	1.22	0.676
4/6	3/6	0.14	0.43	0.43	0.74	0.94	0.94	0.156	0.95	0.91	0.294	0.77	1.14	0.706
4/6	4/6	0.16	0.46	0.38	0.74	0.87	0.87	0.014	0.95	0.91	0.118	0.72	1.05	0.882
4/6	5/6	0.16	0.47	0.37	0.74	0.85	0.85	0.010	0.95	0.91	0.066	0.72	1.01	0.934
4/6	6/6	0.15	0.47	0.38	0.74	0.84	0.84	0.005	0.95	0.90	0.035	0.72	0.98	0.965
5/6	1/6	0.06	0.32	0.62	0.74	1.02	1.02	0.855	0.98	0.95	0.537	0.76	1.37	0.463
5/6	2/6	0.05	0.33	0.62	0.74	1.09	1.09	0.937	0.94	0.89	0.748	0.88	1.34	0.252
5/6	3/6	0.04	0.37	0.59	0.74	1.07	1.07	0.927	0.95	0.91	0.750	0.90	1.28	0.250
5/6	4/6	0.05	0.39	0.56	0.74	0.95	0.95	0.186	0.96	0.91	0.293	0.81	1.11	0.707
5/6	5/6	0.06	0.37	0.57	0.74	0.97	0.97	0.343	0.95	0.91	0.382	0.85	1.12	0.618
5/6	6/6	0.06	0.36	0.58	0.74	0.98	0.98	0.368	0.96	0.91	0.389	0.86	1.11	0.612
6/6	1/6	0.02	0.26	0.72	0.74	1.00	1.00	0.603	0.97	0.94	0.494	0.76	1.31	0.505
6/6	2/6	0.01	0.21	0.78	0.74	0.99	0.99	0.443	0.96	0.93	0.457	0.82	1.19	0.543
6/6	3/6	0.01	0.21	0.78	0.74	0.96	0.96	0.232	0.96	0.92	0.342	0.83	1.12	0.658
6/6	4/6	0.01	0.22	0.77	0.74	0.92	0.92	0.034	0.96	0.93	0.149	0.80	1.05	0.851
6/6	5/6	0.01	0.21	0.78	0.74	0.88	0.88	0.003	0.97	0.93	0.034	0.78	0.99	0.966
6/6	6/6	0.01	0.23	0.76	0.74	0.91	0.91	0.030	0.96	0.92	0.082	0.82	1.02	0.918

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

960 Appendix Table 4.-Summary statistics for tests of relative reproductive success (RRS) of a HxN cross to a NxN cross from
 961 simulations of a low stray rate (15% spawners hatchery-origin) stream with a modeled RRS of 0.500 for a HxH cross to a NxN cross
 962 for different sampling proportions of parents (F_0) and offspring (F_1) ranging from 1/6 to 6/6. Statistics include proportion of offspring
 963 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
 964 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , and the RRS values that we could have
 965 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
 966 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , 90% confidence interval, and the one tailed p-value that RRS is < 1). See
 967 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F_0	F_1	Unassigned	1 Parent	2 Parents	Estimated			RRS Detectability			90% CI			p RRS < 1
					True	Simple	Unbiased	1-tail p	$\alpha = 0.20$	$\alpha = 0.05$	1-tail p	5%	95%	
1/6	1/6	0.70	0.27	0.03	0.75	0.62	0.62	NA	NA	NA	NA	NA	NA	NA
1/6	2/6	0.72	0.26	0.02	0.75	0.58	0.58	0.212	0.58	0.58	0.175	0.23	1.51	0.825
1/6	3/6	0.71	0.27	0.02	0.75	0.74	0.74	0.542	0.55	0.55	0.275	0.32	1.70	0.726
1/6	4/6	0.71	0.27	0.02	0.75	0.89	0.89	0.450	0.78	0.55	0.371	0.50	1.59	0.629
1/6	5/6	0.70	0.28	0.02	0.75	0.74	0.74	0.249	0.74	0.58	0.173	0.44	1.25	0.827
1/6	6/6	0.70	0.28	0.02	0.75	0.66	0.65	0.153	0.72	0.59	0.092	0.39	1.10	0.908
2/6	1/6	0.47	0.43	0.10	0.75	0.82	0.82	0.208	0.82	0.82	0.269	0.49	1.39	0.731
2/6	2/6	0.49	0.41	0.10	0.75	0.92	0.92	0.325	0.92	0.87	0.369	0.62	1.37	0.631
2/6	3/6	0.42	0.44	0.14	0.75	0.85	0.85	0.120	0.91	0.82	0.187	0.63	1.15	0.813
2/6	4/6	0.47	0.43	0.10	0.75	0.87	0.86	0.191	0.89	0.78	0.211	0.64	1.16	0.789
2/6	5/6	0.47	0.43	0.10	0.75	0.82	0.82	0.082	0.88	0.80	0.101	0.64	1.06	0.899
2/6	6/6	0.47	0.42	0.11	0.75	0.85	0.85	0.135	0.88	0.80	0.118	0.67	1.07	0.882
3/6	1/6	0.28	0.52	0.20	0.75	0.89	0.89	0.173	0.95	0.89	0.319	0.59	1.34	0.681
3/6	2/6	0.25	0.51	0.24	0.75	0.83	0.83	0.005	0.95	0.90	0.133	0.63	1.09	0.867
3/6	3/6	0.24	0.49	0.27	0.75	0.98	0.98	0.463	0.93	0.86	0.439	0.79	1.22	0.561
3/6	4/6	0.26	0.48	0.26	0.75	0.90	0.90	0.152	0.93	0.86	0.211	0.74	1.11	0.789
3/6	5/6	0.29	0.49	0.22	0.75	0.82	0.82	0.016	0.92	0.87	0.043	0.68	0.99	0.957
3/6	6/6	0.28	0.49	0.23	0.75	0.90	0.89	0.129	0.92	0.86	0.143	0.76	1.06	0.857

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		α = 0.20	α = 0.05		5%	95%	
4/6	1/6	0.14	0.46	0.40	0.75	0.88	0.88	0.206	0.88	0.81	0.260	0.64	1.22	0.740
4/6	2/6	0.14	0.44	0.42	0.75	0.91	0.91	0.134	0.94	0.88	0.230	0.74	1.12	0.770
4/6	3/6	0.13	0.44	0.43	0.75	0.93	0.93	0.191	0.94	0.88	0.241	0.78	1.11	0.759
4/6	4/6	0.11	0.43	0.46	0.75	0.90	0.90	0.094	0.94	0.88	0.120	0.78	1.04	0.880
4/6	5/6	0.14	0.45	0.41	0.75	0.85	0.85	0.016	0.94	0.88	0.021	0.74	0.97	0.979
4/6	6/6	0.11	0.42	0.47	0.75	0.88	0.88	0.046	0.94	0.88	0.040	0.78	0.99	0.960
5/6	1/6	0.04	0.40	0.56	0.75	0.88	0.88	0.098	0.94	0.88	0.238	0.67	1.18	0.762
5/6	2/6	0.06	0.38	0.56	0.75	0.88	0.88	0.024	0.94	0.90	0.119	0.73	1.05	0.881
5/6	3/6	0.04	0.34	0.62	0.75	0.89	0.89	0.035	0.95	0.91	0.103	0.77	1.04	0.897
5/6	4/6	0.03	0.30	0.67	0.75	0.90	0.90	0.062	0.95	0.90	0.089	0.80	1.02	0.911
5/6	5/6	0.04	0.30	0.66	0.75	0.85	0.85	0.003	0.95	0.91	0.005	0.76	0.94	0.995
5/6	6/6	0.06	0.36	0.58	0.75	0.88	0.88	0.022	0.95	0.90	0.022	0.79	0.98	0.978
6/6	1/6	0.01	0.19	0.80	0.75	0.92	0.92	0.128	0.95	0.90	0.266	0.74	1.14	0.734
6/6	2/6	0.02	0.18	0.80	0.75	0.86	0.86	0.002	0.95	0.92	0.047	0.74	1.00	0.953
6/6	3/6	0.00	0.10	0.90	0.75	0.91	0.91	0.034	0.95	0.92	0.087	0.80	1.02	0.912
6/6	4/6	0.01	0.16	0.83	0.75	0.90	0.90	0.025	0.96	0.91	0.049	0.81	1.00	0.951
6/6	5/6	0.01	0.11	0.88	0.75	0.87	0.87	0.005	0.96	0.92	0.006	0.79	0.95	0.994
6/6	6/6	0.00	0.11	0.89	0.75	0.86	0.86	0.004	0.96	0.92	0.003	0.79	0.94	0.997

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

968 Appendix Table 5.-Summary statistics for tests of relative reproductive success (RRS) of a H dam cross to a N dam cross from
 969 simulations of a high stray rate (50% spawners hatchery-origin) stream with a modeled RRS of 0.500 for a HxH cross to a NxN cross
 970 for different sampling proportions of parents (F₀) and offspring (F₁) ranging from 1/6 to 6/6. Statistics include proportion of offspring
 971 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
 972 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, and the RRS values that we could have
 973 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
 974 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, 90% confidence interval, and the one tailed p-value that RRS is <1). See
 975 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	Estimated			RRS Detectability			90% CI			p RRS < 1
					True	Simple	Unbiased	1-tail p	α = 0.20	α = 0.05	1-tail p	5%	95%	
1/6	1/6	0.69	0.29	0.02	0.69	0.91	0.90	0.438	0.71	0.52	0.378	0.54	1.53	0.622
1/6	2/6	0.70	0.28	0.02	0.69	0.51	0.48	0.005	0.86	0.68	0.004	0.33	0.78	0.996
1/6	3/6	0.70	0.29	0.01	0.69	0.92	0.91	0.379	0.84	0.68	0.340	0.66	1.29	0.660
1/6	4/6	0.71	0.27	0.02	0.69	0.71	0.69	0.046	0.85	0.74	0.037	0.52	0.97	0.963
1/6	5/6	0.70	0.28	0.02	0.69	0.63	0.61	0.005	0.87	0.77	0.004	0.48	0.84	0.996
1/6	6/6	0.70	0.28	0.02	0.69	0.76	0.74	0.044	0.88	0.78	0.037	0.59	0.98	0.963
2/6	1/6	0.51	0.42	0.07	0.69	0.76	0.75	0.140	0.81	0.67	0.126	0.52	1.13	0.874
2/6	2/6	0.45	0.43	0.12	0.69	0.51	0.49	0.000	0.89	0.80	0.000	0.39	0.67	1.000
2/6	3/6	0.45	0.45	0.10	0.69	0.57	0.55	0.000	0.90	0.82	0.000	0.45	0.73	1.000
2/6	4/6	0.47	0.42	0.11	0.69	0.66	0.64	0.001	0.91	0.83	0.000	0.54	0.81	1.000
2/6	5/6	0.47	0.43	0.10	0.69	0.68	0.66	0.000	0.92	0.85	0.000	0.57	0.82	1.000
2/6	6/6	0.46	0.44	0.10	0.69	0.67	0.65	0.000	0.93	0.86	0.000	0.57	0.79	1.000
3/6	1/6	0.27	0.49	0.24	0.69	0.76	0.75	0.080	0.85	0.72	0.070	0.55	1.03	0.930
3/6	2/6	0.30	0.45	0.25	0.69	0.58	0.56	0.000	0.90	0.82	0.000	0.46	0.73	1.000
3/6	3/6	0.29	0.48	0.23	0.69	0.66	0.64	0.000	0.92	0.84	0.000	0.54	0.79	1.000
3/6	4/6	0.29	0.48	0.23	0.69	0.77	0.76	0.005	0.92	0.86	0.004	0.66	0.91	0.996
3/6	5/6	0.29	0.49	0.22	0.69	0.75	0.73	0.001	0.93	0.87	0.000	0.64	0.86	1.000
3/6	6/6	0.28	0.49	0.23	0.69	0.70	0.69	0.000	0.94	0.89	0.000	0.61	0.80	1.000

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		α = 0.20	α = 0.05		5%	95%	
4/6	1/6	0.18	0.42	0.40	0.69	0.84	0.84	0.174	0.87	0.74	0.153	0.64	1.11	0.847
4/6	2/6	0.15	0.49	0.36	0.69	0.61	0.60	0.000	0.92	0.84	0.000	0.49	0.74	1.000
4/6	3/6	0.14	0.43	0.43	0.69	0.66	0.65	0.000	0.93	0.86	0.000	0.56	0.78	1.000
4/6	4/6	0.16	0.46	0.38	0.69	0.76	0.76	0.001	0.94	0.88	0.001	0.67	0.88	0.999
4/6	5/6	0.16	0.47	0.37	0.69	0.71	0.70	0.000	0.94	0.89	0.000	0.62	0.81	1.000
4/6	6/6	0.15	0.47	0.38	0.69	0.71	0.70	0.000	0.94	0.89	0.000	0.63	0.80	1.000
5/6	1/6	0.06	0.32	0.62	0.69	0.75	0.74	0.022	0.89	0.80	0.022	0.59	0.95	0.978
5/6	2/6	0.05	0.33	0.62	0.69	0.64	0.64	0.000	0.92	0.85	0.000	0.54	0.77	1.000
5/6	3/6	0.04	0.37	0.59	0.69	0.64	0.64	0.000	0.94	0.88	0.000	0.55	0.74	1.000
5/6	4/6	0.05	0.39	0.56	0.69	0.71	0.70	0.000	0.94	0.89	0.000	0.62	0.80	1.000
5/6	5/6	0.06	0.37	0.57	0.69	0.69	0.68	0.000	0.95	0.90	0.000	0.61	0.78	1.000
5/6	6/6	0.06	0.36	0.58	0.69	0.69	0.68	0.000	0.95	0.90	0.000	0.61	0.77	1.000
6/6	1/6	0.02	0.26	0.72	0.69	0.71	0.71	0.009	0.89	0.81	0.008	0.56	0.90	0.992
6/6	2/6	0.01	0.21	0.78	0.69	0.62	0.61	0.000	0.93	0.87	0.000	0.52	0.73	1.000
6/6	3/6	0.01	0.21	0.78	0.69	0.66	0.65	0.000	0.94	0.88	0.000	0.57	0.75	1.000
6/6	4/6	0.01	0.22	0.77	0.69	0.71	0.71	0.000	0.95	0.90	0.000	0.63	0.80	1.000
6/6	5/6	0.01	0.21	0.78	0.69	0.68	0.68	0.000	0.95	0.90	0.000	0.61	0.76	1.000
6/6	6/6	0.01	0.23	0.76	0.69	0.66	0.66	0.000	0.96	0.91	0.000	0.60	0.74	1.000

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

976 Appendix Table 6.-Summary statistics for tests of relative reproductive success (RRS) of a H dam cross to a N dam cross from
 977 simulations of a low stray rate (15% spawners hatchery-origin) stream with a modeled RRS of 0.500 for a HxH cross to a NxN cross
 978 for different sampling proportions of parents (F₀) and offspring (F₁) ranging from 1/6 to 6/6. Statistics include proportion of offspring
 979 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
 980 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, and the RRS values that we could have
 981 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
 982 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, 90% confidence interval, and the one tailed p-value that RRS is <1). See
 983 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	Estimated			RRS Detectability			90% CI			p RRS < 1
					True	Simple	Unbiased	1-tail p	α = 0.20	α = 0.05	1-tail p	5%	95%	
1/6	1/6	0.70	0.27	0.03	0.75	0.73	0.70	0.317	0.62	0.40	0.228	0.36	1.46	0.772
1/6	2/6	0.72	0.26	0.02	0.75	0.74	0.71	0.201	0.74	0.57	0.155	0.45	1.21	0.845
1/6	3/6	0.71	0.27	0.02	0.75	0.69	0.66	0.095	0.80	0.65	0.079	0.45	1.06	0.921
1/6	4/6	0.71	0.27	0.02	0.75	0.65	0.61	0.052	0.82	0.65	0.042	0.43	0.98	0.958
1/6	5/6	0.70	0.28	0.02	0.75	0.85	0.84	0.264	0.83	0.67	0.222	0.61	1.20	0.777
1/6	6/6	0.70	0.28	0.02	0.75	0.82	0.80	0.187	0.84	0.71	0.151	0.60	1.13	0.849
2/6	1/6	0.47	0.43	0.10	0.75	0.87	0.86	0.371	0.76	0.58	0.308	0.55	1.37	0.692
2/6	2/6	0.49	0.41	0.10	0.75	0.74	0.72	0.089	0.82	0.71	0.071	0.52	1.04	0.929
2/6	3/6	0.42	0.44	0.14	0.75	0.64	0.61	0.006	0.87	0.76	0.005	0.48	0.85	0.995
2/6	4/6	0.47	0.43	0.10	0.75	0.65	0.63	0.011	0.86	0.75	0.007	0.49	0.87	0.993
2/6	5/6	0.47	0.43	0.10	0.75	0.76	0.74	0.043	0.87	0.77	0.028	0.59	0.96	0.972
2/6	6/6	0.47	0.42	0.11	0.75	0.72	0.70	0.013	0.88	0.78	0.008	0.57	0.90	0.992
3/6	1/6	0.28	0.52	0.20	0.75	0.79	0.78	0.180	0.82	0.65	0.147	0.54	1.15	0.853
3/6	2/6	0.25	0.51	0.24	0.75	0.60	0.57	0.001	0.87	0.77	0.001	0.45	0.79	0.999
3/6	3/6	0.24	0.49	0.27	0.75	0.61	0.58	0.000	0.89	0.80	0.000	0.48	0.77	1.000
3/6	4/6	0.26	0.48	0.26	0.75	0.66	0.64	0.001	0.90	0.81	0.001	0.53	0.82	0.999
3/6	5/6	0.29	0.49	0.22	0.75	0.70	0.69	0.002	0.91	0.82	0.002	0.58	0.86	0.998
3/6	6/6	0.28	0.49	0.23	0.75	0.66	0.65	0.000	0.91	0.83	0.000	0.55	0.79	1.000

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		α = 0.20	α = 0.05		5%	95%	
4/6	1/6	0.14	0.46	0.40	0.75	0.76	0.76	0.116	0.85	0.71	0.093	0.55	1.07	0.907
4/6	2/6	0.14	0.44	0.42	0.75	0.85	0.84	0.140	0.89	0.78	0.120	0.68	1.07	0.880
4/6	3/6	0.13	0.44	0.43	0.75	0.75	0.74	0.008	0.91	0.82	0.007	0.61	0.91	0.993
4/6	4/6	0.11	0.43	0.46	0.75	0.75	0.74	0.004	0.92	0.84	0.003	0.63	0.89	0.997
4/6	5/6	0.14	0.45	0.41	0.75	0.73	0.72	0.001	0.92	0.85	0.001	0.62	0.86	0.999
4/6	6/6	0.11	0.42	0.47	0.75	0.76	0.75	0.002	0.93	0.86	0.001	0.65	0.88	0.999
5/6	1/6	0.04	0.40	0.56	0.75	0.89	0.89	0.291	0.84	0.72	0.257	0.66	1.20	0.743
5/6	2/6	0.06	0.38	0.56	0.75	0.78	0.78	0.040	0.90	0.80	0.036	0.63	0.98	0.964
5/6	3/6	0.04	0.34	0.62	0.75	0.75	0.75	0.007	0.91	0.84	0.006	0.63	0.91	0.994
5/6	4/6	0.03	0.30	0.67	0.75	0.76	0.76	0.004	0.92	0.85	0.004	0.65	0.90	0.997
5/6	5/6	0.04	0.30	0.66	0.75	0.78	0.78	0.004	0.93	0.86	0.004	0.67	0.91	0.996
5/6	6/6	0.06	0.36	0.58	0.75	0.78	0.78	0.003	0.93	0.86	0.002	0.67	0.90	0.998
6/6	1/6	0.01	0.19	0.80	0.75	0.87	0.86	0.220	0.87	0.75	0.193	0.66	1.14	0.807
6/6	2/6	0.02	0.18	0.80	0.75	0.73	0.73	0.007	0.91	0.82	0.006	0.59	0.90	0.994
6/6	3/6	0.00	0.10	0.90	0.75	0.74	0.74	0.002	0.92	0.85	0.001	0.62	0.87	0.999
6/6	4/6	0.01	0.16	0.83	0.75	0.71	0.71	0.000	0.93	0.86	0.000	0.61	0.83	1.000
6/6	5/6	0.01	0.11	0.88	0.75	0.75	0.75	0.000	0.93	0.87	0.000	0.66	0.87	1.000
6/6	6/6	0.00	0.11	0.89	0.75	0.73	0.73	0.000	0.94	0.88	0.000	0.64	0.84	1.000

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

984 Appendix Table 7.-Summary statistics for tests of relative reproductive success (RRS) of a H sire cross to a N sire cross from
985 simulations of a high stray rate (50% spawners hatchery-origin) stream with a modeled RRS of 0.500 for a HxH cross to a NxN cross
986 for different sampling proportions of parents (F₀) and offspring (F₁) ranging from 1/6 to 6/6. Statistics include proportion of offspring
987 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
988 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, and the RRS values that we could have
989 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
990 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, 90% confidence interval, and the one tailed p-value that RRS is <1). See
991 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	Estimated			RRS Detectability			90% CI			
					True	Simple	Unbiased	1-tail p	α = 0.20	α = 0.05	1-tail p	5%	95%	p RRS < 1
1/6	1/6	0.69	0.29	0.02	0.72	0.60	0.59	0.069	0.76	0.60	0.058	0.36	1.02	0.942
1/6	2/6	0.70	0.28	0.02	0.72	0.76	0.74	0.118	0.83	0.68	0.099	0.53	1.08	0.901
1/6	3/6	0.70	0.29	0.01	0.72	0.77	0.76	0.087	0.87	0.75	0.074	0.58	1.04	0.926
1/6	4/6	0.71	0.27	0.02	0.72	0.79	0.78	0.086	0.87	0.75	0.075	0.61	1.03	0.924
1/6	5/6	0.70	0.28	0.02	0.72	0.84	0.83	0.131	0.89	0.78	0.115	0.66	1.07	0.885
1/6	6/6	0.70	0.28	0.02	0.72	0.80	0.79	0.064	0.90	0.79	0.053	0.64	1.00	0.947
2/6	1/6	0.51	0.42	0.07	0.72	0.66	0.64	0.053	0.85	0.66	0.045	0.44	0.99	0.955
2/6	2/6	0.45	0.43	0.12	0.72	0.57	0.55	0.000	0.90	0.78	0.000	0.44	0.75	1.000
2/6	3/6	0.45	0.45	0.10	0.72	0.67	0.65	0.002	0.91	0.81	0.001	0.53	0.83	0.999
2/6	4/6	0.47	0.42	0.11	0.72	0.65	0.64	0.000	0.92	0.85	0.000	0.54	0.79	1.000
2/6	5/6	0.47	0.43	0.10	0.72	0.67	0.66	0.000	0.92	0.85	0.000	0.56	0.80	1.000
2/6	6/6	0.46	0.44	0.10	0.72	0.67	0.66	0.000	0.93	0.87	0.000	0.57	0.79	1.000
3/6	1/6	0.27	0.49	0.24	0.72	0.67	0.65	0.013	0.87	0.77	0.011	0.50	0.89	0.989
3/6	2/6	0.30	0.45	0.25	0.72	0.81	0.80	0.059	0.90	0.81	0.053	0.65	1.00	0.947
3/6	3/6	0.29	0.48	0.23	0.72	0.67	0.66	0.000	0.93	0.85	0.000	0.56	0.79	1.000
3/6	4/6	0.29	0.48	0.23	0.72	0.79	0.79	0.008	0.93	0.86	0.007	0.68	0.93	0.993
3/6	5/6	0.29	0.49	0.22	0.72	0.75	0.75	0.001	0.93	0.87	0.000	0.65	0.87	1.000
3/6	6/6	0.28	0.49	0.23	0.72	0.75	0.75	0.000	0.94	0.88	0.000	0.66	0.86	1.000

