Supplementary Material

1   Supplementary Figures and Tables

Table S1. Estimated census population sizes at each of the four outplant sites. Estimates were made using linear regression between observed and predicted counts from 2011-2017, and then plugging the observed value from the genetic sampling into the resulting equation. Predicted counts were based on the population model reported in Carson et al. (2019). Three different estimates were made; one with all the information from winter surveys from all sites, one with data only from relevant sites (Omaha, Gold, and Baytown – Dragoon is younger than the model), and one for Omaha and Gold, respectively, since these sites were the oldest and had sufficient data to make site-specific estimates..

Observed	Estimated	Detection Assumption	Source	Fit
Omaha				
96	280.1	34%	all sites	$r^2 = 0.32$
96	287.5	33%	relevant sites	$r^2 = 0.46$
96	301.1	32%	Omaha only	$r^2 = 0.72$
Gold				
37	166.8	22%	all sites	$r^2 = 0.32$
37	148.1	25%	relevant sites	$r^2 = 0.46$
37	147.2	25%	Gold only	$r^2 = 0.67$
Baytown				
72	234.0	31%	all sites	$r^2 = 0.32$
72	230.8	31%	relevant sites	$r^2 = 0.46$
Dragoon				
73	235.9	31%	all sites	$r^2 = 0.32$
73	233.2	31%	relevant sites	$r^2 = 0.46$

Table S2. Full output of NeEstimator with N_e estimates for a range of allele frequencies.

