



Supplementary Information for:

Consequences of Seafood Mislabeling for Marine Populations and Fisheries Management

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## Supplementary Information Text

### Linking Mislabeling Data to Apparent Consumption and Production-Method Data

We linked mislabeling data to U.S. apparent consumption estimates (and imports and aquaculture production), using scientific names of the FAO production products from Fishstat [1] and scientific names of mislabeling products that had been previously linked to Fishbase [2] and Sealifebase [3] by Luque and Donlan [4] (see below). In the remainder of the SI we refer to products in Fishstat as FAO production products. Apparent consumption estimation required linking the product group field in the trade data from the U.S. National Oceanic and Atmospheric Administration's National Marine Fisheries Service to FAO production products to calculate apparent consumption as the sum of production and imports minus exports of each product.<sup>1</sup> For most products, we were able to link on the scientific names. However, not all mislabeling data could be linked this way, and we were forced to make a number of assumptions to further clean and link the datasets, which are described below.

Some products in the mislabeling data are ambiguously labeled and consist of more than one species, such as *Pacific salmon*, *tuna*, *cod*, and *snapper*. We identify these products with an asterisk (\*) in Figure 1. In these cases, we manually identified linkages. Pacific salmon, for example, encompasses several species belonging to the genus *Oncorhynchus*. The Pacific salmon macro links to Pink, Chinook, Sockeye, Coho and Chum salmon. For some product labels using taxonomic ambiguous common names, assigning taxonomic resolution is more challenging. In these cases, we identified the closest matching NOAA trade product grouping (based on the product group field) and included all the FAO production products linked to the trade product grouping in order to link it with mislabeling data. We then calculated 2016 total apparent consumption, total imports, and total aquaculture for each of these associated FAO production products. For example, for mislabeling data for *grouper*, we included all of the FAO production products that were previously linked to the NOAA trade product grouping for *grouper*. See Luque and Donlan [4] for more detail on data collection and naming for mislabeling data.

While mislabeling data for most products could be directly linked to an FAO production product name with positive 2016 estimated U.S. apparent consumption and known production method, this was not true for all products. In order to estimate the amount of an FAO production product produced via aquaculture or wild-caught and imported by the U.S., there must be corresponding NOAA trade product import data from at least one producing country with production method information (wild-caught or aquaculture) in 2016. In cases where import data was not available for at least one producer country, a 2016 apparent consumption estimate, import percentage, and aquaculture percentage for the FAO production product was not calculated in the prior steps.

For these cases of *missing* products, we used an alternative method to estimate apparent consumption and production. We took NOAA trade product groupings and calculated the percent of total 2016 global production for the grouping that could be attributed to each FAO production product produced via aquaculture or wild-caught and that had been linked to the grouping, excluding products associated with *nei*. The terms *nei* denotes FAO production *not explicitly identified* and can include multiple species, genera, or families under a single product name (e.g., *Groupers nei*, *Salmonids nei*, and *Snappers nei*). For each NOAA trade product grouping, we identified all linked *nei* FAO production products and summed the 2016 apparent consumption estimates. We used the total apparent consumption estimates for these *nei* products as a baseline to infer the amount of consumption that can be attributed to related *missing* products. We took 2016 global production percentages for *missing* products and multiplied these percentages by their respective NOAA trade product grouping's total *nei* consumption, allowing us to estimate how much of total *nei* product consumption in a grouping can be attributed to related *missing* products (and their known production methods).

We estimated global production for 19 expected and 36 substitute products using these alternative methods (i.e., approximately 72,000 and 10,300 tonnes of apparent consumption, respectively).

### Seafood Watch Scores

Seafood Watch assessments measure the population and management status of specific fisheries and aquaculture operations. We used scores for four factors from their assessments: impacts on species under assessment (i.e., target species), impacts on other species under assessment (i.e., bycatch), management effectiveness, and impacts on habitat and ecosystems. Ratings and recommendations for wild-capture fisheries are given for a single stock or product within a specific fishery, and each fishery is defined by region, gear type, and management body [5]. Each

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<sup>1</sup> Trade data records with product groups without enough product information, such as caviar, fillet, tuna in airtight containers, and canned salmon, were dropped.

of these four scores, and the criteria that determine them, are briefly described below based on Monterey Bay Aquarium Seafood Watch [5].

*Impacts on the Target Species* is based on the Seafood Watch *species under assessment* score, which is based on two primary criteria. The first criterion assesses the current stock abundance, and the goal of maintaining it at a level that does not impair recruitment or productivity. The second criterion assesses fishing mortality, which must be appropriate for the current stock status which is defined at or below maximum sustainable yield.

*Impacts on Other Species* is based on the same two criteria from *Impacts on the Target Species* but applied to bycatch species that are caught within the same fishery. Additional considerations are taken for unknown bycatch. A third criterion, discards and bait use, is also included in the assessment. This criterion focuses on minimizing post-harvest loss and efficient bait use. Waste associated with high discards and bait use reduce the score.