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		α = 0.20	α = 0.05		5%	95%	
4/6	1/6	0.18	0.42	0.40	0.72	0.65	0.65	0.004	0.88	0.78	0.004	0.50	0.85	0.996
4/6	2/6	0.15	0.49	0.36	0.72	0.75	0.74	0.007	0.91	0.84	0.006	0.62	0.90	0.994
4/6	3/6	0.14	0.43	0.43	0.72	0.67	0.66	0.000	0.93	0.87	0.000	0.57	0.78	1.000
4/6	4/6	0.16	0.46	0.38	0.72	0.79	0.78	0.004	0.93	0.87	0.003	0.68	0.91	0.997
4/6	5/6	0.16	0.47	0.37	0.72	0.74	0.73	0.000	0.94	0.89	0.000	0.65	0.83	1.000
4/6	6/6	0.15	0.47	0.38	0.72	0.72	0.72	0.000	0.95	0.90	0.000	0.64	0.81	1.000
5/6	1/6	0.06	0.32	0.62	0.72	0.66	0.65	0.002	0.91	0.81	0.002	0.52	0.83	0.998
5/6	2/6	0.05	0.33	0.62	0.72	0.73	0.73	0.002	0.93	0.85	0.001	0.62	0.87	0.999
5/6	3/6	0.04	0.37	0.59	0.72	0.68	0.67	0.000	0.94	0.88	0.000	0.59	0.78	1.000
5/6	4/6	0.05	0.39	0.56	0.72	0.75	0.74	0.000	0.94	0.89	0.000	0.66	0.84	1.000
5/6	5/6	0.06	0.37	0.57	0.72	0.74	0.74	0.000	0.95	0.90	0.000	0.66	0.83	1.000
5/6	6/6	0.06	0.36	0.58	0.72	0.75	0.75	0.000	0.95	0.91	0.000	0.67	0.83	1.000
6/6	1/6	0.02	0.26	0.72	0.72	0.65	0.65	0.001	0.92	0.83	0.001	0.52	0.81	0.999
6/6	2/6	0.01	0.21	0.78	0.72	0.69	0.69	0.000	0.93	0.87	0.000	0.58	0.80	1.000
6/6	3/6	0.01	0.21	0.78	0.72	0.65	0.65	0.000	0.94	0.89	0.000	0.57	0.75	1.000
6/6	4/6	0.01	0.22	0.77	0.72	0.72	0.72	0.000	0.95	0.90	0.000	0.64	0.81	1.000
6/6	5/6	0.01	0.21	0.78	0.72	0.71	0.71	0.000	0.95	0.91	0.000	0.64	0.79	1.000
6/6	6/6	0.01	0.23	0.76	0.72	0.71	0.71	0.000	0.96	0.92	0.000	0.64	0.78	1.000

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

992 Appendix Table 8.-Summary statistics for tests of relative reproductive success (RRS) of a H sire cross to a N sire cross from
 993 simulations of a low stray rate (15% spawners hatchery-origin) stream with a modeled RRS of 0.500 for a HxH cross to a NxN cross
 994 for different sampling proportions of parents (F₀) and offspring (F₁) ranging from 1/6 to 6/6. Statistics include proportion of offspring
 995 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
 996 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, and the RRS values that we could have
 997 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
 998 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, 90% confidence interval, and the one tailed p-value that RRS is <1). See
 999 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	Estimated			RRS Detectability			90% CI			p RRS < 1
					True	Simple	Unbiased	1-tail p	α = 0.20	α = 0.05	1-tail p	5%	95%	
1/6	1/6	0.70	0.27	0.03	0.73	0.77	0.77	0.371	0.65	0.40	0.282	0.37	1.61	0.718
1/6	2/6	0.72	0.26	0.02	0.73	0.96	0.96	0.518	0.74	0.53	0.449	0.56	1.65	0.551
1/6	3/6	0.71	0.27	0.02	0.73	0.88	0.88	0.365	0.80	0.62	0.318	0.58	1.35	0.682
1/6	4/6	0.71	0.27	0.02	0.73	0.69	0.68	0.080	0.82	0.66	0.065	0.46	1.03	0.935
1/6	5/6	0.70	0.28	0.02	0.73	0.74	0.73	0.108	0.81	0.69	0.084	0.51	1.06	0.916
1/6	6/6	0.70	0.28	0.02	0.73	0.83	0.83	0.214	0.83	0.69	0.180	0.60	1.16	0.820
2/6	1/6	0.47	0.43	0.10	0.73	0.84	0.83	0.327	0.78	0.60	0.271	0.52	1.34	0.729
2/6	2/6	0.49	0.41	0.10	0.73	0.80	0.79	0.160	0.83	0.71	0.139	0.56	1.12	0.861
2/6	3/6	0.42	0.44	0.14	0.73	0.68	0.66	0.017	0.87	0.75	0.014	0.51	0.91	0.986
2/6	4/6	0.47	0.43	0.10	0.73	0.73	0.72	0.031	0.88	0.76	0.027	0.56	0.96	0.973
2/6	5/6	0.47	0.43	0.10	0.73	0.84	0.83	0.130	0.89	0.78	0.116	0.66	1.07	0.884
2/6	6/6	0.47	0.42	0.11	0.73	0.79	0.79	0.060	0.89	0.78	0.052	0.63	1.00	0.948
3/6	1/6	0.28	0.52	0.20	0.73	0.68	0.67	0.063	0.83	0.68	0.053	0.46	1.01	0.947
3/6	2/6	0.25	0.51	0.24	0.73	0.75	0.74	0.044	0.88	0.77	0.040	0.58	0.98	0.960
3/6	3/6	0.24	0.49	0.27	0.73	0.67	0.65	0.003	0.90	0.80	0.003	0.53	0.85	0.997
3/6	4/6	0.26	0.48	0.26	0.73	0.61	0.59	0.000	0.91	0.83	0.000	0.49	0.76	1.000
3/6	5/6	0.29	0.49	0.22	0.73	0.66	0.64	0.000	0.91	0.83	0.000	0.54	0.80	1.000
3/6	6/6	0.28	0.49	0.23	0.73	0.69	0.68	0.000	0.92	0.84	0.000	0.58	0.82	1.000

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		α = 0.20	α = 0.05		5%	95%	
4/6	1/6	0.14	0.46	0.40	0.73	0.69	0.69	0.052	0.83	0.69	0.042	0.48	0.98	0.958
4/6	2/6	0.14	0.44	0.42	0.73	0.83	0.83	0.110	0.89	0.79	0.095	0.66	1.05	0.905
4/6	3/6	0.13	0.44	0.43	0.73	0.67	0.67	0.001	0.91	0.82	0.001	0.55	0.83	0.999
4/6	4/6	0.11	0.43	0.46	0.73	0.74	0.74	0.004	0.92	0.84	0.004	0.62	0.89	0.996
4/6	5/6	0.14	0.45	0.41	0.73	0.79	0.78	0.013	0.91	0.84	0.011	0.66	0.93	0.989
4/6	6/6	0.11	0.42	0.47	0.73	0.77	0.76	0.005	0.92	0.85	0.003	0.66	0.90	0.997
5/6	1/6	0.04	0.40	0.56	0.73	0.56	0.56	0.002	0.87	0.74	0.002	0.40	0.79	0.998
5/6	2/6	0.06	0.38	0.56	0.73	0.72	0.72	0.010	0.90	0.80	0.008	0.58	0.90	0.992
5/6	3/6	0.04	0.34	0.62	0.73	0.68	0.68	0.000	0.92	0.84	0.000	0.57	0.82	1.000
5/6	4/6	0.03	0.30	0.67	0.73	0.69	0.69	0.000	0.93	0.85	0.000	0.59	0.82	1.000
5/6	5/6	0.04	0.30	0.66	0.73	0.77	0.77	0.003	0.93	0.87	0.002	0.66	0.90	0.998
5/6	6/6	0.06	0.36	0.58	0.73	0.75	0.75	0.001	0.93	0.87	0.001	0.65	0.87	0.999
6/6	1/6	0.01	0.19	0.80	0.73	0.63	0.63	0.005	0.87	0.76	0.005	0.47	0.85	0.995
6/6	2/6	0.02	0.18	0.80	0.73	0.77	0.77	0.017	0.91	0.82	0.014	0.63	0.94	0.986
6/6	3/6	0.00	0.10	0.90	0.73	0.67	0.67	0.000	0.92	0.86	0.000	0.56	0.79	1.000
6/6	4/6	0.01	0.16	0.83	0.73	0.70	0.70	0.000	0.93	0.87	0.000	0.60	0.82	1.000
6/6	5/6	0.01	0.11	0.88	0.73	0.73	0.73	0.000	0.93	0.88	0.000	0.64	0.84	1.000
6/6	6/6	0.00	0.11	0.89	0.73	0.74	0.74	0.000	0.94	0.88	0.000	0.65	0.85	1.000

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

1000 Appendix Table 9.-Summary statistics for tests of relative reproductive success (RRS) of a HxH cross to a NxN cross from
 1001 simulations of a high stray rate (50% spawners hatchery-origin) stream with a modeled RRS of 0.625 for a HxH cross to a NxN cross
 1002 for different sampling proportions of parents (F₀) and offspring (F₁) ranging from 1/6 to 6/6. Statistics include proportion of offspring
 1003 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
 1004 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, and the RRS values that we could have
 1005 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
 1006 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, 90% confidence interval, and the one tailed p-value that RRS is <1). See
 1007 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	Estimated			RRS Detectability			90% CI			p RRS < 1
					True	Simple	Unbiased	1-tail p	α = 0.20	α = 0.05	1-tail p	5%	95%	
1/6	1/6	0.72	0.26	0.02	0.63	1.00	1.00	NA	NA	NA	NA	NA	NA	NA
1/6	2/6	0.67	0.29	0.04	0.63	1.00	1.00	NA	NA	NA	NA	NA	NA	NA
1/6	3/6	0.69	0.28	0.03	0.63	0.86	0.85	0.500	0.86	0.86	0.391	0.34	2.14	0.609
1/6	4/6	0.67	0.29	0.04	0.63	0.87	0.86	0.372	0.87	0.87	0.372	0.42	1.78	0.628
1/6	5/6	0.70	0.27	0.03	0.63	0.82	0.81	0.301	0.82	0.82	0.339	0.37	1.81	0.661
1/6	6/6	0.69	0.28	0.03	0.63	0.73	0.72	0.109	0.87	0.73	0.217	0.38	1.41	0.783
2/6	1/6	0.50	0.43	0.07	0.63	1.00	1.00	NA	NA	NA	NA	NA	NA	NA
2/6	2/6	0.44	0.46	0.10	0.63	1.20	1.20	1.000	0.83	0.83	0.672	0.61	2.35	0.328
2/6	3/6	0.49	0.42	0.09	0.63	0.92	0.92	0.353	0.92	0.82	0.400	0.55	1.56	0.600
2/6	4/6	0.46	0.44	0.10	0.63	0.85	0.85	0.112	0.92	0.85	0.271	0.55	1.31	0.729
2/6	5/6	0.48	0.42	0.10	0.63	0.79	0.79	0.058	0.91	0.79	0.177	0.53	1.20	0.823
2/6	6/6	0.48	0.43	0.09	0.63	0.80	0.80	0.045	0.90	0.85	0.168	0.54	1.17	0.832
3/6	1/6	0.28	0.52	0.20	0.63	0.86	0.86	0.432	0.86	0.86	0.376	0.38	1.91	0.624
3/6	2/6	0.23	0.48	0.29	0.63	0.97	0.97	0.522	0.90	0.83	0.452	0.63	1.50	0.548
3/6	3/6	0.27	0.48	0.25	0.63	0.96	0.96	0.419	0.91	0.87	0.417	0.68	1.35	0.583
3/6	4/6	0.28	0.49	0.23	0.63	0.83	0.83	0.014	0.93	0.90	0.167	0.60	1.14	0.833
3/6	5/6	0.28	0.50	0.22	0.63	0.92	0.92	0.206	0.92	0.85	0.314	0.68	1.23	0.686
3/6	6/6	0.28	0.49	0.23	0.63	0.86	0.86	0.073	0.93	0.86	0.171	0.66	1.12	0.829

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		α = 0.20	α = 0.05		5%	95%	
4/6	1/6	0.16	0.51	0.33	0.63	1.00	1.00	NA	NA	NA	NA	NA	NA	NA
4/6	2/6	0.17	0.50	0.33	0.63	0.88	0.88	0.119	0.93	0.88	0.295	0.61	1.29	0.705
4/6	3/6	0.19	0.42	0.39	0.63	0.88	0.88	0.062	0.93	0.88	0.225	0.66	1.17	0.775
4/6	4/6	0.16	0.47	0.37	0.63	0.84	0.84	0.023	0.93	0.89	0.132	0.65	1.08	0.868
4/6	5/6	0.15	0.45	0.40	0.63	0.84	0.84	0.022	0.93	0.87	0.089	0.67	1.04	0.911
4/6	6/6	0.17	0.47	0.36	0.63	0.81	0.81	0.013	0.93	0.87	0.051	0.66	1.00	0.949
5/6	1/6	0.07	0.37	0.56	0.63	0.97	0.97	0.523	0.91	0.91	0.453	0.65	1.46	0.547
5/6	2/6	0.06	0.39	0.55	0.63	0.95	0.95	0.319	0.95	0.89	0.389	0.71	1.27	0.611
5/6	3/6	0.06	0.36	0.58	0.63	0.92	0.92	0.109	0.95	0.90	0.269	0.73	1.15	0.731
5/6	4/6	0.06	0.38	0.56	0.63	0.87	0.87	0.010	0.95	0.91	0.122	0.71	1.06	0.878
5/6	5/6	0.05	0.36	0.59	0.63	0.89	0.89	0.054	0.94	0.89	0.137	0.75	1.06	0.863
5/6	6/6	0.06	0.34	0.60	0.63	0.79	0.79	0.000	0.95	0.90	0.006	0.67	0.92	0.994
6/6	1/6	0.01	0.23	0.76	0.63	0.96	0.96	0.435	0.96	0.92	0.434	0.67	1.39	0.566
6/6	2/6	0.00	0.23	0.77	0.63	0.91	0.91	0.065	0.95	0.91	0.259	0.71	1.16	0.741
6/6	3/6	0.00	0.08	0.92	0.63	0.93	0.93	0.088	0.96	0.92	0.251	0.77	1.11	0.749
6/6	4/6	0.00	0.10	0.90	0.63	0.88	0.88	0.008	0.96	0.93	0.101	0.75	1.04	0.899
6/6	5/6	0.00	0.12	0.88	0.63	0.89	0.89	0.025	0.96	0.91	0.093	0.77	1.03	0.907
6/6	6/6	0.01	0.13	0.86	0.63	0.81	0.81	0.000	0.95	0.91	0.004	0.71	0.92	0.996

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

1008 Appendix Table 10.-Summary statistics for tests of relative reproductive success (RRS) of a HxH cross to a NxN cross from
 1009 simulations of a low stray rate (15% spawners hatchery-origin) stream with a modeled RRS of 0.625 for a HxH cross to a NxN cross
 1010 for different sampling proportions of parents (F_0) and offspring (F_1) ranging from 1/6 to 6/6. Statistics include proportion of offspring
 1011 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
 1012 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , and the RRS values that we could have
 1013 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
 1014 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , 90% confidence interval, and the one tailed p-value that RRS is < 1). See
 1015 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F_0	F_1	Unassigned	1 Parent	2 Parents	True	Estimated		RRS Detectability			90% CI			p RRS < 1
						Simple	Unbiased	1-tail p	$\alpha = 0.20$	$\alpha = 0.05$	1-tail p	5%	95%	
1/6	1/6	0.71	0.26	0.03	0.61	NA	NA	NA	NA	NA	NA	NA	NA	NA
1/6	2/6	0.68	0.28	0.04	0.61	NA	NA	NA	NA	NA	NA	NA	NA	NA
1/6	3/6	0.72	0.25	0.03	0.61	NA	NA	NA	NA	NA	NA	NA	NA	NA
1/6	4/6	0.71	0.26	0.03	0.61	NA	NA	NA	NA	NA	NA	NA	NA	NA
1/6	5/6	0.73	0.24	0.03	0.61	NA	NA	NA	NA	NA	NA	NA	NA	NA
1/6	6/6	0.72	0.25	0.03	0.61	NA	NA	NA	NA	NA	NA	NA	NA	NA
2/6	1/6	0.44	0.45	0.11	0.61	NA	NA	NA	NA	NA	NA	NA	NA	NA
2/6	2/6	0.47	0.41	0.12	0.61	0.99	0.99	0.748	0.73	0.73	0.494	0.43	2.30	0.506
2/6	3/6	0.44	0.43	0.13	0.61	0.89	0.88	0.610	0.66	0.66	0.405	0.38	2.04	0.595
2/6	4/6	0.44	0.43	0.13	0.61	0.78	0.78	0.543	0.58	0.58	0.318	0.33	1.84	0.682
2/6	5/6	0.46	0.43	0.11	0.61	0.74	0.74	0.414	0.55	0.55	0.279	0.32	1.71	0.722
2/6	6/6	0.41	0.44	0.15	0.61	0.82	0.81	0.484	0.70	0.58	0.309	0.42	1.59	0.691
3/6	1/6	0.32	0.46	0.22	0.61	0.88	0.88	0.777	0.88	0.88	0.429	0.27	2.86	0.571
3/6	2/6	0.28	0.50	0.22	0.61	0.97	0.97	0.710	0.77	0.77	0.475	0.46	2.05	0.525
3/6	3/6	0.31	0.48	0.21	0.61	0.87	0.87	0.349	0.87	0.78	0.334	0.51	1.48	0.666
3/6	4/6	0.29	0.47	0.24	0.61	0.82	0.82	0.272	0.82	0.74	0.255	0.49	1.35	0.745
3/6	5/6	0.30	0.48	0.22	0.61	0.91	0.91	0.493	0.81	0.63	0.381	0.54	1.54	0.619
3/6	6/6	0.30	0.48	0.22	0.61	0.84	0.84	0.314	0.84	0.72	0.266	0.54	1.32	0.734

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		$\alpha = 0.20$	$\alpha = 0.05$		5%	95%	
4/6	1/6	0.14	0.49	0.37	0.61	1.11	1.11	0.891	0.88	0.88	0.593	0.53	2.36	0.407
4/6	2/6	0.15	0.47	0.38	0.61	1.07	1.07	0.766	0.76	0.76	0.573	0.57	2.02	0.427
4/6	3/6	0.15	0.48	0.37	0.61	0.78	0.78	0.204	0.78	0.69	0.235	0.45	1.37	0.765
4/6	4/6	0.13	0.48	0.39	0.61	0.71	0.71	0.071	0.82	0.71	0.111	0.45	1.13	0.889
4/6	5/6	0.15	0.48	0.37	0.61	0.74	0.74	0.121	0.84	0.69	0.127	0.48	1.14	0.873
4/6	6/6	0.14	0.48	0.38	0.61	0.93	0.93	0.472	0.79	0.69	0.381	0.63	1.37	0.619
5/6	1/6	0.10	0.36	0.54	0.61	0.87	0.87	0.384	0.87	0.87	0.358	0.46	1.64	0.642
5/6	2/6	0.05	0.36	0.59	0.61	0.83	0.83	0.276	0.83	0.75	0.286	0.49	1.41	0.714
5/6	3/6	0.06	0.38	0.56	0.61	0.89	0.89	0.277	0.89	0.80	0.302	0.61	1.29	0.698
5/6	4/6	0.06	0.33	0.61	0.61	0.91	0.91	0.371	0.88	0.76	0.327	0.65	1.27	0.673
5/6	5/6	0.07	0.38	0.55	0.61	0.77	0.77	0.079	0.86	0.77	0.095	0.56	1.07	0.905
5/6	6/6	0.07	0.38	0.55	0.61	0.81	0.81	0.155	0.84	0.75	0.136	0.60	1.11	0.864
6/6	1/6	0.01	0.19	0.80	0.61	0.96	0.96	0.616	0.84	0.84	0.455	0.53	1.73	0.545
6/6	2/6	0.01	0.20	0.79	0.61	0.97	0.97	0.553	0.90	0.76	0.453	0.62	1.51	0.547
6/6	3/6	0.01	0.18	0.81	0.61	0.86	0.86	0.187	0.90	0.79	0.240	0.61	1.21	0.760
6/6	4/6	0.01	0.19	0.80	0.61	0.85	0.85	0.159	0.88	0.79	0.185	0.63	1.15	0.815
6/6	5/6	0.02	0.18	0.80	0.61	0.78	0.78	0.064	0.88	0.78	0.082	0.58	1.05	0.918
6/6	6/6	0.02	0.18	0.80	0.61	0.79	0.79	0.073	0.87	0.77	0.073	0.60	1.03	0.927

