

Text S1: Development of Single-Nucleotide Polymorphism Assay for Sex Identification

We designed and tested a single-nucleotide polymorphism (SNP) assay for sex identification in Pacific walrus. A putative sex-linked SNP (R083252_FXY – Table S1) was discovered using RADseq as described by Cook et al. (2020) to genotype 96 adult walruses (48 adult males and 48 putative adult females from Cape Seniavin and Point Lay, Alaska, respectively). We specifically selected adult animals from Cape Seniavin because the haulout was exclusively comprised of adult males. In contrast, Point Lay is overwhelmingly comprised of adult females and juveniles of both sexes with occasional adult males. The SNP genotypes at this locus correlated with sex for all but three putative females. To facilitate high-throughput genotyping, we used the ThermoFisher Scientific Custom TaqMan™ Assay Design Tool to develop a Custom TaqMan™ Genotyping Assay for this SNP (Oro_XY_R083252 – Table S1). A three-step procedure was then used to evaluate this assay for sex identification.

First, we used the Oro_XY_R083252 assay to infer sex in the 96 adults described above and compared these results to sex as assigned from the RADseq data for the same individuals. The SNP assay was run on a ThermoFisher Scientific QuantStudio™ 12K Flex System using cycling conditions as follows: Pre-Read Stage - 60°C for 30s, Hold Stage - 95°C for 10 min, PCR Stage – 40 cycles of 95°C for 15s, 60°C for 1 min, followed by Post Read Stage - 60°C for 30s. PCR reactions were conducted in 10 µl volumes using 2 µL of 50 ng/µL template DNA, 5 µL Applied Biosystems™ TaqMan™ Genotyping Master Mix, 0.5 µL Custom TaqMan™ SNP Genotyping Assay, non-human (20x), and deionized H₂O. We found no discrepancies in sex classification between Oro_XY_R083252 and the sequence data from R083252_FXY.

Second, we assayed the same 96 adults using the sex-determining primer ORXY (Fischbach et al. 2008). We used ORXY because it has been previously demonstrated to be 100% accurate for sex determination (Fischbach et al. 2008). We amplified ORXY using PCR and visualized the amplicons with an Applied Biosystems 3730x/ DNA Analyzer. We used PCR cycling (Applied Biosystems Veriti 96-Well Thermal Cycler) profiles as described in Fischbach et al. (2008). PCR reactions were conducted with 10 µL volumes using 2 µL of 50 ng/µL template DNA, 0.5 uM of each forward and reverse primer, 1.0 U Taq DNA Polymerase (NovaTaq DNA Polymerase), 1.0 mM dNTPs, 0.8 mM MgCl₂, 1X PCR buffer and deionized H₂O. Applied Biosystems GeneScan 600 LIZ size standard v2.0 was loaded into each well to ensure consistency of allele scores. We used Applied Biosystems GeneMapper Software 6.0 to

estimate sizes and score fragments. All scores were verified manually. We found no discrepancies in sex assignments between ORXY and Oro_XY_R083252 for 96 adults.

Finally, we analyzed an additional 860 walrus samples with Oro_XY_R083252 and ORXY using the conditions described above. These samples included 125 additional individuals from Cape Seniavin and Point Lay, Alaska and 735 individuals from Beatty et al. (2020) for which we had ample DNA. To test samples with a relatively even distribution of males and females, the latter 735 samples included 452 individuals with estimated ages from 0 (i.e., calf) to 3 years. Results for both markers were identical for all 860 samples.

We discovered a potential single base error in the sequence R083252_FXY after completing the evaluation (Table S1). Therefore, we used the method described above to develop a new Custom TaqMan SNP Genotyping Assay (Oro_XY_R083252_v2, Table S1). We used Oro_XY_R083252_v2 to assay 221 samples from Cape Seniavin and Point Lay, Alaska as well as 126 samples previously analyzed from Beatty et al. (2020). The sex ID results from Oro_XY_R083252 and Oro_XY_R083252_v2 were identical for all 347 individuals. Therefore, we concluded that the putative single base error in the sequence did not influence the accuracy of the Oro_XY_R083252 assay.