| Population	Sample Size	Allele frequency	Ne	Parametric CI		Jackknife CI	
				Low	High	Low	High
Baytown H	36	0.05	19.9	19.9	20	12.8	33.1
		0.02	24.4	24.4	24.4	17.9	34.9
		0.01	40.4	40.4	40.4	28.2	63.9
Dragoon H	36	0.05	12.2	12.2	12.2	7.6	19.3
		0.02	16.9	16.9	17	12.8	22.8
		0.01	26.2	26.2	26.2	18.5	39.5
Gold H	36	0.05	12.6	12.6	12.7	8.4	19
		0.02	18	18	18.1	12.9	26.1
		0.01	27.9	27.9	27.9	18.8	45.4
Omaha H	36	0.05	15.6	15.5	15.6	10.7	23
		0.02	21.5	21.5	21.5	16	29.8
		0.01	35	34.9	35	25.3	51.9
Progeny '17-'20	36	0.05	43.1	43	43.2	27.8	79
		0.02	53.3	53.3	53.4	40.1	76
		0.01	99.9	99.7	100.1	71.3	159.1
Broodstock W	36	0.05	3927.2	3402.7	4641.8	2126.4	25030.4
		0.02	3186	2984.3	3417	1638	52447.2
		0.01	-5099.9	Infinite	Infinite	18175.4	Infinite
San Juan W	36	0.05	-28706.9	271144.8	Infinite	24515.9	Infinite
		0.02	-31366.9	Infinite	Infinite	53211.4	Infinite
		0.01	-1590.3	Infinite	Infinite	Infinite	Infinite
Ketchikan W	36	0.05	1009.9	970.1	1053.1	376.2	Infinite
		0.02	997.9	976.1	1020.6	377.8	Infinite
		0.01	2306.5	2220.4	2399.6	449	Infinite
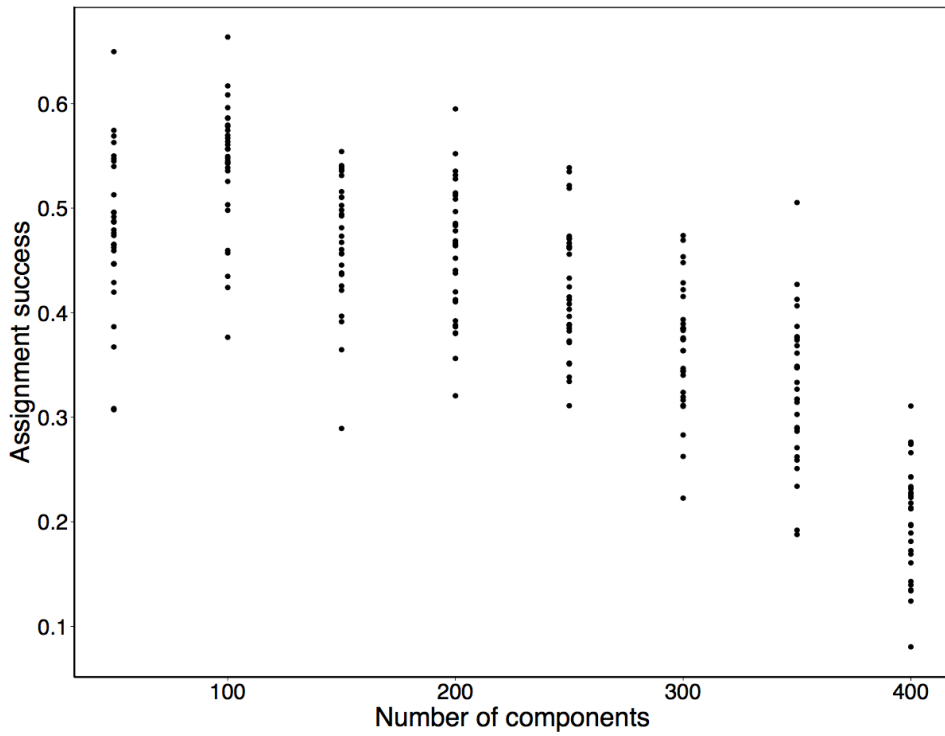
Figure S1. Results of cross validation for the discriminant analysis of principal components (DAPC), testing successful assignment of individuals to their respective groups as a function of the number of principal components used.
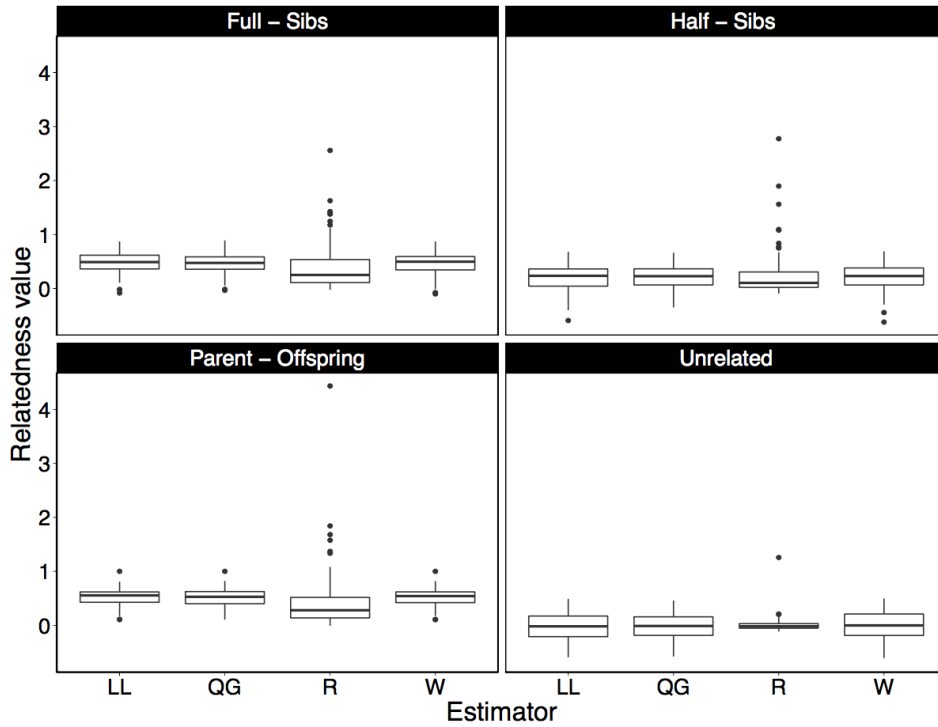
Figure S2. Boxplots of relatedness values of each relatedness estimator based on relationships simulated from the *H. kamtschatkana* SNP dataset. Abbreviations for each estimator are: LL = Lynch-Li, QG = Queller & Goodnight, R = Ritland, W = Wang.
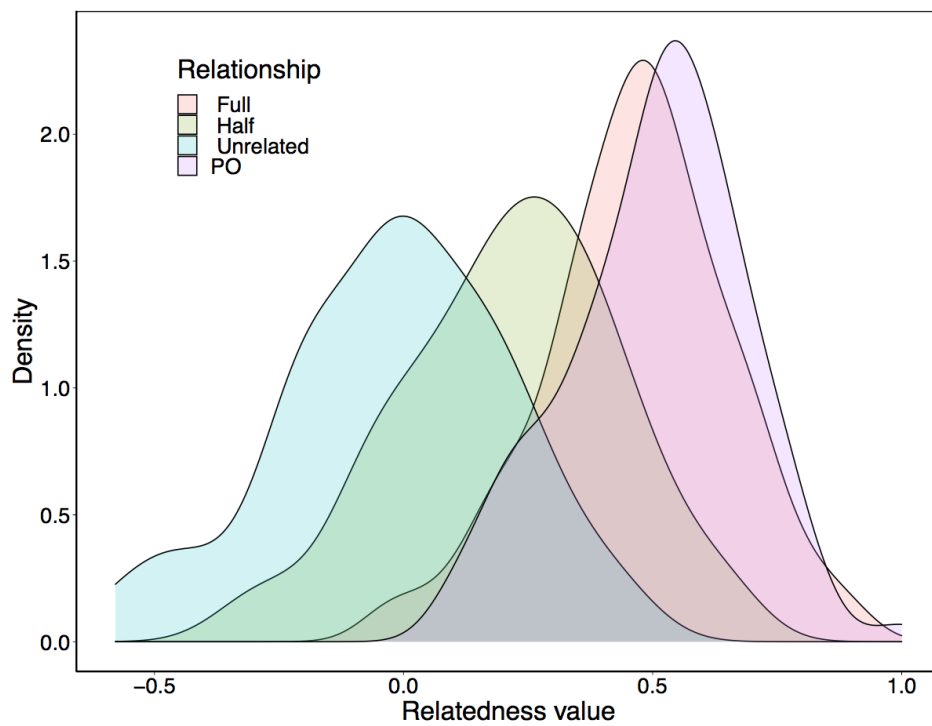
Figure S3. Density plot showing distribution of Queller & Goodnight relatedness values for each simulated relationship (full sibling, half sibling, unrelated, parent-offspring).