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

1016 Appendix Table 11.-Summary statistics for tests of relative reproductive success (RRS) of a HxN cross to a NxN cross from
1017 simulations of a high stray rate (50% spawners hatchery-origin) stream with a modeled RRS of 0.625 for a HxH cross to a NxN cross
1018 for different sampling proportions of parents (F_0) and offspring (F_1) ranging from 1/6 to 6/6. Statistics include proportion of offspring
1019 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
1020 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , and the RRS values that we could have
1021 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
1022 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , 90% confidence interval, and the one tailed p-value that RRS is < 1). See
1023 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F_0	F_1	Unassigned	1 Parent	2 Parents	Estimated			RRS Detectability			90% CI			p RRS < 1
					True	Simple	Unbiased	1-tail p	$\alpha = 0.20$	$\alpha = 0.05$	1-tail p	5%	95%	
1/6	1/6	0.72	0.26	0.02	0.82	1.00	1.00	NA	NA	NA	NA	NA	NA	NA
1/6	2/6	0.67	0.29	0.04	0.82	1.25	1.25	NA	NA	NA	NA	NA	NA	NA
1/6	3/6	0.69	0.28	0.03	0.82	1.29	1.29	0.909	0.71	0.43	0.691	0.56	2.95	0.309
1/6	4/6	0.67	0.29	0.04	0.82	1.05	1.05	0.742	0.80	0.80	0.557	0.59	1.88	0.443
1/6	5/6	0.70	0.27	0.03	0.82	0.94	0.93	0.486	0.79	0.79	0.432	0.49	1.78	0.568
1/6	6/6	0.69	0.28	0.03	0.82	0.86	0.86	0.304	0.86	0.75	0.333	0.49	1.51	0.667
2/6	1/6	0.50	0.43	0.07	0.82	1.00	1.00	NA	NA	NA	NA	NA	NA	NA
2/6	2/6	0.44	0.46	0.10	0.82	1.09	1.09	1.000	0.96	0.83	0.594	0.61	1.94	0.406
2/6	3/6	0.49	0.42	0.09	0.82	1.02	1.02	0.746	0.93	0.84	0.530	0.62	1.69	0.470
2/6	4/6	0.46	0.44	0.10	0.82	0.92	0.92	0.307	0.92	0.81	0.367	0.62	1.37	0.633
2/6	5/6	0.48	0.42	0.10	0.82	0.87	0.87	0.172	0.92	0.83	0.266	0.61	1.25	0.734
2/6	6/6	0.48	0.43	0.09	0.82	0.91	0.91	0.246	0.91	0.83	0.316	0.65	1.27	0.684
3/6	1/6	0.28	0.52	0.20	0.82	0.89	0.89	0.190	0.99	0.89	0.353	0.52	1.50	0.647
3/6	2/6	0.23	0.48	0.29	0.82	1.01	1.01	0.626	0.93	0.86	0.521	0.73	1.39	0.479
3/6	3/6	0.27	0.48	0.25	0.82	1.02	1.02	0.696	0.93	0.90	0.547	0.77	1.36	0.453
3/6	4/6	0.28	0.49	0.23	0.82	1.01	1.01	0.617	0.92	0.85	0.538	0.79	1.31	0.462
3/6	5/6	0.28	0.50	0.22	0.82	1.11	1.11	0.904	0.93	0.85	0.769	0.88	1.39	0.231
3/6	6/6	0.28	0.49	0.23	0.82	0.97	0.97	0.403	0.93	0.86	0.415	0.79	1.20	0.585

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		α = 0.20	α = 0.05		5%	95%	
4/6	1/6	0.16	0.51	0.33	0.82	1.08	1.08	1.000	0.94	0.87	0.618	0.70	1.67	0.383
4/6	2/6	0.17	0.50	0.33	0.82	0.92	0.92	0.166	0.95	0.88	0.319	0.67	1.25	0.681
4/6	3/6	0.19	0.42	0.39	0.82	0.94	0.94	0.199	0.95	0.90	0.315	0.75	1.17	0.685
4/6	4/6	0.16	0.47	0.37	0.82	1.04	1.04	0.725	0.93	0.85	0.635	0.85	1.29	0.365
4/6	5/6	0.15	0.45	0.40	0.82	0.96	0.96	0.342	0.94	0.87	0.369	0.81	1.15	0.631
4/6	6/6	0.17	0.47	0.36	0.82	0.97	0.97	0.364	0.94	0.88	0.384	0.83	1.14	0.616
5/6	1/6	0.07	0.37	0.56	0.82	0.96	0.96	0.367	0.96	0.89	0.422	0.71	1.31	0.578
5/6	2/6	0.06	0.39	0.55	0.82	1.08	1.08	0.893	0.93	0.89	0.698	0.85	1.36	0.302
5/6	3/6	0.06	0.36	0.58	0.82	1.00	1.00	0.513	0.96	0.91	0.486	0.83	1.20	0.514
5/6	4/6	0.06	0.38	0.56	0.82	1.04	1.04	0.753	0.95	0.90	0.645	0.88	1.22	0.355
5/6	5/6	0.05	0.36	0.59	0.82	0.95	0.95	0.208	0.95	0.91	0.275	0.82	1.09	0.725
5/6	6/6	0.06	0.34	0.60	0.82	0.91	0.91	0.050	0.96	0.91	0.098	0.80	1.03	0.902
6/6	1/6	0.01	0.23	0.76	0.82	0.97	0.97	0.345	0.97	0.91	0.427	0.74	1.28	0.573
6/6	2/6	0.00	0.23	0.77	0.82	0.98	0.98	0.375	0.96	0.92	0.426	0.80	1.19	0.574
6/6	3/6	0.00	0.08	0.92	0.82	1.00	1.00	0.509	0.97	0.93	0.491	0.86	1.15	0.509
6/6	4/6	0.00	0.10	0.90	0.82	1.06	1.06	0.880	0.96	0.92	0.759	0.93	1.20	0.241
6/6	5/6	0.00	0.12	0.88	0.82	0.96	0.96	0.237	0.96	0.92	0.298	0.86	1.08	0.702
6/6	6/6	0.01	0.13	0.86	0.82	0.92	0.92	0.051	0.96	0.92	0.094	0.83	1.02	0.906

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

1024 Appendix Table 12.-Summary statistics for tests of relative reproductive success (RRS) of a HxN cross to a NxN cross from
 1025 simulations of a low stray rate (15% spawners hatchery-origin) stream with a modeled RRS of 0.625 for a HxH cross to a NxN cross
 1026 for different sampling proportions of parents (F_0) and offspring (F_1) ranging from 1/6 to 6/6. Statistics include proportion of offspring
 1027 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
 1028 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , and the RRS values that we could have
 1029 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
 1030 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , 90% confidence interval, and the one tailed p-value that RRS is < 1). See
 1031 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F_0	F_1	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		$\alpha = 0.20$	$\alpha = 0.05$		5%	95%	
1/6	1/6	0.71	0.26	0.03	0.80	0.91	0.91	0.767	0.91	0.91	0.442	0.31	2.65	0.558
1/6	2/6	0.68	0.28	0.04	0.80	0.98	0.98	0.667	0.75	0.75	0.485	0.44	2.18	0.515
1/6	3/6	0.72	0.25	0.03	0.80	0.82	0.82	0.535	0.63	0.63	0.340	0.37	1.80	0.660
1/6	4/6	0.71	0.26	0.03	0.80	0.96	0.96	0.579	0.70	0.57	0.461	0.53	1.76	0.539
1/6	5/6	0.73	0.24	0.03	0.80	0.98	0.98	0.600	0.72	0.59	0.477	0.54	1.78	0.523
1/6	6/6	0.72	0.25	0.03	0.80	1.00	1.00	0.593	0.70	0.50	0.500	0.59	1.68	0.500
2/6	1/6	0.44	0.45	0.11	0.80	0.92	0.92	0.421	0.92	0.92	0.403	0.52	1.62	0.597
2/6	2/6	0.47	0.41	0.12	0.80	1.09	1.09	0.756	0.81	0.74	0.630	0.72	1.65	0.370
2/6	3/6	0.44	0.43	0.13	0.80	0.89	0.88	0.276	0.89	0.79	0.259	0.65	1.21	0.741
2/6	4/6	0.44	0.43	0.13	0.80	0.92	0.92	0.376	0.87	0.76	0.315	0.70	1.22	0.685
2/6	5/6	0.46	0.43	0.11	0.80	0.81	0.81	0.084	0.88	0.79	0.098	0.62	1.06	0.902
2/6	6/6	0.41	0.44	0.15	0.80	0.96	0.96	0.442	0.87	0.77	0.391	0.77	1.21	0.609
3/6	1/6	0.32	0.46	0.22	0.80	1.03	1.03	0.737	0.90	0.84	0.542	0.68	1.54	0.458
3/6	2/6	0.28	0.50	0.22	0.80	1.00	1.00	0.566	0.90	0.84	0.492	0.74	1.33	0.508
3/6	3/6	0.31	0.48	0.21	0.80	1.00	1.00	0.579	0.93	0.87	0.505	0.78	1.28	0.495
3/6	4/6	0.29	0.47	0.24	0.80	0.97	0.97	0.416	0.92	0.85	0.397	0.79	1.18	0.603
3/6	5/6	0.30	0.48	0.22	0.80	0.91	0.91	0.190	0.93	0.86	0.218	0.76	1.10	0.782
3/6	6/6	0.30	0.48	0.22	0.80	0.94	0.94	0.255	0.93	0.86	0.262	0.79	1.11	0.738

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Sampling Proportion		Proportion of Offspring Assigned			RRS Estimated			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Simple	Unbiased	1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
									$\alpha = 0.20$	$\alpha = 0.05$		5%	95%	
4/6	1/6	0.14	0.49	0.37	0.80	0.99	0.99	0.560	0.95	0.91	0.472	0.71	1.37	0.528
4/6	2/6	0.15	0.47	0.38	0.80	0.92	0.92	0.166	0.94	0.89	0.268	0.74	1.14	0.732
4/6	3/6	0.15	0.48	0.37	0.80	0.95	0.95	0.272	0.94	0.88	0.310	0.79	1.13	0.690
4/6	4/6	0.13	0.48	0.39	0.80	0.84	0.84	0.012	0.94	0.88	0.034	0.71	0.98	0.966
4/6	5/6	0.15	0.48	0.37	0.80	0.84	0.84	0.015	0.93	0.88	0.024	0.73	0.97	0.976
4/6	6/6	0.14	0.48	0.38	0.80	0.80	0.80	0.002	0.94	0.88	0.003	0.71	0.92	0.997
5/6	1/6	0.10	0.36	0.54	0.80	1.02	1.02	0.711	0.95	0.90	0.552	0.79	1.32	0.448
5/6	2/6	0.05	0.36	0.59	0.80	0.99	0.99	0.501	0.95	0.90	0.472	0.83	1.19	0.528
5/6	3/6	0.06	0.38	0.56	0.80	1.01	1.01	0.612	0.95	0.90	0.549	0.87	1.18	0.451
5/6	4/6	0.06	0.33	0.61	0.80	0.95	0.95	0.244	0.95	0.91	0.267	0.84	1.08	0.733
5/6	5/6	0.07	0.38	0.55	0.80	0.88	0.88	0.021	0.95	0.90	0.037	0.78	0.99	0.963
5/6	6/6	0.07	0.38	0.55	0.80	0.86	0.86	0.010	0.95	0.91	0.012	0.78	0.96	0.988
6/6	1/6	0.01	0.19	0.80	0.80	0.93	0.93	0.089	0.96	0.93	0.275	0.75	1.15	0.725
6/6	2/6	0.01	0.20	0.79	0.80	0.95	0.95	0.185	0.96	0.91	0.286	0.81	1.11	0.714
6/6	3/6	0.01	0.18	0.81	0.80	0.93	0.93	0.095	0.95	0.92	0.183	0.82	1.06	0.817
6/6	4/6	0.01	0.19	0.80	0.80	0.92	0.92	0.070	0.96	0.92	0.112	0.83	1.03	0.888
6/6	5/6	0.02	0.18	0.80	0.80	0.86	0.86	0.002	0.96	0.92	0.006	0.78	0.95	0.994
6/6	6/6	0.02	0.18	0.80	0.80	0.86	0.86	0.002	0.96	0.92	0.003	0.79	0.94	0.997

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

1032 Appendix Table 13.-Summary statistics for tests of relative reproductive success (RRS) of a H dam cross to a N dam cross from
 1033 simulations of a high stray rate (50% spawners hatchery-origin) stream with a modeled RRS of 0.625 for a HxH cross to a NxN cross
 1034 for different sampling proportions of parents (F₀) and offspring (F₁) ranging from 1/6 to 6/6. Statistics include proportion of offspring
 1035 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
 1036 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, and the RRS values that we could have
 1037 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
 1038 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, 90% confidence interval, and the one tailed p-value that RRS is <1). See
 1039 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	Estimated			RRS Detectability			90% CI			p RRS < 1
					True	Simple	Unbiased	1-tail p	α = 0.20	α = 0.05	1-tail p	5%	95%	
1/6	1/6	0.72	0.26	0.02	0.83	1.23	1.26	0.784	0.66	0.37	0.720	0.68	2.24	0.280
1/6	2/6	0.67	0.29	0.04	0.83	0.85	0.82	0.265	0.81	0.68	0.227	0.59	1.22	0.773
1/6	3/6	0.69	0.28	0.03	0.83	1.03	1.04	0.596	0.84	0.67	0.567	0.75	1.43	0.433
1/6	4/6	0.67	0.29	0.04	0.83	0.96	0.95	0.441	0.85	0.71	0.405	0.73	1.27	0.595
1/6	5/6	0.70	0.27	0.03	0.83	1.03	1.03	0.573	0.83	0.67	0.563	0.77	1.37	0.437
1/6	6/6	0.69	0.28	0.03	0.83	0.94	0.93	0.394	0.85	0.72	0.352	0.73	1.21	0.648
2/6	1/6	0.50	0.43	0.07	0.83	0.65	0.65	0.051	0.83	0.65	0.041	0.44	0.98	0.959
2/6	2/6	0.44	0.46	0.10	0.83	1.03	1.03	0.603	0.86	0.73	0.571	0.79	1.34	0.429
2/6	3/6	0.49	0.42	0.09	0.83	0.88	0.87	0.182	0.89	0.80	0.167	0.70	1.10	0.833
2/6	4/6	0.46	0.44	0.10	0.83	0.84	0.83	0.066	0.91	0.82	0.059	0.69	1.01	0.941
2/6	5/6	0.48	0.42	0.10	0.83	0.86	0.85	0.082	0.92	0.84	0.074	0.72	1.02	0.926
2/6	6/6	0.48	0.43	0.09	0.83	0.81	0.80	0.022	0.93	0.85	0.020	0.69	0.96	0.980
3/6	1/6	0.28	0.52	0.20	0.83	0.67	0.66	0.028	0.86	0.73	0.023	0.49	0.93	0.977
3/6	2/6	0.23	0.48	0.29	0.83	0.87	0.87	0.163	0.90	0.80	0.149	0.70	1.08	0.851
3/6	3/6	0.27	0.48	0.25	0.83	0.95	0.95	0.335	0.91	0.82	0.318	0.79	1.14	0.682
3/6	4/6	0.28	0.49	0.23	0.83	0.90	0.90	0.169	0.92	0.85	0.159	0.77	1.07	0.841
3/6	5/6	0.28	0.50	0.22	0.83	0.88	0.87	0.084	0.92	0.85	0.078	0.75	1.02	0.922
3/6	6/6	0.28	0.49	0.23	0.83	0.84	0.83	0.030	0.93	0.86	0.025	0.73	0.97	0.975

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		α = 0.20	α = 0.05		5%	95%	
4/6	1/6	0.16	0.51	0.33	0.83	0.74	0.73	0.045	0.89	0.76	0.038	0.56	0.98	0.962
4/6	2/6	0.17	0.50	0.33	0.83	0.94	0.94	0.331	0.90	0.80	0.310	0.76	1.16	0.690
4/6	3/6	0.19	0.42	0.39	0.83	0.89	0.89	0.140	0.92	0.85	0.129	0.76	1.05	0.871
4/6	4/6	0.16	0.47	0.37	0.83	0.94	0.94	0.268	0.93	0.85	0.252	0.81	1.09	0.748
4/6	5/6	0.15	0.45	0.40	0.83	0.89	0.89	0.081	0.93	0.87	0.073	0.78	1.02	0.927
4/6	6/6	0.17	0.47	0.36	0.83	0.82	0.82	0.008	0.94	0.88	0.006	0.72	0.94	0.994
5/6	1/6	0.07	0.37	0.56	0.83	0.73	0.72	0.023	0.90	0.78	0.019	0.56	0.94	0.981
5/6	2/6	0.06	0.39	0.55	0.83	0.95	0.95	0.349	0.91	0.82	0.330	0.79	1.14	0.670
5/6	3/6	0.06	0.36	0.58	0.83	0.90	0.90	0.127	0.93	0.86	0.117	0.78	1.04	0.883
5/6	4/6	0.06	0.38	0.56	0.83	0.88	0.88	0.071	0.94	0.87	0.066	0.77	1.01	0.934
5/6	5/6	0.05	0.36	0.59	0.83	0.87	0.87	0.030	0.94	0.89	0.027	0.77	0.98	0.973
5/6	6/6	0.06	0.34	0.60	0.83	0.78	0.78	0.000	0.95	0.90	0.000	0.70	0.88	1.000
6/6	1/6	0.01	0.23	0.76	0.83	0.84	0.84	0.118	0.89	0.79	0.107	0.67	1.06	0.893
6/6	2/6	0.00	0.23	0.77	0.83	1.00	1.00	0.527	0.92	0.83	0.508	0.85	1.18	0.492
6/6	3/6	0.00	0.08	0.92	0.83	0.83	0.83	0.008	0.94	0.88	0.007	0.73	0.94	0.993
6/6	4/6	0.00	0.10	0.90	0.83	0.91	0.91	0.095	0.94	0.89	0.088	0.81	1.02	0.912
6/6	5/6	0.00	0.12	0.88	0.83	0.88	0.88	0.034	0.95	0.90	0.029	0.79	0.98	0.971
6/6	6/6	0.01	0.13	0.86	0.83	0.84	0.84	0.003	0.95	0.91	0.003	0.76	0.93	0.997

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

1040 Appendix Table 14.-Summary statistics for tests of relative reproductive success (RRS) of a H dam cross to a N dam cross from
 1041 simulations of a low stray rate (15% spawners hatchery-origin) stream with a modeled RRS of 0.625 for a HxH cross to a NxN cross
 1042 for different sampling proportions of parents (F₀) and offspring (F₁) ranging from 1/6 to 6/6. Statistics include proportion of offspring
 1043 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
 1044 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, and the RRS values that we could have
 1045 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
 1046 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, 90% confidence interval, and the one tailed p-value that RRS is <1). See
 1047 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	Estimated			RRS Detectability			90% CI			p RRS < 1
					True	Simple	Unbiased	1-tail p	α = 0.20	α = 0.05	1-tail p	5%	95%	
1/6	1/6	0.71	0.26	0.03	0.75	0.41	0.35	0.052	0.65	0.41	0.045	0.17	0.98	0.955
1/6	2/6	0.68	0.28	0.04	0.75	0.76	0.71	0.227	0.76	0.59	0.185	0.46	1.26	0.815
1/6	3/6	0.72	0.25	0.03	0.75	0.42	0.35	0.003	0.81	0.64	0.004	0.24	0.72	0.996
1/6	4/6	0.71	0.26	0.03	0.75	0.52	0.47	0.006	0.83	0.67	0.006	0.34	0.80	0.994
1/6	5/6	0.73	0.24	0.03	0.75	0.57	0.54	0.013	0.83	0.69	0.011	0.39	0.85	0.989
1/6	6/6	0.72	0.25	0.03	0.75	0.59	0.55	0.012	0.83	0.69	0.009	0.41	0.85	0.991
2/6	1/6	0.44	0.45	0.11	0.75	0.94	0.94	0.470	0.82	0.64	0.409	0.62	1.43	0.591
2/6	2/6	0.47	0.41	0.12	0.75	0.84	0.82	0.221	0.84	0.69	0.189	0.60	1.17	0.811
2/6	3/6	0.44	0.43	0.13	0.75	0.78	0.76	0.092	0.87	0.75	0.074	0.59	1.03	0.926
2/6	4/6	0.44	0.43	0.13	0.75	0.85	0.84	0.188	0.87	0.76	0.155	0.66	1.10	0.845
2/6	5/6	0.46	0.43	0.11	0.75	0.82	0.81	0.115	0.87	0.78	0.094	0.65	1.05	0.906
2/6	6/6	0.41	0.44	0.15	0.75	0.90	0.89	0.289	0.87	0.77	0.229	0.72	1.13	0.771
3/6	1/6	0.32	0.46	0.22	0.75	0.97	0.97	0.490	0.81	0.65	0.442	0.68	1.38	0.558
3/6	2/6	0.28	0.50	0.22	0.75	0.93	0.92	0.346	0.87	0.75	0.314	0.71	1.20	0.686
3/6	3/6	0.31	0.48	0.21	0.75	0.78	0.77	0.038	0.89	0.80	0.033	0.62	0.97	0.967
3/6	4/6	0.29	0.47	0.24	0.75	0.92	0.91	0.259	0.90	0.81	0.233	0.75	1.12	0.767
3/6	5/6	0.30	0.48	0.22	0.75	0.82	0.82	0.055	0.91	0.82	0.046	0.68	1.00	0.954
3/6	6/6	0.30	0.48	0.22	0.75	0.83	0.82	0.052	0.91	0.83	0.041	0.70	0.99	0.959