Text S2: True Abundance for Study Duration Evaluation

We calculated juvenile and adult female true abundance for the simulations that evaluated the efficacy of a three or five-year study. For all simulations, we set the number of captures in the first year equal to the mean number of first captures + recaptures for all five years in the empirical dataset, which equaled 168 calves (93 females, 75 males), 660 juveniles (389 females, 271 males), 711 adult females, and 113 adult males. We then calculated true abundance of juveniles with the simple formula:

$$N_{J(F)}^{True} = \frac{389}{\rho_J}$$

$$N_{J(M)}^{True} = \frac{271}{\rho_J}$$

where ρ_J is the posterior mean from the model, which was considered true juvenile recapture probability and first capture probability (i.e., probability of capture) for the purposes of the simulations. We calculated N_F^{True} and N_M^{True} for adults with a similar approach. True age-

specific population sizes remained constant for all sampling occasions because we assumed a constant population size and stable age distribution. We now describe the approach used to calculate the number of first captures and recaptures for each state on each occasion. We calculated the number of juvenile females and adult females alive and available for recapture on the second occasion as:

$$\kappa_{2,J(F)} = 93\phi_C + 389\phi_J(1 - \psi)$$

$$\kappa_{2,J(M)} = 75\phi_C + 271\phi_J(1 - \psi)$$

$$\kappa_{2,F} = 389\phi_J\psi + 711\phi_F$$

$$\kappa_{2,M} = 271\phi_J\psi + 113\phi_F$$

We calculated the expected number of recaptures on the second occasion as:

$$n_{2,J(F)}^{recap} = \kappa_{2,J(F)}\rho_J$$

$$n_{2,J(M)}^{recap} = \kappa_{2,J(M)}\rho_J$$

$$n_{2,F}^{recap} = \kappa_{2,F}\rho_F$$

$$n_{2,M}^{recap} = \kappa_{2,M}\rho_M$$

The number of initial captures for calves remained the same throughout the simulation (168) because we assumed a constant population size, a stable age structure, and a constant capture probability. We calculated the expected number of first captures on the second occasion (n_2) as a function of expected number of recaptures on the second occasion (κ_2), true population size (N^{True}), and capture rate (ρ). For the remaining age classes, the expected number of first captures on the second occasion was:

$$n_{2,J(F)}^{first} = (N_{J(F)}^{True} - \kappa_{2,J(F)})\rho_J$$

$$n_{2,J(M)}^{first} = (N_{J(M)}^{True} - \kappa_{2,J(M)})\rho_J$$

$$n_{2,F}^{first} = (N_F^{True} - \kappa_{2,F})\rho_F$$

$$n_{2,M}^{first} = (N_M^{True} - \kappa_{2,M})\rho_M$$

We calculated the number of animals alive and available for recapture on the third occasion:

$$\kappa_{3,J(F)} = 93\phi_C + (\kappa_{2,J(F)} + n_{2,J(F)}^{first})\phi_J(1 - \psi)$$

$$\kappa_{3,J(M)} = 75\phi_C + (\kappa_{2,J(M)} + n_{2,J(M)}^{first})\phi_J(1 - \psi)$$

$$\kappa_{3,F} = (\kappa_{2,J(F)} + n_{2,J(F)}^{first})\phi_J\psi + (\kappa_{2,F} + n_{2,F}^{first})\phi_F$$

$$\kappa_{3,M} = (\kappa_{2,J(M)} + n_{2,J(M)}^{first})\phi_J\psi + (\kappa_{2,M} + n_{2,M}^{first})\phi_M$$

We calculated all remaining quantities for the third, fourth and fifth sampling occasions similarly, but we replaced all values that varied with sampling occasion appropriately. Thus, the number of first captures (females/males) in each sampling occasion for all simulations were:

	Occasion 1	Occasion 2	Occasion 3	Occasion 4	Occasion 5
Calves	93 / 75	93 / 75	93 / 75	93 / 75	93 / 75
Juveniles	389 / 271	386 / 269	385 / 268	384 / 268	384 / 267
Adults	711 / 113	703 / 112	697 / 112	691 / 111	685 / 111

Any use of trade, firm, or product names is for descriptive purposes only and does not imply endorsement by the U.S. Government.

Table S1. Custom genotyping assays for sex identification in Pacific walrus (*Odobenus rosmarus divergens*).

