**Supplemental Methods**

*Genetic Parentage Analysis*

Consistent with the approach used in other evaluations of spring Chinook salmon reintroductions above Upper Willamette tributaries (Banks *et al.* 2013; Banks *et al.* 2016; Banks *et al.* 2014; Evans *et al.* 2019; Evans *et al.* 2016; O’Malley *et al.* 2014; O’Malley *et al.* 2015; Sard *et al.* 2016b; Sard *et al.* 2015), we used COLONY alongside CERVUS to generate a consensus pedigree for analyses. The consensus pedigree approach allows incorporation of multiple sources of information, providing greater confidence in parent-offspring relationships (Walling *et al.* 2010). We chose to use COLONY alongside CERVUS, because CERVUS requires an accurate estimate of the proportion of sampled parents, and previous work has indicated the presence of adfluvial and precocial spawners above the dam (Sard *et al.* 2016a). Furthermore, simulation studies have suggested that parent-offspring relationships identified by COLONY are the most accurate among three pedigree reconstruction methods in frequent use (Harrison *et al.* 2013).

When inferring pedigrees, we attempted to follow the approach of previously published evaluations for the McKenzie River reintroduction as closely as possible. We first made parent(s)-offspring assignments in CERVUS Version 3.07. For each offspring, we first removed impossible parentages. For example, if one parent of a parent-offspring trio was collected as a carcass sample, the recovery date must be after the release date of the other parent. Assignments were then made using a strict 95% confidence criterion, a minimum of seven loci, an assumed parent sampling rate of 95%, and a maximum of one mismatch between parent-offspring pairs (maximum of two mismatches for parent-offspring trios). We then assigned parentage using the combined PLS-FL algorithm implemented in COLONY Version 2.0.6.8 (Jones & Wang 2010). COLONY was run using the following parameters: medium run length, polygamous male and female setting, weak sibship prior of 1, allele dropout and miscalled allele rate prior of 2% per locus, and an assumed 95% rate of sampled parents. We also filtered the raw COLONY pedigree to remove impossible parentages, parent-offspring duos with more than one mismatch, and parent-offspring trios with greater than two mismatches.

To infer the consensus pedigree used for all downstream analyses we combined the results of the CERVUS and COLONY pedigrees. Briefly, for each offspring, disagreements in assignments between CERVUS and COLONY were settled using number of mismatches. Additionally, parent-offspring trio assignments were given precedence over parent-offspring duo assignments, given the smaller non-exclusion probabilities of parent-offspring trios relative to parent-offspring duos (Supplemental Table 1). In the case of ties, assignments made by COLONY were given precedence.

*GLMMimmigrant*

We used a generalized linear mixed model to investigate the relationship between the probability that an NOR salmon collected at the Cougar Trap was produced above the dam or was an NOR immigrant and two fixed predictors (*sex* and *Julian day of sampling* at the Cougar Trap), and their interaction. We fit the model with the binomial distribution using the *glmmTMB* function from the *glmmTMB* package in *R*. To identify the optimal random effects structure we fit the model with a fully saturated fixed effects structure using restricted maximum likelihood and varying the random effects, to include no random effects, a random intercept for *year*, or a random intercept for *year* and a random slope for *Julian day of sampling*. Model selection of random effects was by AIC. After refitting the fully saturated fixed effects model with the final random effects structure using maximum likelihood, we conducted model selection for fixed effects based on both likelihood ratio tests for each predictor and backward stepwise selection using Wald tests for significant effects of each predictor. After a final model was selected (hereafter GLMMimmigrant), we conducted model validation by testing for goodness of fit, overdispersion, and influence of outliers using residuals simulated by the *DHARMa* package in *R*. Effect plots of significant predictors in the GLMMTLF were generated using the *effects* package in *R* and conditioned on the typical values of all other significant predictors in the final model.

*Predictors of Fitness*

We fit a generalized linear mixed model (GLMM) to identify significant predictors of candidate parent TLF from 2007 – 2015 (hereafter GLMMTLF). Our modeling approach primarily followed the recommendations of Zuur et al. (2009) and Bolker (2015). We conducted an exploratory data analysis to identify the distribution and link function that provided the best fit to the data, calculated variance inflation factors of main effects to examine the data for multicollinearity and determined if non-linear effects of *release day,* *release group density,* *release group sex ratio,* or *annual sex ratio* improved the fit to the data. Model fit under different distributions was evaluated using AIC, BIC, rootograms and QQ-plots of randomized quantile residuals from the *COUNTREG* package in *R*, and simulated residuals produced by the *DHARMa* package in R. ﻿To examine collinearity between categorical and continuous predictors we used the general variance inflation factor (Fox & Monette 1992)(GVIF^(1/(2\*Df)), and a conservative cutoff of 2.0. Non-linear effects were evaluated by fitting fully each potentially non-linear predictor as a second order polynomial and comparing to a null (linear) model using AIC, BIC, and likelihood ratio tests.

After exploratory data analysis, we fit our models using the negative binomial distribution and a log link function using the *glmmTMB* function from the *glmmTMB* package in *R*. For model selection, we first identified the best random effects structure by fitting a fully saturated fixed effect model using restricted maximum likelihood and varying the random effects. Model selection of random effects was by AIC. After refitting the fully saturated fixed effects model with the final random effects structure using maximum likelihood, we conducted model selection for fixed effects based on both likelihood ratio tests for each predictor and backward stepwise selection using Wald tests for significant effects of each predictor. When the two model selection criteria disagreed, we chose to be conservative and only retained predictors selected by both approaches. After a final model was selected (hereafter GLMMTLF), we conducted model validation by testing for goodness of fit, overdispersion, and influence of outliers using residuals simulated by the *DHARMa* package in *R*. Effect plots of significant predictors in the GLMMTLF were generated using the *effects* package in *R* and conditioned on the typical values of all other significant predictors in the final model.

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