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		$\alpha = 0.20$	$\alpha = 0.05$		5%	95%	
4/6	1/6	0.14	0.49	0.37	0.75	0.70	0.69	0.044	0.85	0.73	0.041	0.50	0.98	0.959
4/6	2/6	0.15	0.47	0.38	0.75	0.78	0.78	0.058	0.89	0.78	0.052	0.61	1.00	0.948
4/6	3/6	0.15	0.48	0.37	0.75	0.70	0.69	0.003	0.91	0.82	0.003	0.57	0.86	0.997
4/6	4/6	0.13	0.48	0.39	0.75	0.70	0.70	0.001	0.92	0.84	0.001	0.58	0.85	0.999
4/6	5/6	0.15	0.48	0.37	0.75	0.73	0.73	0.002	0.92	0.84	0.002	0.61	0.87	0.999
4/6	6/6	0.14	0.48	0.38	0.75	0.72	0.72	0.001	0.92	0.85	0.000	0.61	0.85	1.000
5/6	1/6	0.10	0.36	0.54	0.75	0.92	0.92	0.350	0.87	0.74	0.316	0.69	1.22	0.683
5/6	2/6	0.05	0.36	0.59	0.75	0.82	0.82	0.069	0.90	0.81	0.062	0.66	1.01	0.938
5/6	3/6	0.06	0.38	0.56	0.75	0.70	0.69	0.001	0.92	0.84	0.001	0.58	0.84	0.999
5/6	4/6	0.06	0.33	0.61	0.75	0.79	0.79	0.010	0.92	0.85	0.009	0.68	0.93	0.991
5/6	5/6	0.07	0.38	0.55	0.75	0.75	0.75	0.001	0.93	0.86	0.001	0.64	0.88	0.999
5/6	6/6	0.07	0.38	0.55	0.75	0.78	0.78	0.003	0.93	0.87	0.002	0.68	0.90	0.998
6/6	1/6	0.01	0.19	0.80	0.75	0.84	0.84	0.151	0.88	0.75	0.135	0.64	1.09	0.865
6/6	2/6	0.01	0.20	0.79	0.75	0.75	0.74	0.010	0.91	0.83	0.009	0.61	0.92	0.991
6/6	3/6	0.01	0.18	0.81	0.75	0.68	0.68	0.000	0.93	0.85	0.000	0.58	0.81	1.000
6/6	4/6	0.01	0.19	0.80	0.75	0.80	0.79	0.007	0.92	0.86	0.006	0.68	0.93	0.994
6/6	5/6	0.02	0.18	0.80	0.75	0.72	0.72	0.000	0.93	0.87	0.000	0.63	0.83	1.000
6/6	6/6	0.02	0.18	0.80	0.75	0.74	0.74	0.000	0.94	0.88	0.000	0.65	0.84	1.000

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

1048 Appendix Table 15.-Summary statistics for tests of relative reproductive success (RRS) of a H sire cross to a N sire cross from
 1049 simulations of a high stray rate (50% spawners hatchery-origin) stream with a modeled RRS of 0.625 for a HxH cross to a NxN cross
 1050 for different sampling proportions of parents (F₀) and offspring (F₁) ranging from 1/6 to 6/6. Statistics include proportion of offspring
 1051 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
 1052 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, and the RRS values that we could have
 1053 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
 1054 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, 90% confidence interval, and the one tailed p-value that RRS is <1). See
 1055 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	Estimated			RRS Detectability			90% CI			p RRS < 1
					True	Simple	Unbiased	1-tail p	α = 0.20	α = 0.05	1-tail p	5%	95%	
1/6	1/6	0.72	0.26	0.02	0.77	1.03	1.03	0.593	0.75	0.48	0.538	0.62	1.71	0.462
1/6	2/6	0.67	0.29	0.04	0.77	0.90	0.90	0.347	0.83	0.68	0.313	0.64	1.27	0.687
1/6	3/6	0.69	0.28	0.03	0.77	0.67	0.64	0.012	0.87	0.77	0.012	0.50	0.90	0.988
1/6	4/6	0.67	0.29	0.04	0.77	0.76	0.73	0.051	0.88	0.76	0.041	0.58	0.99	0.959
1/6	5/6	0.70	0.27	0.03	0.77	0.83	0.82	0.106	0.89	0.78	0.094	0.66	1.05	0.906
1/6	6/6	0.69	0.28	0.03	0.77	0.81	0.79	0.067	0.90	0.80	0.056	0.65	1.01	0.944
2/6	1/6	0.50	0.43	0.07	0.77	1.13	1.13	0.742	0.77	0.58	0.696	0.76	1.68	0.304
2/6	2/6	0.44	0.46	0.10	0.77	0.79	0.78	0.082	0.87	0.76	0.069	0.60	1.03	0.931
2/6	3/6	0.49	0.42	0.09	0.77	0.91	0.90	0.261	0.89	0.79	0.239	0.72	1.14	0.761
2/6	4/6	0.46	0.44	0.10	0.77	0.89	0.88	0.182	0.90	0.81	0.166	0.72	1.09	0.835
2/6	5/6	0.48	0.42	0.10	0.77	0.90	0.90	0.179	0.91	0.82	0.168	0.75	1.08	0.833
2/6	6/6	0.48	0.43	0.09	0.77	0.83	0.83	0.045	0.92	0.84	0.040	0.70	0.99	0.960
3/6	1/6	0.28	0.52	0.20	0.77	0.84	0.84	0.214	0.84	0.69	0.192	0.61	1.16	0.808
3/6	2/6	0.23	0.48	0.29	0.77	0.79	0.79	0.043	0.90	0.81	0.037	0.64	0.98	0.963
3/6	3/6	0.27	0.48	0.25	0.77	0.80	0.80	0.024	0.92	0.84	0.021	0.68	0.96	0.979
3/6	4/6	0.28	0.49	0.23	0.77	0.80	0.79	0.014	0.93	0.85	0.011	0.68	0.94	0.989
3/6	5/6	0.28	0.50	0.22	0.77	0.89	0.88	0.102	0.93	0.86	0.093	0.76	1.03	0.907
3/6	6/6	0.28	0.49	0.23	0.77	0.80	0.80	0.006	0.93	0.87	0.005	0.70	0.93	0.995

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		α = 0.20	α = 0.05		5%	95%	
4/6	1/6	0.16	0.51	0.33	0.77	0.81	0.81	0.122	0.88	0.74	0.107	0.62	1.07	0.893
4/6	2/6	0.17	0.50	0.33	0.77	0.89	0.89	0.173	0.90	0.81	0.158	0.73	1.08	0.842
4/6	3/6	0.19	0.42	0.39	0.77	0.90	0.89	0.136	0.92	0.85	0.124	0.77	1.05	0.876
4/6	4/6	0.16	0.47	0.37	0.77	0.79	0.79	0.005	0.93	0.87	0.004	0.69	0.92	0.996
4/6	5/6	0.15	0.45	0.40	0.77	0.88	0.88	0.054	0.94	0.88	0.049	0.77	1.00	0.951
4/6	6/6	0.17	0.47	0.36	0.77	0.81	0.81	0.003	0.94	0.89	0.002	0.72	0.92	0.998
5/6	1/6	0.07	0.37	0.56	0.77	0.77	0.77	0.047	0.88	0.79	0.040	0.61	0.99	0.960
5/6	2/6	0.06	0.39	0.55	0.77	0.75	0.75	0.005	0.92	0.84	0.004	0.63	0.90	0.996
5/6	3/6	0.06	0.36	0.58	0.77	0.78	0.78	0.002	0.93	0.87	0.002	0.67	0.90	0.998
5/6	4/6	0.06	0.38	0.56	0.77	0.75	0.75	0.000	0.94	0.89	0.000	0.66	0.86	1.000
5/6	5/6	0.05	0.36	0.59	0.77	0.80	0.80	0.001	0.95	0.89	0.001	0.72	0.90	0.999
5/6	6/6	0.06	0.34	0.60	0.77	0.77	0.76	0.000	0.95	0.90	0.000	0.69	0.85	1.000
6/6	1/6	0.01	0.23	0.76	0.77	0.81	0.81	0.063	0.90	0.81	0.055	0.64	1.01	0.945
6/6	2/6	0.00	0.23	0.77	0.77	0.74	0.74	0.002	0.93	0.86	0.001	0.63	0.87	0.999
6/6	3/6	0.00	0.08	0.92	0.77	0.81	0.81	0.005	0.94	0.88	0.004	0.72	0.92	0.996
6/6	4/6	0.00	0.10	0.90	0.77	0.77	0.77	0.000	0.95	0.90	0.000	0.69	0.87	1.000
6/6	5/6	0.00	0.12	0.88	0.77	0.83	0.83	0.002	0.95	0.90	0.002	0.75	0.92	0.998
6/6	6/6	0.01	0.13	0.86	0.77	0.77	0.77	0.000	0.95	0.91	0.000	0.70	0.85	1.000

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

1056 Appendix Table 16.-Summary statistics for tests of relative reproductive success (RRS) of a H sire cross to a N sire cross from
 1057 simulations of a low stray rate (15% spawners hatchery-origin) stream with a modeled RRS of 0.625 for a HxH cross to a NxN cross
 1058 for different sampling proportions of parents (F₀) and offspring (F₁) ranging from 1/6 to 6/6. Statistics include proportion of offspring
 1059 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
 1060 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, and the RRS values that we could have
 1061 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
 1062 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, 90% confidence interval, and the one tailed p-value that RRS is <1). See
 1063 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	Estimated			RRS Detectability			90% CI			p RRS < 1
					True	Simple	Unbiased	1-tail p	α = 0.20	α = 0.05	1-tail p	5%	95%	
1/6	1/6	0.71	0.26	0.03	0.82	0.91	0.89	0.487	0.65	0.39	0.397	0.48	1.69	0.603
1/6	2/6	0.68	0.28	0.04	0.82	0.76	0.72	0.221	0.76	0.59	0.177	0.46	1.24	0.823
1/6	3/6	0.72	0.25	0.03	0.82	0.96	0.96	0.491	0.79	0.61	0.442	0.63	1.46	0.558
1/6	4/6	0.71	0.26	0.03	0.82	0.89	0.88	0.339	0.83	0.67	0.296	0.63	1.27	0.704
1/6	5/6	0.73	0.24	0.03	0.82	0.88	0.87	0.311	0.83	0.67	0.272	0.62	1.25	0.728
1/6	6/6	0.72	0.25	0.03	0.82	0.90	0.89	0.340	0.84	0.68	0.302	0.65	1.25	0.698
2/6	1/6	0.44	0.45	0.11	0.82	0.83	0.83	0.281	0.78	0.64	0.238	0.54	1.27	0.762
2/6	2/6	0.47	0.41	0.12	0.82	0.83	0.82	0.207	0.83	0.70	0.180	0.60	1.15	0.820
2/6	3/6	0.44	0.43	0.13	0.82	0.84	0.84	0.166	0.88	0.76	0.140	0.65	1.09	0.860
2/6	4/6	0.44	0.43	0.13	0.82	0.66	0.64	0.005	0.88	0.77	0.004	0.51	0.86	0.996
2/6	5/6	0.46	0.43	0.11	0.82	0.69	0.68	0.007	0.89	0.79	0.006	0.54	0.88	0.994
2/6	6/6	0.41	0.44	0.15	0.82	0.73	0.71	0.011	0.90	0.81	0.009	0.59	0.91	0.991
3/6	1/6	0.32	0.46	0.22	0.82	0.79	0.78	0.163	0.83	0.68	0.141	0.55	1.13	0.860
3/6	2/6	0.28	0.50	0.22	0.82	0.72	0.72	0.034	0.87	0.76	0.030	0.55	0.96	0.970
3/6	3/6	0.31	0.48	0.21	0.82	0.82	0.81	0.076	0.89	0.80	0.067	0.65	1.02	0.933
3/6	4/6	0.29	0.47	0.24	0.82	0.70	0.69	0.003	0.90	0.82	0.003	0.57	0.87	0.997
3/6	5/6	0.30	0.48	0.22	0.82	0.79	0.78	0.025	0.90	0.83	0.022	0.65	0.96	0.978
3/6	6/6	0.30	0.48	0.22	0.82	0.80	0.79	0.020	0.92	0.84	0.016	0.67	0.95	0.984

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		α = 0.20	α = 0.05		5%	95%	
4/6	1/6	0.14	0.49	0.37	0.82	0.92	0.92	0.359	0.87	0.74	0.324	0.69	1.23	0.676
4/6	2/6	0.15	0.47	0.38	0.82	0.79	0.79	0.048	0.90	0.80	0.044	0.63	0.99	0.956
4/6	3/6	0.15	0.48	0.37	0.82	0.85	0.84	0.074	0.91	0.83	0.068	0.70	1.02	0.932
4/6	4/6	0.13	0.48	0.39	0.82	0.79	0.78	0.013	0.92	0.84	0.011	0.66	0.94	0.989
4/6	5/6	0.15	0.48	0.37	0.82	0.83	0.83	0.034	0.92	0.85	0.029	0.71	0.98	0.971
4/6	6/6	0.14	0.48	0.38	0.82	0.86	0.86	0.055	0.93	0.86	0.047	0.74	1.00	0.953
5/6	1/6	0.10	0.36	0.54	0.82	0.99	0.99	0.525	0.85	0.73	0.488	0.76	1.30	0.512
5/6	2/6	0.05	0.36	0.59	0.82	0.76	0.76	0.020	0.91	0.82	0.018	0.62	0.94	0.982
5/6	3/6	0.06	0.38	0.56	0.82	0.91	0.91	0.190	0.91	0.84	0.172	0.77	1.07	0.828
5/6	4/6	0.06	0.33	0.61	0.82	0.82	0.82	0.026	0.92	0.85	0.022	0.70	0.96	0.978
5/6	5/6	0.07	0.38	0.55	0.82	0.81	0.81	0.012	0.93	0.86	0.011	0.70	0.94	0.989
5/6	6/6	0.07	0.38	0.55	0.82	0.84	0.83	0.018	0.93	0.87	0.015	0.73	0.96	0.985
6/6	1/6	0.01	0.19	0.80	0.82	0.83	0.83	0.117	0.88	0.77	0.105	0.64	1.06	0.895
6/6	2/6	0.01	0.20	0.79	0.82	0.76	0.76	0.009	0.91	0.83	0.009	0.62	0.92	0.991
6/6	3/6	0.01	0.18	0.81	0.82	0.84	0.84	0.034	0.92	0.86	0.031	0.71	0.98	0.969
6/6	4/6	0.01	0.19	0.80	0.82	0.81	0.81	0.012	0.93	0.86	0.010	0.70	0.94	0.990
6/6	5/6	0.02	0.18	0.80	0.82	0.81	0.81	0.006	0.94	0.87	0.005	0.71	0.93	0.995
6/6	6/6	0.02	0.18	0.80	0.82	0.82	0.82	0.006	0.94	0.88	0.005	0.72	0.93	0.995

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

1064 Appendix Table 17.-Summary statistics for tests of relative reproductive success (RRS) of a HxH cross to a NxN cross from
 1065 simulations of a high stray rate (50% spawners hatchery-origin) stream with a modeled RRS of 0.750 for a HxH cross to a NxN cross
 1066 for different sampling proportions of parents (F_0) and offspring (F_1) ranging from 1/6 to 6/6. Statistics include proportion of offspring
 1067 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
 1068 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , and the RRS values that we could have
 1069 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
 1070 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , 90% confidence interval, and the one tailed p-value that RRS is < 1). See
 1071 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F_0	F_1	Unassigned	1 Parent	2 Parents	True	Estimated		RRS Detectability			90% CI			p RRS < 1
						Simple	Unbiased	1-tail p	$\alpha = 0.20$	$\alpha = 0.05$	1-tail p	5%	95%	
1/6	1/6	0.67	0.29	0.04	0.74	1.00	1.00	NA	NA	NA	NA	NA	NA	NA
1/6	2/6	0.70	0.28	0.02	0.74	2.00	2.01	NA	NA	NA	NA	NA	NA	NA
1/6	3/6	0.69	0.29	0.02	0.74	1.00	1.00	NA	NA	NA	NA	NA	NA	NA
1/6	4/6	0.68	0.29	0.03	0.74	0.67	0.66	0.248	0.67	0.67	0.283	0.21	2.13	0.717
1/6	5/6	0.69	0.29	0.02	0.74	0.33	0.33	NA	NA	NA	NA	NA	NA	NA
1/6	6/6	0.70	0.28	0.02	0.74	0.90	0.90	0.540	0.55	0.55	0.431	0.33	2.44	0.569
2/6	1/6	0.52	0.39	0.09	0.74	0.88	0.87	0.636	0.88	0.88	0.414	0.32	2.40	0.586
2/6	2/6	0.44	0.44	0.12	0.74	0.91	0.91	0.500	0.91	0.91	0.409	0.46	1.79	0.591
2/6	3/6	0.48	0.42	0.10	0.74	0.69	0.69	0.289	0.69	0.69	0.243	0.29	1.66	0.757
2/6	4/6	0.47	0.42	0.11	0.74	0.67	0.66	0.051	0.82	0.67	0.107	0.39	1.14	0.893
2/6	5/6	0.47	0.42	0.11	0.74	0.73	0.73	0.075	0.82	0.73	0.175	0.42	1.27	0.825
2/6	6/6	0.46	0.43	0.11	0.74	0.60	0.60	0.003	0.87	0.76	0.034	0.38	0.95	0.966
3/6	1/6	0.28	0.49	0.23	0.74	1.00	1.00	NA	NA	NA	NA	NA	NA	NA
3/6	2/6	0.24	0.50	0.26	0.74	0.97	0.97	0.641	0.97	0.97	0.460	0.61	1.55	0.540
3/6	3/6	0.24	0.49	0.27	0.74	0.96	0.96	0.384	0.92	0.88	0.411	0.69	1.33	0.589
3/6	4/6	0.25	0.49	0.26	0.74	0.84	0.84	0.043	0.93	0.87	0.168	0.62	1.13	0.832
3/6	5/6	0.28	0.50	0.22	0.74	0.97	0.97	0.477	0.91	0.84	0.445	0.72	1.32	0.555
3/6	6/6	0.24	0.49	0.27	0.74	0.87	0.87	0.088	0.93	0.85	0.168	0.68	1.10	0.832

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		α = 0.20	α = 0.05		5%	95%	
4/6	1/6	0.17	0.46	0.37	0.74	0.96	0.96	0.485	0.96	0.89	0.443	0.61	1.50	0.557
4/6	2/6	0.12	0.47	0.41	0.74	0.93	0.93	0.200	0.93	0.93	0.361	0.67	1.30	0.639
4/6	3/6	0.09	0.43	0.48	0.74	0.80	0.80	0.002	0.93	0.89	0.078	0.62	1.04	0.922
4/6	4/6	0.14	0.48	0.38	0.74	0.83	0.82	0.020	0.93	0.87	0.100	0.64	1.06	0.900
4/6	5/6	0.14	0.50	0.36	0.74	0.89	0.89	0.120	0.93	0.87	0.203	0.71	1.12	0.797
4/6	6/6	0.13	0.48	0.39	0.74	0.82	0.82	0.008	0.94	0.88	0.042	0.67	0.99	0.958
5/6	1/6	0.06	0.41	0.53	0.74	0.96	0.96	0.418	0.96	0.91	0.438	0.66	1.41	0.562
5/6	2/6	0.04	0.30	0.66	0.74	0.96	0.96	0.261	0.96	0.93	0.394	0.74	1.24	0.607
5/6	3/6	0.05	0.38	0.57	0.74	0.89	0.89	0.045	0.95	0.91	0.209	0.71	1.13	0.791
5/6	4/6	0.05	0.32	0.63	0.74	1.01	1.01	0.625	0.94	0.89	0.551	0.84	1.22	0.449
5/6	5/6	0.06	0.38	0.56	0.74	0.91	0.91	0.078	0.95	0.90	0.178	0.76	1.08	0.822
5/6	6/6	0.05	0.34	0.61	0.74	0.92	0.92	0.094	0.95	0.90	0.171	0.79	1.07	0.829
6/6	1/6	0.01	0.23	0.76	0.74	1.02	1.02	0.874	0.98	0.94	0.539	0.73	1.42	0.461
6/6	2/6	0.00	0.15	0.85	0.74	0.93	0.93	0.072	0.97	0.93	0.302	0.75	1.17	0.698
6/6	3/6	0.02	0.18	0.80	0.74	0.95	0.95	0.213	0.95	0.91	0.316	0.78	1.15	0.683
6/6	4/6	0.01	0.20	0.79	0.74	0.97	0.97	0.319	0.95	0.91	0.374	0.82	1.14	0.626
6/6	5/6	0.01	0.14	0.85	0.74	0.89	0.89	0.022	0.95	0.91	0.091	0.78	1.03	0.909
6/6	6/6	0.01	0.19	0.80	0.74	0.92	0.92	0.059	0.96	0.92	0.138	0.81	1.04	0.862

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

1072 Appendix Table 18.-Summary statistics for tests of relative reproductive success (RRS) of a HxH cross to a NxN cross from
1073 simulations of a low stray rate (15% spawners hatchery-origin) stream with a modeled RRS of 0.750 for a HxH cross to a NxN cross
1074 for different sampling proportions of parents (F_0) and offspring (F_1) ranging from 1/6 to 6/6. Statistics include proportion of offspring
1075 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
1076 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , and the RRS values that we could have
1077 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
1078 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , 90% confidence interval, and the one tailed p-value that RRS is < 1). See
1079 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F_0	F_1	Unassigned	1 Parent	2 Parents	True	Estimated		RRS Detectability			90% CI			p RRS < 1
						Simple	Unbiased	1-tail p	$\alpha = 0.20$	$\alpha = 0.05$	1-tail p	5%	95%	
1/6	1/6	0.62	0.33	0.05	0.74	0.82	0.82	0.866	0.82	0.82	0.425	0.15	4.48	0.575
1/6	2/6	0.64	0.31	0.05	0.74	0.79	0.79	0.874	0.79	0.79	0.410	0.15	4.21	0.590
1/6	3/6	0.67	0.30	0.03	0.74	0.65	0.64	0.757	0.65	0.65	0.337	0.12	3.52	0.663
1/6	4/6	0.63	0.32	0.05	0.74	0.73	0.71	0.845	0.73	0.73	0.377	0.14	3.82	0.623
1/6	5/6	0.64	0.31	0.05	0.74	1.02	1.03	0.805	0.67	0.67	0.515	0.37	2.86	0.485
1/6	6/6	0.64	0.32	0.04	0.74	0.95	0.95	0.776	0.62	0.62	0.469	0.33	2.74	0.531
2/6	1/6	0.40	0.42	0.18	0.74	0.86	0.86	0.794	0.86	0.86	0.415	0.26	2.79	0.585
2/6	2/6	0.46	0.41	0.13	0.74	1.83	1.83	NA	NA	NA	NA	NA	NA	NA
2/6	3/6	0.41	0.44	0.15	0.74	0.74	0.73	0.300	0.74	0.74	0.251	0.35	1.56	0.749
2/6	4/6	0.38	0.44	0.18	0.74	1.03	1.03	0.693	0.79	0.67	0.530	0.59	1.79	0.470
2/6	5/6	0.41	0.44	0.15	0.74	0.83	0.83	0.416	0.72	0.61	0.303	0.46	1.50	0.697
2/6	6/6	0.38	0.44	0.18	0.74	0.96	0.96	0.587	0.69	0.60	0.453	0.57	1.63	0.547
3/6	1/6	0.23	0.49	0.28	0.74	0.91	0.91	0.683	0.91	0.91	0.431	0.40	2.12	0.569
3/6	2/6	0.27	0.50	0.23	0.74	0.97	0.96	0.645	0.82	0.82	0.464	0.51	1.83	0.536
3/6	3/6	0.24	0.48	0.28	0.74	0.78	0.78	0.298	0.78	0.78	0.259	0.42	1.47	0.741
3/6	4/6	0.25	0.48	0.27	0.74	0.97	0.97	0.589	0.81	0.73	0.452	0.61	1.54	0.548
3/6	5/6	0.27	0.49	0.24	0.74	0.90	0.90	0.454	0.83	0.68	0.350	0.56	1.43	0.649
3/6	6/6	0.23	0.49	0.28	0.74	1.05	1.05	0.686	0.74	0.67	0.571	0.67	1.64	0.429