SNP Assay Name	SNP	Primers (5'-3')	Reporter 1 (VIC/NFQ)	Context Sequence
			Reporter 2 (FAM/NFQ)	
Oro_XY_R083252	A/T	F: GGATCTCCAGGCCTCCAGAA	1: CGGCAGAGACAGCTG	TCCAGGCCTCCAGAACGCGGCAGAG[A/T]CAGCTGAACGAGGAGATCTGCACCC
Oro_XY_R083252	A/T	R: GGGTGCAGATCTCCTCGTT	2: CGGCAGAGTCAGCTG	
Oro_XY_R083252_v2	A/G	F: GATCTCCAGGCCTCCAGAAC	1: TTCAGCTGTCTCTGCCG	TCCAGGCCTCCAGAACGCGGCAGAG[A/G]CAGCTGAACGAGGAGATCTGCACCC
Oro_XY_R083252_v2	A/G	R: ACGCAGGGTGCAGATCTC	2: AGCTGCCTCTGCCG	

Table S2. Parameter definitions for the Pacific walrus multievent mark-recapture model.

Parameter	Definition
ρ_J	Probability a juvenile was recaptured in a sampling occasion
ρ_F	Probability an adult female was recaptured in a sampling occasion
ρ_M	Probability an adult male was recaptured in a sampling occasion
θ_{C1}	Probability a calf was enumerated exactly once in a sampling occasion, given it was captured in that sampling occasion
θ_{C2}	Probability a calf was enumerated exactly twice in a sampling occasion, given it was captured in that sampling occasion
θ_{C3}	Probability a calf was enumerated at least thrice in a sampling occasion, given it was captured in that sampling occasion
θ_{J1}	Probability a juvenile was enumerated exactly once in a sampling occasion, given it was (re)captured in that sampling occasion
θ_{J2}	Probability a juvenile was enumerated exactly twice in a sampling occasion, given it was (re)captured in that sampling occasion
θ_{J3}	Probability a juvenile was enumerated at least thrice in a sampling occasion, given it was (re)captured in that sampling occasion
θ_{F1}	Probability an adult female was enumerated exactly once in a sampling occasion, given it was (re)captured in that sampling occasion
θ_{F2}	Probability an adult female was enumerated exactly twice in a sampling occasion, given it was (re)captured in that sampling occasion
θ_{F3}	Probability an adult female was enumerated at least thrice in a sampling occasion, given it was (re)captured in that sampling occasion
θ_{M1}	Probability an adult male was enumerated exactly once in a sampling occasion, given it was (re)captured in that sampling occasion
θ_{M2}	Probability an adult male was enumerated exactly twice in a sampling occasion, given it was (re)captured in that sampling occasion
θ_{M3}	Probability an adult male was enumerated at least thrice in a sampling occasion, given it was (re)captured in that sampling occasion
ϕ_C	Annual calf survival
ϕ_J	Annual juvenile survival
ϕ_F	Annual adult female survival
ϕ_M	Annual adult male survival
$\delta_{C C}$	Probability an enumerated animal was assigned calf given it was a calf
$\delta_{J C}$	Probability an enumerated animal was assigned juvenile given it was a calf
$\delta_{A C}$	Probability an enumerated animal was assigned adult given it was a calf
$\delta_{C J}$	Probability an enumerated animal was assigned calf given it was a juvenile
$\delta_{J J}$	Probability an enumerated animal was assigned juvenile given it was a juvenile
$\delta_{A J}$	Probability an enumerated animal was assigned adult given it was a juvenile
$\delta_{C A}$	Probability an enumerated animal was assigned calf given it was an adult
$\delta_{J A}$	Probability an enumerated animal was assigned juvenile given it was an adult
$\delta_{A A}$	Probability an enumerated animal was assigned adult given it was an adult
N_C	Calf abundance
N_J	Juvenile abundance
N_F	Adult female abundance
N_{CJF}	Calf, juvenile, and adult female abundance
N	Total abundance (calves, juveniles, adults of both sexes)

Table S3. Results from simulations to evaluate bias and precision of a multievent mark-recapture study to estimate Pacific walrus survival and abundance for a five-year project. “True Value” was the posterior mean from the empirical data that was used to generate 50 different simulated datasets. “Mean” was the mean of the 50 posterior means for the simulated datasets.

