Supplemental Info 1. JAGS Code for the Pollock's Robust Design model used in this study.

```
# Model specification ----
modelString = "
model {
  # Priors
    # Survival and emigration
      for(i in 1:(n.ind)){
        for(t in 1:(n.years-1)){
          # Logit-scale predictor of apparent survival (species)
            logit(r_phi[i,t]) <- l_phi_i[i,t]
            l_phi_i[i,t] <-  l_phi[species[i],t]

          # Logit-scale predictor of site fidelity (species)
            logit(r_gamma[i,t]) <- l_gamma_i[i,t]
            l_gamma_i[i,t] <- l_gamma[species[i],t]
        }
      }

    # Species- and time-specific priors on
    # phi and gamma
      for(s in 1:n.species){
        for(t in 1:(n.years-1)){
          l_phi[s,t] ~ dnorm(0, 1)
          l_gamma[s,t] ~ dnorm(0, 1)

          logit(phi[s,t]) <- l_phi[s,t]
          logit(gamma[s,t]) <- l_gamma[s,t]
        }
      }

    # Secondary occasions p
      # Logit-scale linear predictor on
      # p by year and secondary occasion
        for (i in 1:n.ind){
          for (t in 1:n.years){
            for (j in 1:(n.sec[t])){
                logit(p[i,t,j]) <- lp[i,t,j]
                lp[i,t,j] <- inprod(beta[t,j, ], X[i, ])
                yes[i,t,j] ~ dbin(p[i,t,j], total[i,t,j])
            }
          }
        }
      # Betas (intercepts & 'slopes') for linear predictor of logit-scale
      # p, varying by time-period
      for(t in 1:n.years){
        for(j in 1:(n.sec[t])){
```

```
      for(n in 1:nX){
        beta[t,j,n] ~ dnorm(0, 0.001)
      }
    }
  }

  # Primary occasions p
  for(i in 1:n.ind){
    for(t in 1:n.years){
      pstar[i,t] <- (1 - prod(1 - p[i,t,]) ) * (1 - p_loss[i])
    }
  }

# State (presence/absence) and observation (detection)
# process likelihoods
  for (i in 1:n.ind){

    # Initialize first capture
    z[i,first[i]] <- ch[i,first[i]]

    # Likelihood for state process
    for (t in (first[i]+1):n.years){
      mu1[i,t] <- z[i,t-1] * r_phi[i, t-1]
      mu2[i,t] <- z[i,t] * r_gamma[i, t-1] * pstar[i,t]
      z[i,t] ~ dbern(mu1[i,t])
      ch[i,t] ~ dbern(mu2[i,t])
    }
  }

# Count process likelihood (abundance)
# Population abundance estimated using n-mixture
# approach. We assume that observed abundance
# is the outcome (C) of a binomial process with some
# unknown probability of success (pstar) and some
# starting number of trials (N)
for(s in 1:n.species){
  # Initialize counts for each species
  N[s, 1] ~ dpois(maxes[s])

  log(lambda[s]) <- mu[s]
  mu[s] ~ dunif(-10, 10)

  # Total number alive at time t as function of
  # number alive at t-1, survival, and site fidelity
  for(t in 2:n.years){
    N[s,t] ~ dpois(N[s, t-1]*phi[s, t-1]*gamma[s,t-1])
```

```
    }

    for(t in 1:n.years){
      C[s, t] ~ dpois(N[s,t]/mean(pstar[,t]))
    }

  }

}
"
```

Supplemental Table 1. Secondary period detection probabilities for the upper and lower sites in the Colorado River. Presented are secondary period detection probability estimates, along with 95% credible intervals (lower bound (LB), upper bound (UB)).

Site	Primary Period	Secondary Period	Estimate	LB	UB
Upper	1	1	0.502	0.496	0.513
	1	2	0.502	0.496	0.513
	1	3	0.502	0.496	0.513
	2	1	0.502	0.492	0.507
	2	2	0.502	0.492	0.507
	2	3	0.502	0.492	0.507
	3	1	0.502	0.491	0.512
	3	2	0.502	0.491	0.512
	3	3	0.502	0.491	0.512
	4	1	0.502	0.497	0.507
	4	2	0.502	0.497	0.507
	4	3	0.502	0.497	0.507
	5	1	0.502	0.489	0.509
	5	2	0.502	0.489	0.509
	5	3	0.502	0.489	0.509
Lower	1	1	0.365	0.345	0.428
	1	2	0.365	0.354	0.403
	1	3	0.365	0.355	0.408
	2	1	0.363	0.333	0.383
	2	2	0.363	0.334	0.381
	2	3	0.363	0.330	0.381
	3	1	0.364	0.359	0.367
	3	2	0.364	0.358	0.369
	3	3	0.364	0.345	0.368
	4	1	0.364	0.343	0.401
	4	2	0.364	0.340	0.403
	4	3	0.364	0.347	0.398
	5	1	0.363	0.314	0.385
	5	2	0.363	0.319	0.373
	5	3	0.363	0.315	0.382

Supplemental Table 2. Tagging configuration detection probabilities for the upper and lower sites in the Colorado River. Presented are primary period detection probability estimates, along with 95% credible intervals (lower bound (LB), upper bound (UB)).

Site	Tagging Configuration	Estimate	LB	UB
Upper	1 shellfish	0.855	0.847	0.862
	1 shellfish/1 PIT	0.875	0.872	0.879
	2 shellfish	0.876	0.868	0.883
	2 shellfish/1 PIT	0.876	0.873	0.879
Lower	1 shellfish	0.723	0.665	0.778
	1 shellfish/1 PIT	0.742	0.736	0.748
	2 shellfish	0.742	0.720	0.762
	2 shellfish/1 PIT	0.730	0.565	0.857