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		α = 0.20	α = 0.05		5%	95%	
4/6	1/6	0.15	0.50	0.35	0.74	0.85	0.85	0.738	0.85	0.85	0.412	0.26	2.76	0.588
4/6	2/6	0.12	0.43	0.45	0.74	1.10	1.10	0.807	0.84	0.75	0.632	0.69	1.75	0.368
4/6	3/6	0.12	0.44	0.44	0.74	0.81	0.81	0.285	0.81	0.72	0.251	0.48	1.37	0.749
4/6	4/6	0.13	0.45	0.42	0.74	0.84	0.84	0.307	0.84	0.72	0.253	0.55	1.29	0.747
4/6	5/6	0.11	0.45	0.44	0.74	0.83	0.83	0.311	0.78	0.67	0.236	0.54	1.27	0.764
4/6	6/6	0.14	0.47	0.39	0.74	0.73	0.73	0.145	0.78	0.65	0.116	0.48	1.12	0.884
5/6	1/6	0.05	0.38	0.57	0.74	0.90	0.90	0.652	0.90	0.90	0.419	0.39	2.07	0.581
5/6	2/6	0.02	0.31	0.67	0.74	1.01	1.01	0.670	0.82	0.73	0.515	0.61	1.67	0.485
5/6	3/6	0.03	0.31	0.66	0.74	0.94	0.94	0.510	0.79	0.71	0.405	0.59	1.48	0.595
5/6	4/6	0.03	0.30	0.67	0.74	0.84	0.84	0.284	0.84	0.70	0.239	0.57	1.25	0.761
5/6	5/6	0.03	0.29	0.68	0.74	0.68	0.68	0.063	0.81	0.68	0.070	0.44	1.04	0.930
5/6	6/6	0.05	0.36	0.59	0.74	0.79	0.79	0.207	0.79	0.67	0.163	0.54	1.17	0.837
6/6	1/6	0.01	0.12	0.87	0.74	0.88	0.88	0.538	0.88	0.88	0.384	0.42	1.84	0.616
6/6	2/6	0.00	0.11	0.89	0.74	1.08	1.08	0.790	0.88	0.83	0.637	0.76	1.54	0.363
6/6	3/6	0.00	0.12	0.88	0.74	0.86	0.86	0.254	0.86	0.77	0.248	0.59	1.24	0.752
6/6	4/6	0.00	0.10	0.90	0.74	0.88	0.88	0.302	0.84	0.74	0.264	0.63	1.23	0.736
6/6	5/6	0.01	0.14	0.85	0.74	0.75	0.75	0.058	0.86	0.75	0.064	0.54	1.02	0.936
6/6	6/6	0.00	0.09	0.91	0.74	0.78	0.78	0.098	0.84	0.75	0.082	0.58	1.05	0.918

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

1080 Appendix Table 19.-Summary statistics for tests of relative reproductive success (RRS) of a HxN cross to a NxN cross from
 1081 simulations of a high stray rate (50% spawners hatchery-origin) stream with a modeled RRS of 0.750 for a HxH cross to a NxN cross
 1082 for different sampling proportions of parents (F_0) and offspring (F_1) ranging from 1/6 to 6/6. Statistics include proportion of offspring
 1083 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
 1084 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , and the RRS values that we could have
 1085 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
 1086 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , 90% confidence interval, and the one tailed p-value that RRS is < 1). See
 1087 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F_0	F_1	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		$\alpha = 0.20$	$\alpha = 0.05$		5%	95%	
1/6	1/6	0.67	0.29	0.04	0.84	1.00	1.00	NA	NA	NA	NA	NA	NA	NA
1/6	2/6	0.70	0.28	0.02	0.84	1.29	1.29	NA	NA	NA	NA	NA	NA	NA
1/6	3/6	0.69	0.29	0.02	0.84	1.10	1.10	1.000	0.67	0.67	0.558	0.38	3.21	0.442
1/6	4/6	0.68	0.29	0.03	0.84	0.67	0.66	0.101	1.04	0.67	0.258	0.24	1.86	0.742
1/6	5/6	0.69	0.29	0.02	0.84	0.36	0.35	NA	NA	NA	NA	NA	NA	NA
1/6	6/6	0.70	0.28	0.02	0.84	0.72	0.71	NA	NA	NA	NA	NA	NA	NA
2/6	1/6	0.52	0.39	0.09	0.84	0.95	0.95	0.640	0.95	0.75	0.459	0.45	2.02	0.541
2/6	2/6	0.44	0.44	0.12	0.84	1.04	1.04	0.751	0.88	0.81	0.555	0.66	1.64	0.445
2/6	3/6	0.48	0.42	0.10	0.84	0.84	0.84	0.148	0.90	0.79	0.237	0.57	1.25	0.762
2/6	4/6	0.47	0.42	0.11	0.84	0.71	0.71	0.008	0.89	0.82	0.045	0.51	0.99	0.955
2/6	5/6	0.47	0.42	0.11	0.84	0.92	0.92	0.256	0.92	0.82	0.315	0.68	1.23	0.685
2/6	6/6	0.46	0.43	0.11	0.84	0.83	0.83	0.061	0.91	0.83	0.135	0.63	1.09	0.865
3/6	1/6	0.28	0.49	0.23	0.84	1.09	1.09	1.000	0.97	0.85	0.602	0.62	1.93	0.398
3/6	2/6	0.24	0.50	0.26	0.84	1.15	1.15	0.993	0.93	0.85	0.754	0.82	1.61	0.245
3/6	3/6	0.24	0.49	0.27	0.84	1.09	1.09	0.937	0.95	0.87	0.704	0.83	1.42	0.296
3/6	4/6	0.25	0.49	0.26	0.84	1.04	1.04	0.698	0.91	0.85	0.609	0.82	1.32	0.391
3/6	5/6	0.28	0.50	0.22	0.84	1.11	1.11	0.904	0.92	0.86	0.761	0.88	1.40	0.239
3/6	6/6	0.24	0.49	0.27	0.84	1.01	1.01	0.598	0.93	0.87	0.550	0.84	1.23	0.450

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		α = 0.20	α = 0.05		5%	95%	
4/6	1/6	0.17	0.46	0.37	0.84	1.03	1.03	0.785	0.96	0.90	0.541	0.68	1.54	0.459
4/6	2/6	0.12	0.47	0.41	0.84	1.11	1.11	0.944	0.93	0.87	0.746	0.86	1.44	0.254
4/6	3/6	0.09	0.43	0.48	0.84	0.93	0.93	0.159	0.95	0.91	0.281	0.77	1.14	0.719
4/6	4/6	0.14	0.48	0.38	0.84	0.91	0.91	0.122	0.94	0.88	0.208	0.75	1.10	0.792
4/6	5/6	0.14	0.50	0.36	0.84	0.94	0.94	0.229	0.94	0.89	0.301	0.79	1.13	0.699
4/6	6/6	0.13	0.48	0.39	0.84	0.85	0.85	0.014	0.95	0.89	0.040	0.73	0.99	0.960
5/6	1/6	0.06	0.41	0.53	0.84	1.07	1.07	0.919	0.92	0.88	0.616	0.75	1.52	0.384
5/6	2/6	0.04	0.30	0.66	0.84	1.08	1.08	0.918	0.94	0.89	0.706	0.86	1.34	0.294
5/6	3/6	0.05	0.38	0.57	0.84	0.98	0.98	0.394	0.96	0.92	0.430	0.82	1.18	0.570
5/6	4/6	0.05	0.32	0.63	0.84	1.01	1.01	0.573	0.95	0.90	0.532	0.86	1.18	0.468
5/6	5/6	0.06	0.38	0.56	0.84	0.95	0.95	0.196	0.96	0.91	0.286	0.82	1.10	0.714
5/6	6/6	0.05	0.34	0.61	0.84	0.95	0.95	0.178	0.95	0.91	0.243	0.83	1.08	0.757
6/6	1/6	0.01	0.23	0.76	0.84	1.09	1.09	0.994	0.96	0.93	0.695	0.82	1.46	0.305
6/6	2/6	0.00	0.15	0.85	0.84	1.05	1.05	0.873	0.95	0.91	0.678	0.87	1.27	0.322
6/6	3/6	0.02	0.18	0.80	0.84	0.97	0.97	0.319	0.96	0.92	0.390	0.84	1.14	0.610
6/6	4/6	0.01	0.20	0.79	0.84	0.97	0.97	0.275	0.96	0.92	0.349	0.84	1.11	0.651
6/6	5/6	0.01	0.14	0.85	0.84	0.94	0.94	0.117	0.96	0.92	0.204	0.84	1.06	0.796
6/6	6/6	0.01	0.19	0.80	0.84	0.92	0.92	0.055	0.96	0.92	0.118	0.83	1.03	0.882

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

1088 Appendix Table 20.-Summary statistics for tests of relative reproductive success (RRS) of a HxN cross to a NxN cross from
 1089 simulations of a low stray rate (15% spawners hatchery-origin) stream with a modeled RRS of 0.750 for a HxH cross to a NxN cross
 1090 for different sampling proportions of parents (F_0) and offspring (F_1) ranging from 1/6 to 6/6. Statistics include proportion of offspring
 1091 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
 1092 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , and the RRS values that we could have
 1093 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
 1094 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , 90% confidence interval, and the one tailed p-value that RRS is < 1). See
 1095 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F_0	F_1	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		$\alpha = 0.20$	$\alpha = 0.05$		5%	95%	
1/6	1/6	0.62	0.33	0.05	0.88	0.82	0.82	0.757	0.82	0.82	0.398	0.24	2.82	0.603
1/6	2/6	0.64	0.31	0.05	0.88	0.79	0.79	0.427	0.79	0.79	0.288	0.40	1.56	0.712
1/6	3/6	0.67	0.30	0.03	0.88	0.86	0.86	0.578	0.73	0.59	0.355	0.46	1.64	0.645
1/6	4/6	0.63	0.32	0.05	0.88	0.93	0.92	0.531	0.77	0.69	0.398	0.57	1.50	0.602
1/6	5/6	0.64	0.31	0.05	0.88	0.81	0.79	0.384	0.73	0.66	0.242	0.49	1.34	0.758
1/6	6/6	0.64	0.32	0.04	0.88	0.87	0.85	0.444	0.73	0.59	0.312	0.53	1.41	0.688
2/6	1/6	0.40	0.42	0.18	0.88	0.91	0.91	0.371	0.91	0.84	0.374	0.58	1.45	0.626
2/6	2/6	0.46	0.41	0.13	0.88	0.91	0.91	0.337	0.87	0.78	0.337	0.64	1.30	0.663
2/6	3/6	0.41	0.44	0.15	0.88	0.95	0.95	0.386	0.89	0.81	0.374	0.72	1.25	0.626
2/6	4/6	0.38	0.44	0.18	0.88	0.88	0.87	0.147	0.91	0.83	0.171	0.70	1.10	0.829
2/6	5/6	0.41	0.44	0.15	0.88	0.94	0.94	0.334	0.91	0.83	0.320	0.76	1.17	0.680
2/6	6/6	0.38	0.44	0.18	0.88	0.95	0.95	0.370	0.90	0.82	0.336	0.79	1.15	0.664
3/6	1/6	0.23	0.49	0.28	0.88	1.04	1.04	0.843	0.94	0.88	0.569	0.72	1.51	0.431
3/6	2/6	0.27	0.50	0.23	0.88	0.93	0.93	0.232	0.93	0.88	0.334	0.72	1.22	0.666
3/6	3/6	0.24	0.48	0.28	0.88	1.03	1.03	0.704	0.93	0.88	0.611	0.85	1.26	0.389
3/6	4/6	0.25	0.48	0.27	0.88	1.03	1.03	0.704	0.93	0.87	0.625	0.87	1.23	0.375
3/6	5/6	0.27	0.49	0.24	0.88	1.00	1.00	0.529	0.93	0.86	0.497	0.85	1.18	0.502
3/6	6/6	0.23	0.49	0.28	0.88	1.03	1.03	0.679	0.93	0.87	0.652	0.90	1.19	0.348

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		
						Simple	Unbiased		α = 0.20	α = 0.05		5%	95%	p RRS < 1
4/6	1/6	0.15	0.50	0.35	0.88	0.95	0.94	0.344	0.95	0.87	0.389	0.68	1.32	0.611
4/6	2/6	0.12	0.43	0.45	0.88	0.86	0.86	0.010	0.95	0.90	0.103	0.70	1.05	0.897
4/6	3/6	0.12	0.44	0.44	0.88	0.85	0.85	0.015	0.94	0.89	0.048	0.73	1.00	0.952
4/6	4/6	0.13	0.45	0.42	0.88	0.92	0.92	0.144	0.94	0.89	0.168	0.80	1.06	0.832
4/6	5/6	0.11	0.45	0.44	0.88	0.87	0.87	0.025	0.94	0.89	0.028	0.77	0.98	0.973
4/6	6/6	0.14	0.47	0.39	0.88	0.85	0.85	0.015	0.94	0.88	0.013	0.75	0.96	0.987
5/6	1/6	0.05	0.38	0.57	0.88	0.97	0.97	0.397	0.95	0.93	0.433	0.76	1.25	0.567
5/6	2/6	0.02	0.31	0.67	0.88	0.84	0.84	0.000	0.96	0.92	0.044	0.72	0.99	0.956
5/6	3/6	0.03	0.31	0.66	0.88	0.93	0.93	0.121	0.95	0.91	0.173	0.82	1.06	0.827
5/6	4/6	0.03	0.30	0.67	0.88	0.92	0.92	0.096	0.95	0.91	0.120	0.82	1.03	0.880
5/6	5/6	0.03	0.29	0.68	0.88	0.90	0.90	0.045	0.95	0.90	0.042	0.81	0.99	0.958
5/6	6/6	0.05	0.36	0.59	0.88	0.90	0.90	0.046	0.95	0.90	0.042	0.81	0.99	0.958
6/6	1/6	0.01	0.12	0.87	0.88	0.99	0.99	0.457	0.95	0.92	0.453	0.80	1.21	0.547
6/6	2/6	0.00	0.11	0.89	0.88	0.86	0.86	0.001	0.96	0.93	0.049	0.75	1.00	0.951
6/6	3/6	0.00	0.12	0.88	0.88	0.89	0.89	0.014	0.96	0.92	0.050	0.80	1.00	0.950
6/6	4/6	0.00	0.10	0.90	0.88	0.92	0.92	0.059	0.96	0.92	0.085	0.84	1.02	0.915
6/6	5/6	0.01	0.14	0.85	0.88	0.86	0.86	0.002	0.96	0.92	0.003	0.78	0.94	0.997
6/6	6/6	0.00	0.09	0.91	0.88	0.90	0.90	0.019	0.96	0.92	0.016	0.82	0.97	0.984

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

1096 Appendix Table 21.-Summary statistics for tests of relative reproductive success (RRS) of a H dam cross to a N dam cross from
 1097 simulations of a high stray rate (50% spawners hatchery-origin) stream with a modeled RRS of 0.750 for a HxH cross to a NxN cross
 1098 for different sampling proportions of parents (F₀) and offspring (F₁) ranging from 1/6 to 6/6. Statistics include proportion of offspring
 1099 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
 1100 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, and the RRS values that we could have
 1101 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
 1102 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, 90% confidence interval, and the one tailed p-value that RRS is < 1). See
 1103 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		RRS Detectability			90% CI			p RRS < 1
						Simple	Unbiased	1-tail p	α = 0.20	α = 0.05	1-tail p	5%	95%	
1/6	1/6	0.67	0.29	0.04	0.84	0.99	0.98	0.547	0.69	0.48	0.483	0.58	1.69	0.517
1/6	2/6	0.70	0.28	0.02	0.84	0.89	0.88	0.351	0.80	0.63	0.313	0.61	1.31	0.687
1/6	3/6	0.69	0.29	0.02	0.84	0.66	0.64	0.024	0.86	0.72	0.019	0.48	0.92	0.981
1/6	4/6	0.68	0.29	0.03	0.84	0.88	0.86	0.230	0.88	0.75	0.206	0.68	1.14	0.794
1/6	5/6	0.69	0.29	0.02	0.84	0.86	0.86	0.174	0.88	0.78	0.156	0.68	1.09	0.844
1/6	6/6	0.70	0.28	0.02	0.84	0.90	0.89	0.231	0.90	0.79	0.209	0.72	1.12	0.791
2/6	1/6	0.52	0.39	0.09	0.84	0.86	0.86	0.310	0.81	0.66	0.267	0.59	1.27	0.733
2/6	2/6	0.44	0.44	0.12	0.84	0.84	0.83	0.128	0.89	0.78	0.112	0.66	1.06	0.888
2/6	3/6	0.48	0.42	0.10	0.84	0.68	0.67	0.003	0.90	0.82	0.003	0.54	0.85	0.997
2/6	4/6	0.47	0.42	0.11	0.84	0.81	0.79	0.037	0.91	0.83	0.032	0.67	0.98	0.968
2/6	5/6	0.47	0.42	0.11	0.84	0.79	0.77	0.014	0.92	0.84	0.011	0.66	0.94	0.989
2/6	6/6	0.46	0.43	0.11	0.84	0.83	0.82	0.034	0.93	0.86	0.030	0.71	0.98	0.970
3/6	1/6	0.28	0.49	0.23	0.84	0.94	0.93	0.394	0.84	0.70	0.361	0.69	1.27	0.639
3/6	2/6	0.24	0.50	0.26	0.84	0.83	0.82	0.091	0.90	0.80	0.077	0.67	1.03	0.923
3/6	3/6	0.24	0.49	0.27	0.84	0.74	0.73	0.004	0.92	0.84	0.003	0.62	0.89	0.997
3/6	4/6	0.25	0.49	0.26	0.84	0.87	0.86	0.090	0.92	0.85	0.081	0.74	1.03	0.919
3/6	5/6	0.28	0.50	0.22	0.84	0.79	0.78	0.007	0.93	0.86	0.006	0.68	0.92	0.994
3/6	6/6	0.24	0.49	0.27	0.84	0.83	0.82	0.014	0.94	0.87	0.010	0.72	0.95	0.990

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		$\alpha = 0.20$	$\alpha = 0.05$		5%	95%	
4/6	1/6	0.17	0.46	0.37	0.84	0.88	0.88	0.243	0.88	0.76	0.220	0.67	1.15	0.780
4/6	2/6	0.12	0.47	0.41	0.84	0.74	0.73	0.005	0.92	0.84	0.004	0.61	0.89	0.996
4/6	3/6	0.09	0.43	0.48	0.84	0.73	0.72	0.000	0.93	0.87	0.000	0.62	0.85	1.000
4/6	4/6	0.14	0.48	0.38	0.84	0.85	0.85	0.039	0.93	0.87	0.035	0.74	0.99	0.965
4/6	5/6	0.14	0.50	0.36	0.84	0.80	0.79	0.003	0.94	0.88	0.003	0.70	0.91	0.997
4/6	6/6	0.13	0.48	0.39	0.84	0.80	0.80	0.002	0.94	0.89	0.001	0.71	0.91	0.999
5/6	1/6	0.06	0.41	0.53	0.84	0.95	0.95	0.398	0.89	0.75	0.371	0.74	1.22	0.629
5/6	2/6	0.04	0.30	0.66	0.84	0.93	0.93	0.265	0.91	0.84	0.249	0.79	1.10	0.751
5/6	3/6	0.05	0.38	0.57	0.84	0.77	0.77	0.003	0.93	0.87	0.002	0.66	0.90	0.998
5/6	4/6	0.05	0.32	0.63	0.84	0.86	0.86	0.036	0.94	0.88	0.031	0.76	0.98	0.969
5/6	5/6	0.06	0.38	0.56	0.84	0.81	0.80	0.002	0.94	0.89	0.002	0.71	0.91	0.998
5/6	6/6	0.05	0.34	0.61	0.84	0.88	0.88	0.030	0.95	0.89	0.025	0.79	0.98	0.975
6/6	1/6	0.01	0.23	0.76	0.84	0.95	0.95	0.380	0.89	0.78	0.357	0.76	1.19	0.642
6/6	2/6	0.00	0.15	0.85	0.84	0.86	0.86	0.068	0.93	0.86	0.061	0.74	1.01	0.939
6/6	3/6	0.02	0.18	0.80	0.84	0.75	0.75	0.000	0.94	0.88	0.000	0.66	0.86	1.000
6/6	4/6	0.01	0.20	0.79	0.84	0.90	0.89	0.074	0.94	0.88	0.068	0.79	1.01	0.932
6/6	5/6	0.01	0.14	0.85	0.84	0.84	0.84	0.004	0.95	0.90	0.003	0.76	0.93	0.997
6/6	6/6	0.01	0.19	0.80	0.84	0.86	0.86	0.008	0.95	0.91	0.007	0.78	0.95	0.993