Parameter	True Value	Mean	Standard Error	Coefficient of Variation	Absolute Bias	Relative Bias
ρ_J	0.008	0.010	0.003	0.343	0.002	0.236
ρ_F	0.011	0.014	0.003	0.187	0.003	0.239
ρ_M	0.010	0.031	0.025	0.792	0.021	2.117
θ_{C1}	0.916	0.913	0.011	0.012	-0.003	-0.004
θ_{C2}	0.075	0.077	0.009	0.123	0.002	0.024
θ_{C3}	0.009	0.011	0.003	0.295	0.002	0.177
θ_{J1}	0.924	0.923	0.005	0.005	-0.001	-0.001
θ_{J2}	0.070	0.071	0.005	0.068	0.001	0.011
θ_{J3}	0.006	0.006	0.002	0.247	0.000	0.051
θ_{F1}	0.910	0.907	0.005	0.006	-0.003	-0.004
θ_{F2}	0.082	0.084	0.005	0.063	0.002	0.030
θ_{F3}	0.008	0.009	0.001	0.167	0.001	0.088
θ_{M1}	0.952	0.954	0.008	0.009	0.002	0.002
θ_{M2}	0.046	0.043	0.008	0.186	-0.003	-0.062
θ_{M3}	0.002	0.003	0.001	0.398	0.001	0.362
ϕ_C	0.489	0.483	0.151	0.313	-0.006	-0.012
ϕ_J	0.626	0.600	0.095	0.158	-0.026	-0.041
ϕ_F	0.904	0.850	0.061	0.071	-0.054	-0.060
ϕ_M	0.535	0.405	0.166	0.410	-0.130	-0.244
$\delta_{C C}$	0.818	0.803	0.050	0.062	-0.015	-0.018
$\delta_{J C}$	0.083	0.095	0.043	0.451	0.012	0.148
$\delta_{A C}$	0.099	0.102	0.037	0.363	0.003	0.027
$\delta_{C J}$	0.032	0.033	0.011	0.332	0.001	0.030
$\delta_{J J}$	0.865	0.858	0.029	0.034	-0.007	-0.008
$\delta_{A J}$	0.103	0.109	0.030	0.272	0.006	0.055
$\delta_{C A}$	0.026	0.029	0.008	0.271	0.003	0.103
$\delta_{J A}$	0.044	0.038	0.015	0.402	-0.006	-0.141
$\delta_{A A}$	0.930	0.934	0.016	0.017	0.004	0.004
ψ	0.068	0.063	0.023	0.370	-0.005	-0.081
$N_J + N_F$	163565	136883	28085	0.205	-26682	-0.163

Table S4. Results from simulations to evaluate bias and precision of a multievent mark-recapture study to estimate Pacific walrus survival and abundance for a three-year project. “True Value” was the posterior mean from the empirical data that was used to generate 50 different simulated datasets. “Mean” was the mean of the 50 posterior means for the simulated datasets.

Parameter	True Value	Mean	Standard Error	Coefficient of Variation	Absolute Bias	Relative Bias
ρ_J	0.008	0.026	0.020	0.752	0.018	2.303
ρ_F	0.011	0.025	0.016	0.648	0.014	1.314
ρ_M	0.010	0.071	0.060	0.837	0.061	6.114
θ_{C1}	0.916	0.909	0.015	0.017	-0.007	-0.007
θ_{C2}	0.075	0.079	0.015	0.185	0.004	0.053
θ_{C3}	0.009	0.012	0.006	0.482	0.003	0.283
θ_{J1}	0.924	0.921	0.006	0.007	-0.003	-0.003
θ_{J2}	0.070	0.072	0.006	0.085	0.002	0.028
θ_{J3}	0.006	0.007	0.002	0.281	0.001	0.147
θ_{F1}	0.910	0.906	0.006	0.007	-0.004	-0.005
θ_{F2}	0.082	0.086	0.006	0.067	0.004	0.044
θ_{F3}	0.008	0.009	0.002	0.217	0.001	0.080
θ_{M1}	0.952	0.954	0.010	0.011	0.002	0.002
θ_{M2}	0.046	0.042	0.010	0.235	-0.004	-0.088
θ_{M3}	0.002	0.004	0.002	0.513	0.002	1.082
ϕ_C	0.489	0.382	0.139	0.364	-0.107	-0.219
ϕ_J	0.626	0.400	0.151	0.378	-0.226	-0.362
ϕ_F	0.904	0.626	0.136	0.217	-0.278	-0.307
ϕ_M	0.535	0.308	0.115	0.374	-0.227	-0.424
$\delta_{C C}$	0.818	0.799	0.069	0.086	-0.019	-0.024
$\delta_{J C}$	0.083	0.090	0.041	0.458	0.007	0.089
$\delta_{A C}$	0.099	0.111	0.046	0.417	0.012	0.120
$\delta_{C J}$	0.032	0.033	0.014	0.410	0.001	0.029
$\delta_{J J}$	0.865	0.866	0.040	0.046	0.001	0.001
$\delta_{A J}$	0.103	0.101	0.036	0.353	-0.002	-0.018
$\delta_{C A}$	0.026	0.028	0.012	0.433	0.002	0.069
$\delta_{J A}$	0.044	0.045	0.024	0.534	0.001	0.024
$\delta_{A A}$	0.930	0.927	0.027	0.029	-0.003	-0.003
ψ	0.068	0.108	0.054	0.502	0.040	0.595
$N_J + N_F$	163565	94989	28010	0.295	-68575	-0.419