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

1104 Appendix Table 22.-Summary statistics for tests of relative reproductive success (RRS) of a H dam cross to a N dam cross from
 1105 simulations of a low stray rate (15% spawners hatchery-origin) stream with a modeled RRS of 0.750 for a HxH cross to a NxN cross
 1106 for different sampling proportions of parents (F_0) and offspring (F_1) ranging from 1/6 to 6/6. Statistics include proportion of offspring
 1107 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
 1108 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , and the RRS values that we could have
 1109 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
 1110 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , 90% confidence interval, and the one tailed p-value that RRS is < 1). See
 1111 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F_0	F_1	Unassigned	1 Parent	2 Parents	Estimated			RRS Detectability			90% CI			
					True	Simple	Unbiased	1-tail p	$\alpha = 0.20$	$\alpha = 0.05$	1-tail p	5%	95%	p RRS < 1
1/6	1/6	0.62	0.33	0.05	0.88	0.87	0.85	0.399	0.72	0.56	0.335	0.52	1.47	0.665
1/6	2/6	0.64	0.31	0.05	0.88	0.88	0.85	0.345	0.79	0.63	0.304	0.58	1.34	0.696
1/6	3/6	0.67	0.30	0.03	0.88	1.02	1.03	0.588	0.80	0.68	0.547	0.73	1.44	0.453
1/6	4/6	0.63	0.32	0.05	0.88	0.69	0.62	0.050	0.84	0.69	0.039	0.49	0.98	0.961
1/6	5/6	0.64	0.31	0.05	0.88	0.90	0.88	0.319	0.85	0.71	0.290	0.66	1.23	0.710
1/6	6/6	0.64	0.32	0.04	0.88	0.80	0.76	0.112	0.86	0.74	0.098	0.59	1.06	0.902
2/6	1/6	0.40	0.42	0.18	0.88	0.58	0.52	0.027	0.82	0.66	0.022	0.38	0.91	0.978
2/6	2/6	0.46	0.41	0.13	0.88	0.88	0.87	0.265	0.86	0.74	0.238	0.66	1.18	0.761
2/6	3/6	0.41	0.44	0.15	0.88	0.80	0.78	0.095	0.87	0.76	0.078	0.62	1.04	0.922
2/6	4/6	0.38	0.44	0.18	0.88	0.79	0.76	0.045	0.90	0.80	0.036	0.63	0.98	0.964
2/6	5/6	0.41	0.44	0.15	0.88	0.85	0.83	0.106	0.90	0.80	0.093	0.69	1.04	0.907
2/6	6/6	0.38	0.44	0.18	0.88	0.82	0.80	0.062	0.90	0.82	0.050	0.68	1.00	0.950
3/6	1/6	0.23	0.49	0.28	0.88	0.71	0.69	0.088	0.81	0.68	0.069	0.49	1.04	0.931
3/6	2/6	0.27	0.50	0.23	0.88	0.83	0.82	0.145	0.87	0.76	0.121	0.65	1.08	0.879
3/6	3/6	0.24	0.48	0.28	0.88	0.81	0.79	0.089	0.88	0.78	0.070	0.64	1.02	0.930
3/6	4/6	0.25	0.48	0.27	0.88	0.78	0.75	0.031	0.89	0.81	0.021	0.63	0.95	0.979
3/6	5/6	0.27	0.49	0.24	0.88	0.83	0.81	0.073	0.90	0.81	0.053	0.68	1.00	0.947
3/6	6/6	0.23	0.49	0.28	0.88	0.85	0.83	0.105	0.90	0.81	0.071	0.71	1.02	0.929

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		α = 0.20	α = 0.05		5%	95%	
4/6	1/6	0.15	0.50	0.35	0.88	0.60	0.59	0.011	0.86	0.71	0.011	0.42	0.87	0.989
4/6	2/6	0.12	0.43	0.45	0.88	0.86	0.86	0.132	0.90	0.81	0.119	0.70	1.06	0.881
4/6	3/6	0.12	0.44	0.44	0.88	0.87	0.86	0.131	0.90	0.81	0.114	0.71	1.05	0.886
4/6	4/6	0.13	0.45	0.42	0.88	0.83	0.82	0.046	0.92	0.83	0.039	0.69	0.99	0.961
4/6	5/6	0.11	0.45	0.44	0.88	0.78	0.77	0.009	0.92	0.85	0.007	0.66	0.92	0.993
4/6	6/6	0.14	0.47	0.39	0.88	0.82	0.81	0.024	0.92	0.85	0.019	0.69	0.96	0.981
5/6	1/6	0.05	0.38	0.57	0.88	0.69	0.69	0.025	0.86	0.76	0.023	0.51	0.94	0.977
5/6	2/6	0.02	0.31	0.67	0.88	0.82	0.82	0.057	0.90	0.82	0.051	0.67	1.00	0.949
5/6	3/6	0.03	0.31	0.66	0.88	0.88	0.87	0.120	0.91	0.83	0.108	0.73	1.05	0.891
5/6	4/6	0.03	0.30	0.67	0.88	0.79	0.79	0.008	0.92	0.85	0.007	0.67	0.92	0.993
5/6	5/6	0.03	0.29	0.68	0.88	0.83	0.83	0.026	0.92	0.86	0.019	0.72	0.96	0.981
5/6	6/6	0.05	0.36	0.59	0.88	0.84	0.84	0.031	0.92	0.86	0.023	0.73	0.97	0.977
6/6	1/6	0.01	0.12	0.87	0.88	0.65	0.65	0.005	0.88	0.78	0.006	0.49	0.86	0.994
6/6	2/6	0.00	0.11	0.89	0.88	0.81	0.81	0.041	0.91	0.83	0.035	0.67	0.98	0.965
6/6	3/6	0.00	0.12	0.88	0.88	0.82	0.82	0.027	0.92	0.85	0.024	0.69	0.97	0.976
6/6	4/6	0.00	0.10	0.90	0.88	0.80	0.80	0.007	0.93	0.87	0.006	0.69	0.93	0.994
6/6	5/6	0.01	0.14	0.85	0.88	0.82	0.82	0.012	0.93	0.87	0.010	0.71	0.94	0.990
6/6	6/6	0.00	0.09	0.91	0.88	0.84	0.84	0.015	0.94	0.88	0.012	0.74	0.95	0.988

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

1112 Appendix Table 23.-Summary statistics for tests of relative reproductive success (RRS) of a H sire cross to a N sire cross from
 1113 simulations of a high stray rate (50% spawners hatchery-origin) stream with a modeled RRS of 0.750 for a HxH cross to a NxN cross
 1114 for different sampling proportions of parents (F₀) and offspring (F₁) ranging from 1/6 to 6/6. Statistics include proportion of offspring
 1115 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
 1116 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, and the RRS values that we could have
 1117 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
 1118 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, 90% confidence interval, and the one tailed p-value that RRS is < 1). See
 1119 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	Estimated			RRS Detectability			90% CI			p RRS < 1
					True	Simple	Unbiased	1-tail p	α = 0.20	α = 0.05	1-tail p	5%	95%	
1/6	1/6	0.67	0.29	0.04	0.88	0.92	0.91	0.433	0.77	0.56	0.386	0.56	1.51	0.614
1/6	2/6	0.70	0.28	0.02	0.88	1.03	1.03	0.592	0.82	0.61	0.549	0.70	1.50	0.451
1/6	3/6	0.69	0.29	0.02	0.88	0.85	0.84	0.229	0.85	0.70	0.200	0.62	1.17	0.800
1/6	4/6	0.68	0.29	0.03	0.88	1.02	1.02	0.581	0.85	0.73	0.553	0.78	1.34	0.447
1/6	5/6	0.69	0.29	0.02	0.88	0.99	0.99	0.498	0.87	0.73	0.475	0.77	1.28	0.525
1/6	6/6	0.70	0.28	0.02	0.88	1.02	1.03	0.584	0.88	0.76	0.566	0.81	1.30	0.434
2/6	1/6	0.52	0.39	0.09	0.88	0.95	0.95	0.457	0.79	0.63	0.412	0.64	1.41	0.588
2/6	2/6	0.44	0.44	0.12	0.88	1.07	1.08	0.689	0.85	0.71	0.659	0.81	1.41	0.341
2/6	3/6	0.48	0.42	0.10	0.88	0.81	0.81	0.083	0.90	0.78	0.072	0.65	1.03	0.928
2/6	4/6	0.47	0.42	0.11	0.88	0.89	0.88	0.175	0.90	0.81	0.161	0.72	1.08	0.839
2/6	5/6	0.47	0.42	0.11	0.88	0.87	0.86	0.100	0.92	0.84	0.091	0.73	1.03	0.909
2/6	6/6	0.46	0.43	0.11	0.88	0.88	0.88	0.115	0.92	0.84	0.104	0.75	1.04	0.896
3/6	1/6	0.28	0.49	0.23	0.88	1.02	1.02	0.582	0.86	0.70	0.547	0.76	1.38	0.453
3/6	2/6	0.24	0.50	0.26	0.88	0.92	0.92	0.278	0.89	0.80	0.259	0.75	1.13	0.741
3/6	3/6	0.24	0.49	0.27	0.88	0.93	0.93	0.264	0.91	0.83	0.247	0.78	1.11	0.753
3/6	4/6	0.25	0.49	0.26	0.88	0.93	0.93	0.219	0.93	0.86	0.207	0.80	1.08	0.793
3/6	5/6	0.28	0.50	0.22	0.88	0.95	0.95	0.293	0.93	0.86	0.280	0.83	1.10	0.720
3/6	6/6	0.24	0.49	0.27	0.88	0.93	0.93	0.197	0.94	0.88	0.186	0.83	1.06	0.814

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		$\alpha = 0.20$	$\alpha = 0.05$		5%	95%	
4/6	1/6	0.17	0.46	0.37	0.88	1.18	1.18	0.873	0.85	0.71	0.853	0.91	1.54	0.147
4/6	2/6	0.12	0.47	0.41	0.88	1.06	1.06	0.717	0.90	0.82	0.701	0.88	1.27	0.299
4/6	3/6	0.09	0.43	0.48	0.88	0.91	0.91	0.160	0.92	0.86	0.150	0.78	1.06	0.850
4/6	4/6	0.14	0.48	0.38	0.88	0.87	0.86	0.050	0.94	0.87	0.045	0.75	1.00	0.955
4/6	5/6	0.14	0.50	0.36	0.88	0.91	0.91	0.123	0.94	0.88	0.115	0.81	1.03	0.885
4/6	6/6	0.13	0.48	0.39	0.88	0.91	0.91	0.092	0.94	0.89	0.085	0.81	1.02	0.915
5/6	1/6	0.06	0.41	0.53	0.88	0.96	0.96	0.412	0.88	0.76	0.385	0.76	1.21	0.615
5/6	2/6	0.04	0.30	0.66	0.88	0.89	0.89	0.134	0.92	0.85	0.123	0.76	1.05	0.877
5/6	3/6	0.05	0.38	0.57	0.88	0.80	0.79	0.004	0.94	0.87	0.004	0.69	0.92	0.996
5/6	4/6	0.05	0.32	0.63	0.88	0.79	0.79	0.001	0.94	0.89	0.001	0.70	0.90	0.999
5/6	5/6	0.06	0.38	0.56	0.88	0.78	0.78	0.000	0.95	0.90	0.000	0.70	0.87	1.000
5/6	6/6	0.05	0.34	0.61	0.88	0.81	0.81	0.000	0.95	0.91	0.000	0.73	0.90	1.000
6/6	1/6	0.01	0.23	0.76	0.88	1.05	1.05	0.661	0.89	0.78	0.635	0.84	1.30	0.365
6/6	2/6	0.00	0.15	0.85	0.88	0.93	0.93	0.216	0.93	0.85	0.203	0.79	1.08	0.797
6/6	3/6	0.02	0.18	0.80	0.88	0.85	0.85	0.024	0.94	0.88	0.021	0.75	0.97	0.979
6/6	4/6	0.01	0.20	0.79	0.88	0.86	0.86	0.017	0.94	0.89	0.015	0.76	0.96	0.985
6/6	5/6	0.01	0.14	0.85	0.88	0.86	0.86	0.007	0.95	0.90	0.006	0.77	0.95	0.994
6/6	6/6	0.01	0.19	0.80	0.88	0.89	0.89	0.020	0.95	0.91	0.018	0.81	0.97	0.982

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

1120 Appendix Table 24.-Summary statistics for tests of relative reproductive success (RRS) of a H sire cross to a N sire cross from
 1121 simulations of a low stray rate (15% spawners hatchery-origin) stream with a modeled RRS of 0.750 for a HxH cross to a NxN cross
 1122 for different sampling proportions of parents (F₀) and offspring (F₁) ranging from 1/6 to 6/6. Statistics include proportion of offspring
 1123 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
 1124 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, and the RRS values that we could have
 1125 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
 1126 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, 90% confidence interval, and the one tailed p-value that RRS is <1). See
 1127 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	Estimated			RRS Detectability			90% CI			p RRS < 1
					True	Simple	Unbiased	1-tail p	α = 0.20	α = 0.05	1-tail p	5%	95%	
1/6	1/6	0.62	0.33	0.05	0.88	0.45	0.38	0.048	0.75	0.55	0.042	0.21	0.96	0.958
1/6	2/6	0.64	0.31	0.05	0.88	0.54	0.46	0.040	0.80	0.59	0.033	0.31	0.94	0.967
1/6	3/6	0.67	0.30	0.03	0.88	0.70	0.67	0.153	0.78	0.58	0.113	0.43	1.14	0.887
1/6	4/6	0.63	0.32	0.05	0.88	0.79	0.76	0.191	0.82	0.66	0.148	0.55	1.14	0.852
1/6	5/6	0.64	0.31	0.05	0.88	0.65	0.60	0.040	0.83	0.67	0.029	0.45	0.95	0.971
1/6	6/6	0.64	0.32	0.04	0.88	0.64	0.60	0.029	0.83	0.70	0.020	0.45	0.92	0.980
2/6	1/6	0.40	0.42	0.18	0.88	0.87	0.85	0.321	0.82	0.62	0.276	0.58	1.29	0.724
2/6	2/6	0.46	0.41	0.13	0.88	0.94	0.94	0.416	0.85	0.69	0.373	0.68	1.29	0.627
2/6	3/6	0.41	0.44	0.15	0.88	0.91	0.90	0.329	0.86	0.73	0.300	0.69	1.21	0.700
2/6	4/6	0.38	0.44	0.18	0.88	1.06	1.07	0.675	0.87	0.77	0.658	0.84	1.33	0.342
2/6	5/6	0.41	0.44	0.15	0.88	0.89	0.88	0.231	0.88	0.78	0.203	0.71	1.12	0.797
2/6	6/6	0.38	0.44	0.18	0.88	0.98	0.98	0.465	0.89	0.79	0.438	0.79	1.21	0.562
3/6	1/6	0.23	0.49	0.28	0.88	1.07	1.07	0.682	0.86	0.70	0.646	0.80	1.42	0.354
3/6	2/6	0.27	0.50	0.23	0.88	0.95	0.94	0.386	0.88	0.76	0.357	0.74	1.21	0.643
3/6	3/6	0.24	0.48	0.28	0.88	0.98	0.98	0.450	0.90	0.79	0.425	0.80	1.20	0.575
3/6	4/6	0.25	0.48	0.27	0.88	1.04	1.05	0.676	0.91	0.82	0.660	0.88	1.24	0.340
3/6	5/6	0.27	0.49	0.24	0.88	0.95	0.95	0.355	0.91	0.82	0.329	0.80	1.14	0.671
3/6	6/6	0.23	0.49	0.28	0.88	0.97	0.96	0.378	0.92	0.84	0.357	0.82	1.13	0.642

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		α = 0.20	α = 0.05		5%	95%	
4/6	1/6	0.15	0.50	0.35	0.88	0.87	0.87	0.261	0.84	0.73	0.230	0.64	1.18	0.770
4/6	2/6	0.12	0.43	0.45	0.88	0.98	0.98	0.462	0.88	0.79	0.434	0.79	1.21	0.566
4/6	3/6	0.12	0.44	0.44	0.88	0.95	0.95	0.346	0.90	0.81	0.321	0.78	1.15	0.679
4/6	4/6	0.13	0.45	0.42	0.88	0.99	0.99	0.472	0.91	0.83	0.450	0.83	1.17	0.550
4/6	5/6	0.11	0.45	0.44	0.88	0.94	0.94	0.302	0.92	0.84	0.281	0.80	1.11	0.719
4/6	6/6	0.14	0.47	0.39	0.88	0.94	0.94	0.294	0.92	0.85	0.270	0.81	1.10	0.730
5/6	1/6	0.05	0.38	0.57	0.88	0.86	0.85	0.194	0.88	0.75	0.171	0.65	1.12	0.829
5/6	2/6	0.02	0.31	0.67	0.88	0.89	0.89	0.188	0.91	0.82	0.174	0.74	1.09	0.826
5/6	3/6	0.03	0.31	0.66	0.88	0.96	0.95	0.351	0.91	0.83	0.330	0.80	1.13	0.670
5/6	4/6	0.03	0.30	0.67	0.88	0.94	0.94	0.280	0.92	0.85	0.257	0.81	1.09	0.743
5/6	5/6	0.03	0.29	0.68	0.88	0.84	0.84	0.033	0.92	0.86	0.027	0.73	0.97	0.973
5/6	6/6	0.05	0.36	0.59	0.88	0.87	0.87	0.064	0.93	0.87	0.055	0.76	1.00	0.945
6/6	1/6	0.01	0.12	0.87	0.88	0.82	0.82	0.112	0.88	0.77	0.099	0.64	1.06	0.901
6/6	2/6	0.00	0.11	0.89	0.88	0.92	0.92	0.238	0.91	0.83	0.221	0.77	1.10	0.779
6/6	3/6	0.00	0.12	0.88	0.88	0.93	0.93	0.234	0.92	0.84	0.218	0.79	1.09	0.782
6/6	4/6	0.00	0.10	0.90	0.88	0.95	0.95	0.288	0.93	0.86	0.268	0.83	1.09	0.732
6/6	5/6	0.01	0.14	0.85	0.88	0.85	0.85	0.032	0.93	0.87	0.027	0.74	0.98	0.973
6/6	6/6	0.00	0.09	0.91	0.88	0.87	0.87	0.036	0.93	0.88	0.030	0.76	0.98	0.970

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

1128 Appendix Table 25.-Summary statistics for tests of relative reproductive success (RRS) of a HxH cross to a NxN cross from
 1129 simulations of a high stray rate (50% spawners hatchery-origin) stream with a modeled RRS of 0.875 for a HxH cross to a NxN cross
 1130 for different sampling proportions of parents (F_0) and offspring (F_1) ranging from 1/6 to 6/6. Statistics include proportion of offspring
 1131 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
 1132 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , and the RRS values that we could have
 1133 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
 1134 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , 90% confidence interval, and the one tailed p-value that RRS is < 1). See
 1135 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM				
F_0	F_1	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1	
						Simple	Unbiased		$\alpha = 0.20$	$\alpha = 0.05$		5%	95%		
1/6	1/6	0.70	0.27	0.03	0.88	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
1/6	2/6	0.60	0.32	0.08	0.88	1.20	1.21	1.000	0.83	0.83	0.624	0.46	3.10	0.376	
1/6	3/6	0.65	0.32	0.03	0.88	1.00	1.00	NA	NA	NA	NA	NA	NA	NA	
1/6	4/6	0.67	0.29	0.04	0.88	1.25	1.26	1.000	0.71	0.71	0.675	0.56	2.81	0.325	
1/6	5/6	0.68	0.29	0.03	0.88	1.40	1.42	1.000	0.60	0.60	0.717	0.53	3.67	0.283	
1/6	6/6	0.66	0.31	0.03	0.88	1.25	1.27	1.000	0.82	0.82	0.695	0.61	2.56	0.305	
2/6	1/6	0.39	0.44	0.17	0.88	0.78	0.78	0.101	0.94	0.78	0.278	0.39	1.57	0.722	
2/6	2/6	0.43	0.42	0.15	0.88	1.06	1.06	0.834	0.94	0.83	0.565	0.61	1.81	0.435	
2/6	3/6	0.44	0.42	0.14	0.88	1.14	1.14	0.890	0.89	0.73	0.681	0.72	1.81	0.319	
2/6	4/6	0.46	0.42	0.12	0.88	0.89	0.89	0.249	0.89	0.83	0.317	0.59	1.33	0.683	
2/6	5/6	0.47	0.41	0.12	0.88	0.95	0.95	0.437	0.84	0.73	0.414	0.64	1.40	0.586	
2/6	6/6	0.47	0.41	0.12	0.88	1.01	1.01	0.591	0.86	0.77	0.518	0.70	1.45	0.482	
3/6	1/6	0.25	0.54	0.21	0.88	0.88	0.87	0.396	0.88	0.88	0.379	0.43	1.78	0.621	
3/6	2/6	0.21	0.51	0.28	0.88	1.01	1.01	0.737	0.92	0.83	0.517	0.62	1.65	0.483	
3/6	3/6	0.28	0.51	0.21	0.88	0.91	0.91	0.218	0.91	0.86	0.327	0.63	1.30	0.673	
3/6	4/6	0.24	0.51	0.25	0.88	0.87	0.87	0.102	0.93	0.87	0.226	0.64	1.18	0.774	
3/6	5/6	0.21	0.53	0.26	0.88	0.87	0.87	0.075	0.92	0.87	0.194	0.67	1.13	0.806	
3/6	6/6	0.26	0.53	0.21	0.88	0.91	0.91	0.193	0.93	0.86	0.273	0.70	1.18	0.727	