$$\begin{aligned}
 & \text{(a)} \quad \begin{bmatrix} 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \\ 1 & 0 & 0 & 0 \end{bmatrix} \times \text{(b)} \quad \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \theta_{C1} & \theta_{C2} & \theta_{C3} & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \theta_{J1} & \theta_{J2} & \theta_{J3} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \theta_{F1} & \theta_{F2} & \theta_{F3} \end{bmatrix} = \\
 & \text{(c)} \quad \begin{bmatrix} 0 & \theta_{C1} & \theta_{C2} & \theta_{C3} & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \theta_{J1} & \theta_{J2} & \theta_{J3} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \theta_{F1} & \theta_{F2} & \theta_{F3} \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix} \\
 & \text{(d)} \quad \begin{bmatrix} 1 & 0 & 0 & 0 \\ 1 - \rho_J & 0 & \rho_J & 0 \\ 1 - \rho_F & 0 & 0 & \rho_F \\ 1 & 0 & 0 & 0 \end{bmatrix} \times \text{(e)} \quad \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \theta_{C1} & \theta_{C2} & \theta_{C3} & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \theta_{J1} & \theta_{J2} & \theta_{J3} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \theta_{F1} & \theta_{F2} & \theta_{F3} \end{bmatrix} = \\
 & \text{(f)} \quad \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 - \rho_J & 0 & 0 & 0 & \rho_J \theta_{J1} & \rho_J \theta_{J2} & \rho_J \theta_{J3} & 0 & 0 & 0 \\ 1 - \rho_F & 0 & 0 & 0 & 0 & 0 & 0 & \rho_F \theta_{F1} & \rho_F \theta_{F2} & \rho_F \theta_{F3} \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}
 \end{aligned}$$

Fig. S1. Matrix multiplication to generate joint (re)capture/enumeration probabilities, which equals the marginal probabilities an individual was enumerated exactly once, exactly twice or at least thrice during a sampling occasion. In sampling occasions with the first capture event, \mathbf{P}^0 (a) was multiplied by Θ (b) to generate the joint capture/enumeration matrix $\mathbf{P}^0\Theta$ (c). For all subsequent sampling occasions, \mathbf{P}^F (d) was multiplied by Θ (e) to generate the joint recapture/enumeration matrix $\mathbf{P}^F\Theta$ (f). \mathbf{P}^F was replaced with \mathbf{P}^M as appropriate (not shown).

$$\mathbf{O} = [\mathbf{O}_1 \quad \mathbf{O}_2]$$

\mathbf{O}_1

$$= \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 - \rho_J & \rho_J \theta_{J1} \delta_{C|J} & \rho_J \theta_{J1} \delta_{J|J} & \rho_J \theta_{J1} \delta_{A|J} & \rho_J \theta_{J2} \delta_{C|J}^2 & \rho_J \theta_{J2} 2\delta_{C|J} \delta_{A|J} & \rho_J \theta_{J2} 2\delta_{C|J} \delta_{J|J} & \rho_J \theta_{J2} \delta_{A|J}^2 & \rho_J \theta_{J2} 2\delta_{A|J} \delta_{J|J} & \rho_J \theta_{J2} \delta_{J|J}^2 & \rho_J \theta_{J3} 6\delta_{C|J} \delta_{A|J} \delta_{J|J} \\ 1 - \rho_F & \rho_F \theta_{F1} \delta_{C|A} & \rho_F \theta_{F1} \delta_{J|A} & \rho_F \theta_{F1} \delta_{A|A} & \rho_F \theta_{F2} \delta_{C|A}^2 & \rho_F \theta_{F2} 2\delta_{C|A} \delta_{A|A} & \rho_F \theta_{F2} 2\delta_{C|A} \delta_{J|A} & \rho_F \theta_{F2} \delta_{A|A}^2 & \rho_F \theta_{F2} 2\delta_{A|A} \delta_{J|A} & \rho_F \theta_{F2} \delta_{J|A}^2 & \rho_F \theta_{F3} 6\delta_{C|A} \delta_{A|A} \delta_{J|A} \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