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		α = 0.20	α = 0.05		5%	95%	
4/6	1/6	0.15	0.47	0.38	0.88	1.01	1.01	0.817	0.93	0.93	0.514	0.63	1.61	0.486
4/6	2/6	0.13	0.42	0.45	0.88	0.96	0.96	0.400	0.92	0.89	0.424	0.70	1.33	0.576
4/6	3/6	0.16	0.51	0.33	0.88	1.07	1.07	0.866	0.94	0.87	0.642	0.80	1.43	0.357
4/6	4/6	0.13	0.45	0.42	0.88	0.98	0.98	0.425	0.94	0.88	0.429	0.78	1.23	0.571
4/6	5/6	0.17	0.49	0.34	0.88	1.03	1.03	0.660	0.93	0.86	0.576	0.82	1.29	0.424
4/6	6/6	0.18	0.48	0.34	0.88	1.02	1.02	0.646	0.93	0.86	0.569	0.83	1.26	0.431
5/6	1/6	0.05	0.31	0.64	0.88	1.01	1.01	0.778	0.96	0.90	0.521	0.69	1.49	0.479
5/6	2/6	0.04	0.28	0.68	0.88	1.07	1.07	0.920	0.95	0.90	0.676	0.83	1.38	0.324
5/6	3/6	0.06	0.32	0.62	0.88	0.98	0.98	0.416	0.94	0.91	0.436	0.79	1.22	0.564
5/6	4/6	0.07	0.32	0.61	0.88	1.08	1.08	0.920	0.94	0.90	0.750	0.89	1.31	0.250
5/6	5/6	0.07	0.35	0.58	0.88	1.01	1.01	0.612	0.94	0.89	0.550	0.85	1.21	0.450
5/6	6/6	0.07	0.33	0.60	0.88	1.04	1.04	0.764	0.95	0.89	0.663	0.89	1.22	0.337
6/6	1/6	0.01	0.16	0.83	0.88	0.94	0.94	0.217	0.94	0.94	0.386	0.67	1.32	0.614
6/6	2/6	0.00	0.11	0.89	0.88	1.06	1.06	0.916	0.96	0.92	0.660	0.84	1.32	0.340
6/6	3/6	0.01	0.22	0.77	0.88	1.01	1.01	0.646	0.95	0.91	0.539	0.83	1.23	0.461
6/6	4/6	0.01	0.23	0.76	0.88	1.01	1.01	0.633	0.96	0.91	0.545	0.85	1.20	0.455
6/6	5/6	0.01	0.17	0.82	0.88	0.99	0.99	0.436	0.96	0.92	0.444	0.85	1.14	0.556
6/6	6/6	0.00	0.17	0.83	0.88	0.99	0.99	0.472	0.96	0.91	0.466	0.87	1.13	0.534

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

1136 Appendix Table 26.-Summary statistics for tests of relative reproductive success (RRS) of a HxH cross to a NxN cross from
 1137 simulations of a low stray rate (15% spawners hatchery-origin) stream with a modeled RRS of 0.875 for a HxH cross to a NxN cross
 1138 for different sampling proportions of parents (F_0) and offspring (F_1) ranging from 1/6 to 6/6. Statistics include proportion of offspring
 1139 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
 1140 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , and the RRS values that we could have
 1141 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
 1142 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , 90% confidence interval, and the one tailed p-value that RRS is < 1). See
 1143 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F_0	F_1	Unassigned	1 Parent	2 Parents	True	Estimated		RRS Detectability			90% CI			p RRS < 1
						Simple	Unbiased	1-tail p	$\alpha = 0.20$	$\alpha = 0.05$	1-tail p	5%	95%	
1/6	1/6	0.69	0.28	0.03	0.89	NA	NA	NA	NA	NA	NA	NA	NA	NA
1/6	2/6	0.73	0.24	0.03	0.89	NA	NA	NA	NA	NA	NA	NA	NA	NA
1/6	3/6	0.70	0.28	0.02	0.89	NA	NA	NA	NA	NA	NA	NA	NA	NA
1/6	4/6	0.70	0.27	0.03	0.89	NA	NA	NA	NA	NA	NA	NA	NA	NA
1/6	5/6	0.70	0.27	0.03	0.89	NA	NA	NA	NA	NA	NA	NA	NA	NA
1/6	6/6	0.71	0.26	0.03	0.89	NA	NA	NA	NA	NA	NA	NA	NA	NA
2/6	1/6	0.45	0.42	0.13	0.89	0.85	0.85	0.832	0.85	0.85	0.438	0.16	4.51	0.562
2/6	2/6	0.46	0.43	0.11	0.89	1.60	1.61	0.979	0.77	0.77	0.819	0.69	3.73	0.181
2/6	3/6	0.44	0.46	0.10	0.89	3.58	3.61	NA	NA	NA	NA	NA	NA	NA
2/6	4/6	0.47	0.44	0.09	0.89	1.40	1.40	0.953	0.67	0.67	0.787	0.70	2.78	0.213
2/6	5/6	0.47	0.43	0.10	0.89	3.56	3.60	NA	NA	NA	NA	NA	NA	NA
2/6	6/6	0.47	0.43	0.10	0.89	2.75	2.79	0.999	0.53	0.53	1.000	1.75	4.35	0.000
3/6	1/6	0.30	0.47	0.23	0.89	0.90	0.90	0.800	0.90	0.90	0.443	0.28	2.94	0.557
3/6	2/6	0.23	0.53	0.24	0.89	0.69	0.69	0.313	0.69	0.69	0.265	0.27	1.81	0.735
3/6	3/6	0.24	0.52	0.24	0.89	1.06	1.06	0.730	0.82	0.70	0.572	0.61	1.86	0.428
3/6	4/6	0.28	0.51	0.21	0.89	1.27	1.28	0.878	0.78	0.62	0.750	0.71	2.30	0.250
3/6	5/6	0.28	0.50	0.22	0.89	1.27	1.27	0.861	0.77	0.56	0.801	0.80	2.02	0.199
3/6	6/6	0.29	0.50	0.21	0.89	1.48	1.48	0.914	0.66	0.55	0.913	0.92	2.37	0.087

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		α = 0.20	α = 0.05		5%	95%	
4/6	1/6	0.14	0.46	0.40	0.89	1.07	1.07	0.844	0.85	0.85	0.560	0.51	2.27	0.440
4/6	2/6	0.14	0.48	0.38	0.89	1.01	1.01	0.686	0.71	0.71	0.511	0.54	1.90	0.488
4/6	3/6	0.14	0.47	0.39	0.89	0.89	0.89	0.378	0.82	0.75	0.339	0.56	1.41	0.661
4/6	4/6	0.14	0.48	0.38	0.89	0.82	0.82	0.265	0.82	0.70	0.238	0.53	1.29	0.762
4/6	5/6	0.14	0.48	0.38	0.89	0.96	0.96	0.504	0.81	0.71	0.423	0.66	1.39	0.577
4/6	6/6	0.15	0.47	0.38	0.89	0.92	0.92	0.427	0.83	0.69	0.350	0.64	1.32	0.650
5/6	1/6	0.07	0.40	0.53	0.89	0.87	0.87	0.441	0.87	0.87	0.372	0.44	1.73	0.628
5/6	2/6	0.05	0.35	0.60	0.89	0.88	0.88	0.497	0.73	0.73	0.383	0.45	1.74	0.617
5/6	3/6	0.07	0.37	0.56	0.89	0.79	0.79	0.140	0.86	0.73	0.204	0.50	1.26	0.796
5/6	4/6	0.06	0.39	0.55	0.89	0.74	0.74	0.053	0.87	0.74	0.106	0.49	1.10	0.893
5/6	5/6	0.06	0.38	0.56	0.89	0.82	0.82	0.168	0.86	0.74	0.174	0.57	1.16	0.826
5/6	6/6	0.05	0.36	0.59	0.89	0.67	0.67	0.014	0.84	0.76	0.026	0.48	0.94	0.974
6/6	1/6	0.01	0.20	0.79	0.89	1.00	1.00	0.733	0.87	0.87	0.495	0.55	1.80	0.504
6/6	2/6	0.00	0.18	0.82	0.89	0.82	0.82	0.209	0.82	0.74	0.269	0.49	1.39	0.731
6/6	3/6	0.00	0.19	0.81	0.89	0.83	0.83	0.112	0.90	0.79	0.188	0.58	1.18	0.812
6/6	4/6	0.02	0.18	0.80	0.89	0.84	0.84	0.153	0.87	0.77	0.192	0.60	1.17	0.808
6/6	5/6	0.00	0.12	0.88	0.89	0.90	0.90	0.250	0.90	0.80	0.232	0.70	1.15	0.768
6/6	6/6	0.01	0.19	0.80	0.89	0.90	0.90	0.259	0.88	0.80	0.232	0.70	1.14	0.768

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

1144 Appendix Table 27.-Summary statistics for tests of relative reproductive success (RRS) of a HxN cross to a NxN cross from
 1145 simulations of a high stray rate (50% spawners hatchery-origin) stream with a modeled RRS of 0.875 for a HxH cross to a NxN cross
 1146 for different sampling proportions of parents (F_0) and offspring (F_1) ranging from 1/6 to 6/6. Statistics include proportion of offspring
 1147 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
 1148 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , and the RRS values that we could have
 1149 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
 1150 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , 90% confidence interval, and the one tailed p-value that RRS is < 1). See
 1151 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F_0	F_1	Unassigned	1 Parent	2 Parents	True	Estimated		RRS Detectability			90% CI			p RRS < 1
						Simple	Unbiased	1-tail p	$\alpha = 0.20$	$\alpha = 0.05$	1-tail p	5%	95%	
1/6	1/6	0.70	0.27	0.03	0.92	1.00	1.00	NA	NA	NA	NA	NA	NA	NA
1/6	2/6	0.60	0.32	0.08	0.92	1.08	1.09	NA	NA	NA	NA	NA	NA	NA
1/6	3/6	0.65	0.32	0.03	0.92	1.12	1.13	1.000	0.83	0.83	0.588	0.47	2.68	0.412
1/6	4/6	0.67	0.29	0.04	0.92	1.15	1.16	NA	NA	NA	NA	NA	NA	NA
1/6	5/6	0.68	0.29	0.03	0.92	1.16	1.16	1.000	0.65	0.65	0.616	0.51	2.62	0.384
1/6	6/6	0.66	0.31	0.03	0.92	1.16	1.17	1.000	0.77	0.64	0.662	0.65	2.08	0.338
2/6	1/6	0.39	0.44	0.17	0.92	0.82	0.82	0.181	0.98	0.82	0.313	0.42	1.60	0.687
2/6	2/6	0.43	0.42	0.15	0.92	1.00	1.00	0.662	0.92	0.83	0.500	0.62	1.61	0.500
2/6	3/6	0.44	0.42	0.14	0.92	1.01	1.01	0.634	0.88	0.82	0.519	0.67	1.53	0.481
2/6	4/6	0.46	0.42	0.12	0.92	0.88	0.88	0.191	0.93	0.83	0.284	0.60	1.28	0.716
2/6	5/6	0.47	0.41	0.12	0.92	0.86	0.85	0.163	0.90	0.81	0.237	0.60	1.22	0.763
2/6	6/6	0.47	0.41	0.12	0.92	1.07	1.07	0.718	0.87	0.75	0.626	0.77	1.47	0.374
3/6	1/6	0.25	0.54	0.21	0.92	0.94	0.94	0.456	0.94	0.85	0.429	0.56	1.59	0.571
3/6	2/6	0.21	0.51	0.28	0.92	0.99	0.99	0.535	0.94	0.90	0.475	0.70	1.40	0.525
3/6	3/6	0.28	0.51	0.21	0.92	0.97	0.97	0.422	0.94	0.87	0.430	0.72	1.30	0.570
3/6	4/6	0.24	0.51	0.25	0.92	0.92	0.92	0.193	0.94	0.88	0.298	0.72	1.19	0.702
3/6	5/6	0.21	0.53	0.26	0.92	0.88	0.88	0.051	0.95	0.88	0.168	0.71	1.09	0.832
3/6	6/6	0.26	0.53	0.21	0.92	0.92	0.92	0.185	0.94	0.87	0.268	0.74	1.14	0.732

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		$\alpha = 0.20$	$\alpha = 0.05$		5%	95%	
4/6	1/6	0.15	0.47	0.38	0.92	0.99	0.99	0.619	0.99	0.93	0.477	0.66	1.47	0.523
4/6	2/6	0.13	0.42	0.45	0.92	0.97	0.97	0.344	0.97	0.92	0.417	0.74	1.26	0.583
4/6	3/6	0.16	0.51	0.33	0.92	1.02	1.02	0.658	0.95	0.90	0.542	0.79	1.31	0.458
4/6	4/6	0.13	0.45	0.42	0.92	1.02	1.02	0.622	0.94	0.89	0.551	0.84	1.23	0.449
4/6	5/6	0.17	0.49	0.34	0.92	1.01	1.01	0.570	0.94	0.88	0.522	0.83	1.22	0.478
4/6	6/6	0.18	0.48	0.34	0.92	1.03	1.03	0.721	0.94	0.89	0.624	0.87	1.23	0.376
5/6	1/6	0.05	0.31	0.64	0.92	1.02	1.02	0.693	0.95	0.88	0.548	0.75	1.40	0.452
5/6	2/6	0.04	0.28	0.68	0.92	0.98	0.98	0.385	0.96	0.93	0.437	0.79	1.21	0.563
5/6	3/6	0.06	0.32	0.62	0.92	0.97	0.97	0.360	0.95	0.90	0.410	0.81	1.18	0.590
5/6	4/6	0.07	0.32	0.61	0.92	1.12	1.12	0.975	0.95	0.89	0.867	0.95	1.32	0.133
5/6	5/6	0.07	0.35	0.58	0.92	1.00	1.00	0.526	0.95	0.90	0.504	0.86	1.17	0.496
5/6	6/6	0.07	0.33	0.60	0.92	1.04	1.04	0.762	0.96	0.91	0.671	0.91	1.19	0.329
6/6	1/6	0.01	0.16	0.83	0.92	0.97	0.97	0.343	0.97	0.95	0.431	0.75	1.27	0.569
6/6	2/6	0.00	0.11	0.89	0.92	1.01	1.01	0.648	0.97	0.93	0.532	0.84	1.21	0.468
6/6	3/6	0.01	0.22	0.77	0.92	0.99	0.99	0.437	0.96	0.93	0.455	0.84	1.16	0.545
6/6	4/6	0.01	0.23	0.76	0.92	1.01	1.01	0.626	0.96	0.92	0.552	0.87	1.17	0.448
6/6	5/6	0.01	0.17	0.82	0.92	0.94	0.94	0.105	0.96	0.92	0.207	0.83	1.06	0.792
6/6	6/6	0.00	0.17	0.83	0.92	0.99	0.99	0.470	0.96	0.92	0.469	0.89	1.11	0.531

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

1152 Appendix Table 28.-Summary statistics for tests of relative reproductive success (RRS) of a HxN cross to a NxN cross from
 1153 simulations of a low stray rate (15% spawners hatchery-origin) stream with a modeled RRS of 0.875 for a HxH cross to a NxN cross
 1154 for different sampling proportions of parents (F_0) and offspring (F_1) ranging from 1/6 to 6/6. Statistics include proportion of offspring
 1155 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
 1156 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , and the RRS values that we could have
 1157 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
 1158 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1 , 90% confidence interval, and the one tailed p-value that RRS is < 1). See
 1159 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F_0	F_1	Unassigned	1 Parent	2 Parents	Estimated			RRS Detectability			90% CI			p RRS < 1
					True	Simple	Unbiased	1-tail p	$\alpha = 0.20$	$\alpha = 0.05$	1-tail p	5%	95%	
1/6	1/6	0.69	0.28	0.03	0.95	1.00	1.00	NA	NA	NA	NA	NA	NA	NA
1/6	2/6	0.73	0.24	0.03	0.95	0.78	0.78	0.630	0.78	0.78	0.370	0.23	2.63	0.630
1/6	3/6	0.70	0.28	0.02	0.95	0.67	0.66	0.343	0.67	0.67	0.253	0.24	1.81	0.747
1/6	4/6	0.70	0.27	0.03	0.95	0.67	0.66	0.224	0.67	0.67	0.196	0.31	1.45	0.804
1/6	5/6	0.70	0.27	0.03	0.95	0.80	0.79	0.298	0.80	0.70	0.260	0.45	1.41	0.740
1/6	6/6	0.71	0.26	0.03	0.95	0.69	0.68	0.185	0.78	0.61	0.142	0.40	1.22	0.858
2/6	1/6	0.45	0.42	0.13	0.95	0.91	0.91	0.281	0.91	0.83	0.368	0.56	1.46	0.632
2/6	2/6	0.46	0.43	0.11	0.95	0.94	0.94	0.370	0.94	0.84	0.392	0.64	1.37	0.608
2/6	3/6	0.44	0.46	0.10	0.95	0.93	0.93	0.313	0.93	0.82	0.354	0.68	1.28	0.646
2/6	4/6	0.47	0.44	0.09	0.95	0.92	0.92	0.263	0.92	0.85	0.332	0.68	1.26	0.668
2/6	5/6	0.47	0.43	0.10	0.95	1.03	1.03	0.642	0.90	0.82	0.567	0.79	1.33	0.433
2/6	6/6	0.47	0.43	0.10	0.95	0.89	0.89	0.177	0.91	0.84	0.206	0.71	1.12	0.794
3/6	1/6	0.30	0.47	0.23	0.95	0.94	0.94	0.309	0.94	0.89	0.396	0.64	1.38	0.604
3/6	2/6	0.23	0.53	0.24	0.95	0.87	0.87	0.102	0.92	0.85	0.192	0.68	1.13	0.808
3/6	3/6	0.24	0.52	0.24	0.95	0.94	0.94	0.279	0.92	0.88	0.324	0.76	1.17	0.676
3/6	4/6	0.28	0.51	0.21	0.95	0.97	0.97	0.398	0.93	0.87	0.399	0.80	1.18	0.601
3/6	5/6	0.28	0.50	0.22	0.95	0.96	0.96	0.374	0.92	0.85	0.354	0.81	1.14	0.646
3/6	6/6	0.29	0.50	0.21	0.95	0.97	0.97	0.404	0.93	0.85	0.381	0.83	1.14	0.619

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		α = 0.20	α = 0.05		5%	95%	
4/6	1/6	0.14	0.46	0.40	0.95	0.99	0.99	0.550	0.92	0.89	0.472	0.73	1.34	0.528
4/6	2/6	0.14	0.48	0.38	0.95	0.88	0.88	0.067	0.93	0.88	0.165	0.71	1.09	0.835
4/6	3/6	0.14	0.47	0.39	0.95	0.93	0.93	0.155	0.95	0.90	0.230	0.78	1.10	0.770
4/6	4/6	0.14	0.48	0.38	0.95	0.93	0.93	0.170	0.94	0.88	0.197	0.80	1.07	0.803
4/6	5/6	0.14	0.48	0.38	0.95	0.96	0.96	0.296	0.94	0.88	0.291	0.84	1.09	0.709
4/6	6/6	0.15	0.47	0.38	0.95	0.91	0.91	0.108	0.94	0.88	0.101	0.80	1.03	0.899
5/6	1/6	0.07	0.40	0.53	0.95	1.01	1.01	0.628	0.96	0.92	0.516	0.79	1.28	0.484
5/6	2/6	0.05	0.35	0.60	0.95	0.95	0.95	0.207	0.95	0.91	0.299	0.80	1.12	0.701
5/6	3/6	0.07	0.37	0.56	0.95	0.91	0.91	0.059	0.96	0.91	0.148	0.79	1.05	0.852
5/6	4/6	0.06	0.39	0.55	0.95	0.93	0.93	0.103	0.95	0.91	0.154	0.82	1.05	0.846
5/6	5/6	0.06	0.38	0.56	0.95	0.94	0.94	0.171	0.95	0.91	0.195	0.84	1.05	0.805
5/6	6/6	0.05	0.36	0.59	0.95	0.90	0.90	0.041	0.95	0.91	0.041	0.82	0.99	0.959
6/6	1/6	0.01	0.20	0.79	0.95	1.05	1.05	0.874	0.95	0.92	0.655	0.86	1.29	0.345
6/6	2/6	0.00	0.18	0.82	0.95	0.97	0.97	0.282	0.96	0.93	0.354	0.84	1.11	0.646
6/6	3/6	0.00	0.19	0.81	0.95	0.94	0.94	0.099	0.96	0.92	0.184	0.84	1.05	0.816
6/6	4/6	0.02	0.18	0.80	0.95	1.02	1.02	0.640	0.96	0.92	0.597	0.92	1.12	0.403
6/6	5/6	0.00	0.12	0.88	0.95	1.00	1.00	0.534	0.96	0.92	0.515	0.92	1.09	0.485
6/6	6/6	0.01	0.19	0.80	0.95	0.98	0.98	0.362	0.96	0.92	0.354	0.90	1.07	0.646

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

1160 Appendix Table 29.-Summary statistics for tests of relative reproductive success (RRS) of a H dam cross to a N dam cross from
 1161 simulations of a high stray rate (50% spawners hatchery-origin) stream with a modeled RRS of 0.875 for a HxH cross to a NxN cross
 1162 for different sampling proportions of parents (F₀) and offspring (F₁) ranging from 1/6 to 6/6. Statistics include proportion of offspring
 1163 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
 1164 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, and the RRS values that we could have
 1165 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
 1166 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, 90% confidence interval, and the one tailed p-value that RRS is <1). See
 1167 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		RRS Detectability			90% CI			p RRS < 1
						Simple	Unbiased	1-tail p	α = 0.20	α = 0.05	1-tail p	5%	95%	
1/6	1/6	0.70	0.27	0.03	1.00	1.20	1.26	0.770	0.73	0.44	0.727	0.73	1.99	0.273
1/6	2/6	0.60	0.32	0.08	1.00	1.46	1.68	0.973	0.78	0.58	0.974	1.06	2.02	0.026
1/6	3/6	0.65	0.32	0.03	1.00	1.17	1.22	0.844	0.85	0.71	0.833	0.89	1.55	0.168
1/6	4/6	0.67	0.29	0.04	1.00	1.26	1.32	0.899	0.83	0.65	0.910	0.95	1.66	0.090
1/6	5/6	0.68	0.29	0.03	1.00	1.28	1.31	0.951	0.84	0.72	0.954	1.01	1.62	0.046
1/6	6/6	0.66	0.31	0.03	1.00	1.19	1.23	0.900	0.86	0.74	0.901	0.95	1.48	0.099
2/6	1/6	0.39	0.44	0.17	1.00	1.04	1.04	0.604	0.82	0.65	0.568	0.73	1.47	0.432
2/6	2/6	0.43	0.42	0.15	1.00	1.07	1.08	0.699	0.86	0.72	0.672	0.83	1.39	0.328
2/6	3/6	0.44	0.42	0.14	1.00	1.12	1.13	0.821	0.88	0.77	0.808	0.90	1.40	0.192
2/6	4/6	0.46	0.42	0.12	1.00	1.31	1.34	0.989	0.88	0.77	0.987	1.07	1.60	0.013
2/6	5/6	0.47	0.41	0.12	1.00	1.26	1.28	0.983	0.89	0.79	0.980	1.05	1.51	0.020
2/6	6/6	0.47	0.41	0.12	1.00	1.09	1.10	0.808	0.91	0.82	0.799	0.92	1.29	0.201
3/6	1/6	0.25	0.54	0.21	1.00	0.63	0.61	0.015	0.85	0.72	0.012	0.45	0.88	0.988
3/6	2/6	0.21	0.51	0.28	1.00	0.99	0.99	0.495	0.89	0.78	0.471	0.79	1.24	0.529
3/6	3/6	0.28	0.51	0.21	1.00	0.87	0.86	0.128	0.90	0.82	0.117	0.72	1.05	0.883
3/6	4/6	0.24	0.51	0.25	1.00	0.91	0.90	0.187	0.92	0.83	0.174	0.76	1.08	0.826
3/6	5/6	0.21	0.53	0.26	1.00	0.91	0.90	0.172	0.92	0.86	0.160	0.78	1.06	0.840
3/6	6/6	0.26	0.53	0.21	1.00	0.85	0.84	0.036	0.93	0.87	0.034	0.74	0.98	0.966

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		α = 0.20	α = 0.05		5%	95%	
4/6	1/6	0.15	0.47	0.38	1.00	0.81	0.80	0.110	0.88	0.76	0.099	0.62	1.06	0.901
4/6	2/6	0.13	0.42	0.45	1.00	1.00	1.00	0.508	0.91	0.80	0.485	0.82	1.21	0.515
4/6	3/6	0.16	0.51	0.33	1.00	1.08	1.08	0.784	0.91	0.83	0.770	0.91	1.27	0.230
4/6	4/6	0.13	0.45	0.42	1.00	1.01	1.01	0.559	0.92	0.85	0.543	0.87	1.17	0.457
4/6	5/6	0.17	0.49	0.34	1.00	1.06	1.06	0.746	0.92	0.86	0.737	0.92	1.21	0.263
4/6	6/6	0.18	0.48	0.34	1.00	0.96	0.96	0.318	0.94	0.88	0.306	0.85	1.09	0.694
5/6	1/6	0.05	0.31	0.64	1.00	0.83	0.83	0.119	0.89	0.77	0.105	0.65	1.06	0.895
5/6	2/6	0.04	0.28	0.68	1.00	1.05	1.05	0.709	0.91	0.83	0.692	0.89	1.25	0.308
5/6	3/6	0.06	0.32	0.62	1.00	1.01	1.01	0.563	0.93	0.86	0.546	0.88	1.16	0.454
5/6	4/6	0.07	0.32	0.61	1.00	1.11	1.12	0.917	0.93	0.86	0.911	0.98	1.27	0.089
5/6	5/6	0.07	0.35	0.58	1.00	1.06	1.06	0.787	0.93	0.87	0.776	0.94	1.19	0.224
5/6	6/6	0.07	0.33	0.60	1.00	1.00	1.00	0.537	0.94	0.89	0.524	0.90	1.12	0.476
6/6	1/6	0.01	0.16	0.83	1.00	0.85	0.85	0.131	0.90	0.78	0.115	0.68	1.06	0.885
6/6	2/6	0.00	0.11	0.89	1.00	1.08	1.08	0.792	0.92	0.84	0.779	0.92	1.26	0.221
6/6	3/6	0.01	0.22	0.77	1.00	1.02	1.02	0.601	0.93	0.86	0.588	0.89	1.17	0.412
6/6	4/6	0.01	0.23	0.76	1.00	1.09	1.09	0.877	0.93	0.87	0.867	0.96	1.23	0.133
6/6	5/6	0.01	0.17	0.82	1.00	1.06	1.06	0.818	0.94	0.89	0.810	0.95	1.18	0.190
6/6	6/6	0.00	0.17	0.83	1.00	1.01	1.01	0.598	0.95	0.90	0.588	0.92	1.12	0.412

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

1168 Appendix Table 30.-Summary statistics for tests of relative reproductive success (RRS) of a H dam cross to a N dam cross from
 1169 simulations of a low stray rate (15% spawners hatchery-origin) stream with a modeled RRS of 0.875 for a HxH cross to a NxN cross
 1170 for different sampling proportions of parents (F₀) and offspring (F₁) ranging from 1/6 to 6/6. Statistics include proportion of offspring
 1171 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
 1172 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, and the RRS values that we could have
 1173 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
 1174 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, 90% confidence interval, and the one tailed p-value that RRS is <1). See
 1175 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		RRS Detectability			90% CI			p RRS < 1
						Simple	Unbiased	1-tail p	α = 0.20	α = 0.05	1-tail p	5%	95%	
1/6	1/6	0.69	0.28	0.03	0.97	0.73	0.70	0.284	0.73	0.40	0.219	0.37	1.43	0.781
1/6	2/6	0.73	0.24	0.03	0.97	1.23	1.27	0.818	0.74	0.56	0.779	0.79	1.92	0.221
1/6	3/6	0.70	0.28	0.02	0.97	1.03	1.04	0.603	0.81	0.62	0.560	0.71	1.50	0.440
1/6	4/6	0.70	0.27	0.03	0.97	0.87	0.85	0.288	0.84	0.69	0.249	0.61	1.23	0.751
1/6	5/6	0.70	0.27	0.03	0.97	0.92	0.90	0.357	0.85	0.71	0.318	0.67	1.25	0.681
1/6	6/6	0.71	0.26	0.03	0.97	0.89	0.87	0.283	0.85	0.72	0.250	0.67	1.19	0.750
2/6	1/6	0.45	0.42	0.13	0.97	0.88	0.87	0.355	0.78	0.63	0.303	0.58	1.33	0.697
2/6	2/6	0.46	0.43	0.11	0.97	0.88	0.87	0.307	0.83	0.69	0.261	0.64	1.22	0.739
2/6	3/6	0.44	0.46	0.10	0.97	1.30	1.33	0.963	0.85	0.73	0.965	1.02	1.65	0.035
2/6	4/6	0.47	0.44	0.09	0.97	1.02	1.02	0.591	0.87	0.76	0.560	0.81	1.30	0.440
2/6	5/6	0.47	0.43	0.10	0.97	1.05	1.05	0.660	0.89	0.78	0.640	0.84	1.30	0.360
2/6	6/6	0.47	0.43	0.10	0.97	1.08	1.08	0.733	0.89	0.79	0.722	0.88	1.32	0.278
3/6	1/6	0.30	0.47	0.23	0.97	0.97	0.97	0.484	0.83	0.69	0.439	0.70	1.35	0.561
3/6	2/6	0.23	0.53	0.24	0.97	1.06	1.06	0.681	0.88	0.77	0.657	0.84	1.35	0.343
3/6	3/6	0.24	0.52	0.24	0.97	0.95	0.95	0.347	0.91	0.81	0.326	0.78	1.15	0.674
3/6	4/6	0.28	0.51	0.21	0.97	1.01	1.01	0.550	0.90	0.81	0.527	0.83	1.22	0.473
3/6	5/6	0.28	0.50	0.22	0.97	1.02	1.02	0.602	0.90	0.82	0.579	0.85	1.22	0.421
3/6	6/6	0.29	0.50	0.21	0.97	1.01	1.01	0.562	0.91	0.83	0.546	0.86	1.20	0.454

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		α = 0.20	α = 0.05		5%	95%	
4/6	1/6	0.14	0.46	0.40	0.97	0.90	0.89	0.314	0.84	0.72	0.280	0.66	1.22	0.720
4/6	2/6	0.14	0.48	0.38	0.97	0.88	0.87	0.196	0.89	0.79	0.178	0.69	1.11	0.822
4/6	3/6	0.14	0.47	0.39	0.97	1.03	1.03	0.632	0.90	0.81	0.611	0.86	1.24	0.389
4/6	4/6	0.14	0.48	0.38	0.97	0.89	0.89	0.168	0.91	0.83	0.151	0.74	1.07	0.849
4/6	5/6	0.14	0.48	0.38	0.97	0.95	0.95	0.299	0.92	0.85	0.282	0.81	1.11	0.718
4/6	6/6	0.15	0.47	0.38	0.97	0.94	0.93	0.248	0.93	0.85	0.228	0.81	1.08	0.772
5/6	1/6	0.07	0.40	0.53	0.97	1.03	1.03	0.602	0.87	0.73	0.562	0.78	1.35	0.438
5/6	2/6	0.05	0.35	0.60	0.97	0.89	0.89	0.213	0.89	0.80	0.195	0.72	1.11	0.805
5/6	3/6	0.07	0.37	0.56	0.97	0.99	0.99	0.499	0.91	0.83	0.477	0.84	1.18	0.523
5/6	4/6	0.06	0.39	0.55	0.97	0.90	0.90	0.167	0.92	0.84	0.155	0.77	1.06	0.845
5/6	5/6	0.06	0.38	0.56	0.97	0.91	0.91	0.164	0.93	0.86	0.152	0.79	1.06	0.848
5/6	6/6	0.05	0.36	0.59	0.97	0.93	0.93	0.217	0.93	0.87	0.203	0.82	1.07	0.797
6/6	1/6	0.01	0.20	0.79	0.97	1.02	1.02	0.575	0.87	0.76	0.539	0.79	1.30	0.461
6/6	2/6	0.00	0.18	0.82	0.97	0.99	0.99	0.498	0.90	0.82	0.475	0.82	1.20	0.525
6/6	3/6	0.00	0.19	0.81	0.97	1.07	1.07	0.769	0.92	0.85	0.757	0.91	1.25	0.243
6/6	4/6	0.02	0.18	0.80	0.97	1.02	1.02	0.612	0.93	0.85	0.594	0.88	1.18	0.406
6/6	5/6	0.00	0.12	0.88	0.97	1.04	1.04	0.718	0.93	0.87	0.705	0.92	1.19	0.295
6/6	6/6	0.01	0.19	0.80	0.97	1.03	1.03	0.670	0.94	0.87	0.658	0.91	1.17	0.342

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

1176 Appendix Table 31.-Summary statistics for tests of relative reproductive success (RRS) of a H sire cross to a N sire cross from
 1177 simulations of a high stray rate (50% spawners hatchery-origin) stream with a modeled RRS of 0.875 for a HxH cross to a NxN cross
 1178 for different sampling proportions of parents (F₀) and offspring (F₁) ranging from 1/6 to 6/6. Statistics include proportion of offspring
 1179 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
 1180 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, and the RRS values that we could have
 1181 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
 1182 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, 90% confidence interval, and the one tailed p-value that RRS is <1). See
 1183 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	Estimated			RRS Detectability			90% CI			p RRS < 1
					True	Simple	Unbiased	1-tail p	α = 0.20	α = 0.05	1-tail p	5%	95%	
1/6	1/6	0.70	0.27	0.03	0.88	0.43	0.35	0.019	0.76	0.59	0.014	0.23	0.81	0.986
1/6	2/6	0.60	0.32	0.08	0.88	0.73	0.64	0.067	0.86	0.73	0.055	0.52	1.01	0.945
1/6	3/6	0.65	0.32	0.03	0.88	0.76	0.72	0.083	0.84	0.73	0.070	0.55	1.03	0.930
1/6	4/6	0.67	0.29	0.04	0.88	1.03	1.04	0.604	0.87	0.75	0.576	0.80	1.33	0.424
1/6	5/6	0.68	0.29	0.03	0.88	0.90	0.88	0.266	0.88	0.75	0.247	0.69	1.17	0.753
1/6	6/6	0.66	0.31	0.03	0.88	0.90	0.88	0.225	0.90	0.80	0.208	0.72	1.12	0.792
2/6	1/6	0.39	0.44	0.17	0.88	0.91	0.91	0.362	0.83	0.68	0.325	0.65	1.27	0.675
2/6	2/6	0.43	0.42	0.15	0.88	0.81	0.81	0.101	0.88	0.77	0.088	0.63	1.05	0.912
2/6	3/6	0.44	0.42	0.14	0.88	0.81	0.80	0.050	0.90	0.82	0.043	0.66	0.99	0.957
2/6	4/6	0.46	0.42	0.12	0.88	0.87	0.86	0.123	0.91	0.82	0.112	0.71	1.05	0.888
2/6	5/6	0.47	0.41	0.12	0.88	0.86	0.86	0.093	0.92	0.83	0.086	0.72	1.03	0.914
2/6	6/6	0.47	0.41	0.12	0.88	0.84	0.83	0.035	0.92	0.85	0.033	0.71	0.98	0.967
3/6	1/6	0.25	0.54	0.21	0.88	0.77	0.76	0.090	0.88	0.74	0.076	0.57	1.04	0.924
3/6	2/6	0.21	0.51	0.28	0.88	0.76	0.75	0.018	0.91	0.81	0.016	0.62	0.94	0.984
3/6	3/6	0.28	0.51	0.21	0.88	0.82	0.81	0.032	0.92	0.85	0.028	0.69	0.97	0.972
3/6	4/6	0.24	0.51	0.25	0.88	0.86	0.86	0.060	0.93	0.86	0.054	0.74	1.00	0.946
3/6	5/6	0.21	0.53	0.26	0.88	0.90	0.90	0.120	0.93	0.87	0.110	0.79	1.03	0.890
3/6	6/6	0.26	0.53	0.21	0.88	0.84	0.84	0.015	0.94	0.88	0.013	0.74	0.96	0.987

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		α = 0.20	α = 0.05		5%	95%	
4/6	1/6	0.15	0.47	0.38	0.88	0.87	0.86	0.207	0.87	0.75	0.185	0.67	1.13	0.815
4/6	2/6	0.13	0.42	0.45	0.88	0.76	0.76	0.008	0.91	0.84	0.007	0.63	0.91	0.993
4/6	3/6	0.16	0.51	0.33	0.88	0.87	0.87	0.089	0.92	0.85	0.082	0.75	1.02	0.918
4/6	4/6	0.13	0.45	0.42	0.88	0.89	0.89	0.087	0.94	0.87	0.081	0.78	1.02	0.919
4/6	5/6	0.17	0.49	0.34	0.88	0.91	0.91	0.111	0.94	0.88	0.103	0.80	1.03	0.897
4/6	6/6	0.18	0.48	0.34	0.88	0.87	0.87	0.026	0.95	0.89	0.024	0.77	0.98	0.976
5/6	1/6	0.05	0.31	0.64	0.88	0.87	0.87	0.180	0.89	0.78	0.162	0.69	1.10	0.838
5/6	2/6	0.04	0.28	0.68	0.88	0.75	0.74	0.002	0.93	0.85	0.002	0.63	0.88	0.998
5/6	3/6	0.06	0.32	0.62	0.88	0.82	0.82	0.012	0.93	0.87	0.011	0.72	0.95	0.989
5/6	4/6	0.07	0.32	0.61	0.88	0.88	0.88	0.058	0.94	0.88	0.052	0.78	1.00	0.948
5/6	5/6	0.07	0.35	0.58	0.88	0.88	0.88	0.042	0.94	0.89	0.039	0.79	0.99	0.961
5/6	6/6	0.07	0.33	0.60	0.88	0.89	0.89	0.032	0.95	0.90	0.029	0.80	0.98	0.971
6/6	1/6	0.01	0.16	0.83	0.88	0.89	0.89	0.204	0.89	0.79	0.189	0.71	1.11	0.811
6/6	2/6	0.00	0.11	0.89	0.88	0.76	0.76	0.002	0.93	0.87	0.001	0.65	0.88	0.999
6/6	3/6	0.01	0.22	0.77	0.88	0.84	0.84	0.012	0.94	0.88	0.011	0.74	0.95	0.989
6/6	4/6	0.01	0.23	0.76	0.88	0.89	0.89	0.059	0.94	0.89	0.055	0.79	1.00	0.945
6/6	5/6	0.01	0.17	0.82	0.88	0.91	0.91	0.068	0.95	0.90	0.065	0.82	1.01	0.935
6/6	6/6	0.00	0.17	0.83	0.88	0.88	0.88	0.017	0.95	0.91	0.015	0.80	0.97	0.985

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.

1184 Appendix Table 32.-Summary statistics for tests of relative reproductive success (RRS) of a H sire cross to a N sire cross from
 1185 simulations of a low stray rate (15% spawners hatchery-origin) stream with a modeled RRS of 0.875 for a HxH cross to a NxN cross
 1186 for different sampling proportions of parents (F₀) and offspring (F₁) ranging from 1/6 to 6/6. Statistics include proportion of offspring
 1187 assigned to zero, only one and two parents, true and estimated RRS (both simple and unbiased), results from a non-parametric
 1188 permutation test to determine if RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, and the RRS values that we could have
 1189 detected with 80% and 95% probability), and results from a parametric negative binomial general linear model (GLM) to determine if
 1190 RRS is significantly < 1 (one tailed p-value that RRS is ≤ 1, 90% confidence interval, and the one tailed p-value that RRS is < 1). See
 1191 text for details. NAs denote simulations were tests could not be performed due to low sample size.

Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	Estimated			RRS Detectability			90% CI			p RRS < 1
					True	Simple	Unbiased	1-tail p	α = 0.20	α = 0.05	1-tail p	5%	95%	
1/6	1/6	0.69	0.28	0.03	0.92	0.54	0.53	0.108	0.75	0.44	0.084	0.26	1.13	0.916
1/6	2/6	0.73	0.24	0.03	0.92	0.50	0.47	0.038	0.75	0.56	0.032	0.27	0.92	0.968
1/6	3/6	0.70	0.28	0.02	0.92	0.59	0.57	0.038	0.78	0.62	0.031	0.37	0.94	0.969
1/6	4/6	0.70	0.27	0.03	0.92	0.53	0.51	0.014	0.81	0.64	0.010	0.34	0.83	0.990
1/6	5/6	0.70	0.27	0.03	0.92	0.69	0.67	0.073	0.81	0.67	0.055	0.47	1.01	0.945
1/6	6/6	0.71	0.26	0.03	0.92	0.66	0.64	0.042	0.81	0.68	0.030	0.46	0.95	0.970
2/6	1/6	0.45	0.42	0.13	0.92	1.01	1.01	0.578	0.81	0.66	0.522	0.70	1.47	0.478
2/6	2/6	0.46	0.43	0.11	0.92	0.95	0.95	0.441	0.84	0.69	0.403	0.69	1.31	0.597
2/6	3/6	0.44	0.46	0.10	0.92	1.05	1.05	0.650	0.85	0.74	0.619	0.80	1.39	0.381
2/6	4/6	0.47	0.44	0.09	0.92	0.90	0.89	0.254	0.88	0.77	0.231	0.70	1.15	0.769
2/6	5/6	0.47	0.43	0.10	0.92	1.02	1.02	0.594	0.88	0.78	0.570	0.82	1.28	0.430
2/6	6/6	0.47	0.43	0.10	0.92	0.95	0.94	0.352	0.89	0.81	0.327	0.77	1.16	0.673
3/6	1/6	0.30	0.47	0.23	0.92	1.02	1.02	0.585	0.83	0.68	0.540	0.74	1.41	0.460
3/6	2/6	0.23	0.53	0.24	0.92	0.94	0.94	0.383	0.88	0.76	0.354	0.73	1.22	0.646
3/6	3/6	0.24	0.52	0.24	0.92	1.01	1.01	0.560	0.89	0.79	0.537	0.82	1.25	0.463
3/6	4/6	0.28	0.51	0.21	0.92	0.93	0.93	0.301	0.89	0.80	0.281	0.76	1.14	0.719
3/6	5/6	0.28	0.50	0.22	0.92	0.97	0.97	0.433	0.90	0.82	0.411	0.81	1.17	0.589
3/6	6/6	0.29	0.50	0.21	0.92	0.95	0.95	0.342	0.91	0.83	0.321	0.80	1.13	0.679

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Sampling Proportion		Proportion of Offspring Assigned			RRS			Permutation Test			Negative Binomial GLM			
F ₀	F ₁	Unassigned	1 Parent	2 Parents	True	Estimated		1-tail p	RRS Detectability		1-tail p	90% CI		p RRS < 1
						Simple	Unbiased		$\alpha = 0.20$	$\alpha = 0.05$		5%	95%	
4/6	1/6	0.14	0.46	0.40	0.92	0.84	0.84	0.197	0.86	0.74	0.172	0.62	1.14	0.828
4/6	2/6	0.14	0.48	0.38	0.92	0.83	0.83	0.116	0.89	0.78	0.105	0.66	1.06	0.895
4/6	3/6	0.14	0.47	0.39	0.92	0.97	0.97	0.436	0.91	0.82	0.410	0.81	1.17	0.590
4/6	4/6	0.14	0.48	0.38	0.92	0.92	0.92	0.227	0.91	0.83	0.214	0.77	1.10	0.786
4/6	5/6	0.14	0.48	0.38	0.92	0.95	0.95	0.305	0.92	0.84	0.289	0.81	1.11	0.711
4/6	6/6	0.15	0.47	0.38	0.92	0.91	0.91	0.167	0.93	0.86	0.156	0.78	1.06	0.844
5/6	1/6	0.07	0.40	0.53	0.92	1.06	1.06	0.668	0.85	0.74	0.638	0.82	1.37	0.362
5/6	2/6	0.05	0.35	0.60	0.92	0.85	0.85	0.101	0.90	0.81	0.093	0.69	1.04	0.907
5/6	3/6	0.07	0.37	0.56	0.92	0.89	0.89	0.138	0.92	0.83	0.131	0.74	1.06	0.869
5/6	4/6	0.06	0.39	0.55	0.92	0.86	0.85	0.062	0.92	0.85	0.057	0.73	1.01	0.943
5/6	5/6	0.06	0.38	0.56	0.92	0.90	0.90	0.131	0.93	0.86	0.122	0.78	1.04	0.878
5/6	6/6	0.05	0.36	0.59	0.92	0.89	0.89	0.080	0.93	0.87	0.073	0.78	1.02	0.927
6/6	1/6	0.01	0.20	0.79	0.92	0.97	0.97	0.464	0.88	0.76	0.429	0.76	1.24	0.571
6/6	2/6	0.00	0.18	0.82	0.92	0.87	0.87	0.126	0.91	0.82	0.118	0.72	1.06	0.882
6/6	3/6	0.00	0.19	0.81	0.92	0.97	0.97	0.400	0.92	0.85	0.381	0.83	1.13	0.619
6/6	4/6	0.02	0.18	0.80	0.92	0.90	0.90	0.130	0.93	0.86	0.122	0.78	1.04	0.878
6/6	5/6	0.00	0.12	0.88	0.92	0.97	0.97	0.379	0.93	0.87	0.364	0.85	1.11	0.636
6/6	6/6	0.01	0.19	0.80	0.92	0.94	0.94	0.222	0.94	0.88	0.206	0.83	1.06	0.794

Note: F₀ parental and F₁ offspring were generated and sampled once for a given stray rate and effect size.