\mathbf{O}_2

$$= \begin{bmatrix} 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \rho_J \theta_{J3} 3(\delta_{C|J}^2) \delta_{A|J} & \rho_J \theta_{J3} 3(\delta_{C|J}^2) \delta_{J|J} & \rho_J \theta_{J3} 3(\delta_{J|J}^2) \delta_{A|J} & \rho_J \theta_{J3} 3(\delta_{J|J}^2) \delta_{C|J} & \rho_J \theta_{J3} 3(\delta_{A|J}^2) \delta_{C|J} & \rho_J \theta_{J3} 3\delta_{A|J}^2 \delta_{J|J} & \rho_J \theta_{J3} \delta_{C|J}^3 & \rho_J \theta_{J3} \delta_{A|J}^3 & \rho_J \theta_{J3} \delta_{J|J}^3 \\ \rho_F \theta_{F3} 3(\delta_{C|A}^2) \delta_{A|A} & \rho_F \theta_{F3} 3(\delta_{C|A}^2) \delta_{J|A} & \rho_F \theta_{F3} 3(\delta_{J|A}^2) \delta_{A|A} & \rho_F \theta_{F3} 3(\delta_{J|A}^2) \delta_{C|A} & \rho_F \theta_{F3} 3(\delta_{A|A}^2) \delta_{C|A} & \rho_F \theta_{F3} 3\delta_{A|A}^2 \delta_{J|A} & \rho_F \theta_{F3} \delta_{C|A}^3 & \rho_F \theta_{F3} \delta_{A|A}^3 & \rho_F \theta_{F3} \delta_{J|A}^3 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

Fig. S2. In recapture years, the observation matrix (\mathbf{O}) for the Pacific walrus multievent model was the product of the recapture matrix (\mathbf{P}^F or \mathbf{P}^M), the conditional enumeration matrix (Θ^F or Θ^M), and the age assignment matrix (Δ). In the first capture year, the observation matrix (\mathbf{O}^0 , not shown) was the product of the initial capture matrix (\mathbf{P}^0), the conditional enumeration matrix (Θ^F or Θ^M), and the age assignment matrix (Δ).

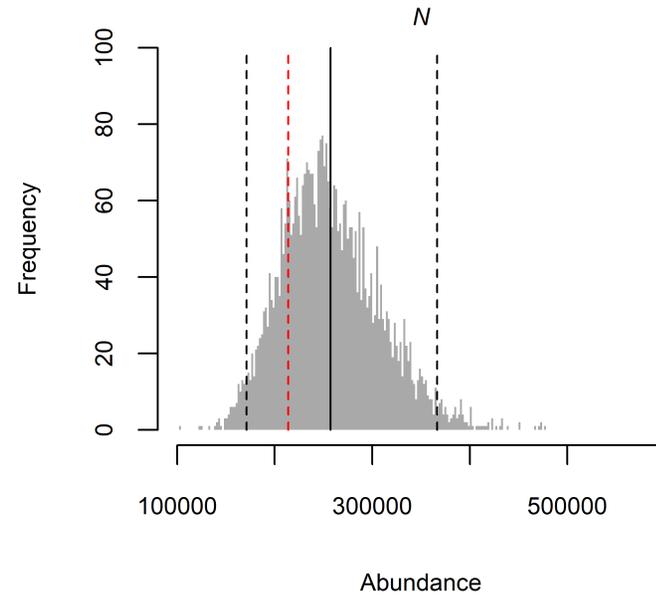


Fig. S3. Posterior distributions for Pacific walrus total abundance. Posterior means (black lines), 95% credible intervals (dotted black lines), and minimum abundance estimate (red dotted line) are also shown.