*Management Effectiveness* is assessed according to five criteria. First, strategy and implementation considers whether a fisheries' management strategy has a high chance of preventing stock declines. Second, bycatch strategy assesses how management prevents negative impacts on species susceptible to bycatch. Third, scientific research and monitoring assesses whether managers use independent, robust, peer-reviewed, and up-to-date science, as well as appropriate monitoring of non-target species. Fourth, enforcement of management regulations assesses whether a fishery has appropriate permits, regulations, and requirements, along with the capacity to ensure and report compliance. Last, stakeholder inclusion assesses if there is transparency in the management process and stakeholder input.

*Impacts on Habitat and Ecosystems* is based on three criteria. The first considers the physical impact of fishing gear on habitat and substrate, with the goal of having no adverse impacts. The second criterion assesses the mitigation of gear impacts or the mitigation of damage to seafloor through habitat protection. Only gear that contacts the seafloor is considered. Mitigation efforts increase the score. The last criterion assesses the use of ecosystem-based fisheries management such that stocks are maintained at levels that promote a functioning ecosystem and food web.

The score reports can vary in their specificity. Some reports target an entire product, regardless of the origin of production, and are meant to have a global scope. Many reports are specific to a particular fishery or aquaculture operation, using a specific type of gear, and located in a specific country or region. The Seafood Watch scores are linked to the mislabeling and mislabeled apparent consumption data using either the production product name and country name, the production product name and FAO region, or simply the production product name.

In cases where Seafood Watch scores were available by country or FAO region and U.S. apparent consumption was from multiple assessed units, we calculated a weighted average score for each product. Specifically, we weighted the Seafood Watch scores for each assessed unit by the estimated U.S. apparent consumption associated with each assessed unit.

Finally, when the mislabeling product was a macro and consisted of multiple FAO production product names, we used another weighting process. Here we calculated a weighted average score where the weight was the apparent consumption associated with each product.

### Mislabeling Substitution Rate Calculations

*Data.* Data was compiled from a review of published literature up to December 2017, which resulted in 141 studies from peer-reviewed (117) and non-peer-reviewed (24) sources. The entire dataset consists of 27,313 samples, covering 401 products that have been tested. Data collection and filters are described in detail in Luque and Donlan 2019 [4]. In order to have sufficient data to estimate expected-substitute pair mislabeling rates and their uncertainty, we pooled samples across studies and used a global dataset. But for our primary analysis, we restricted the dataset to include only expected products that have been tested for mislabeling in the U.S. Thus, data used to estimate expected-substitute pair mislabeling rates included 246 pairs with  $\geq 50$  total samples and where the expected product had been tested in the U.S. at least once. The mean expected-substitute pair sample size was 533 (range: 51-2,528; median=219; mode=1,007). Central tendency estimates (i.e., posterior mean, median, and mode), HDIs, and sample size for each expected-substitute product pair are shown in Table SI-1.

*Meta-Analysis Model.* The hierarchical model is represented in Figure SI-2, which illustrates the parameter definitions, as well as the relationships between the parameters and the data. Starting with the data ( $y_i$ ), the likelihood function is described as

$$y_i | \theta_i \sim \text{Bin}(\theta_i, N_i)$$

where,  $y_i$  represents the number of an expected product that have been identified as a certain substitute species  $i$  out of  $N_i$  (i.e., total # tested samples of the expected product).  $Y_i$  is assumed to be a random variable from a binomial distribution that is defined by its mean  $\theta_i$  and the number of samples ( $N_i$ ). There are as many  $\theta_i$  as product pairs,

which is a proportion and thus can only take values between 0 and 1. We transform the parameters  $\theta_i$  using a logistic transformation and use a  $t$  distribution as a conjugate prior of the likelihood function.<sup>2</sup> The transformation can be defined as

$$\alpha_i = \text{logit}(\theta_i).$$

The estimated  $\alpha_i$  are  $t$  distributed random values around the central tendency  $\mu$ . A  $t$  distribution is similar to a normal distribution with two parameters that control its mean  $\mu$  and its width  $\sigma$ . The  $t$  distribution has a third parameter that controls the heaviness of its tails, the normality parameter  $\nu$ , and describes any deviation from normality when there are outliers (i.e., data values that fall unusually far from a model's expected value). Thus, the  $t$  distribution is robust against outliers (i.e., robust logistic regression), and the parameters  $\alpha_i$  can be described as,

$$\alpha_i | \mu, \sigma, \nu \sim t(\mu, \sigma, \nu)$$

where the probability of  $\alpha_i$  given the three hyperparameters follows a  $t$  distribution described by the  $\mu$ ,  $\sigma$ , and  $\nu$  (Fig. SI-2). The three hyperparameters are described below.

**$\mu \sim \text{Norm}(\mathbf{M}_\mu, \mathbf{S}_\mu)$ .** The estimated overall mislabeling rate is denoted by  $\mu$ , which is the mean of a normal distribution that describes the spread of mislabeling rates of  $i$  pairs ( $\theta_i$ ). The mean  $\mu$  of the  $t$  distribution is estimated and given a normal prior. The prior on  $\mu$  can be whatever is an appropriate description of real prior knowledge. In our case prior knowledge is limited, and we use a non-informative prior that is described by the two parameters  $M_\mu$  and  $S_\mu$ . The prior should be broad on the scale of the transformed data. To establish a generic value, we consider two extreme probabilities near 0.001 and 0.999. The corresponding inverse-logistic values are -6.9 and +6.9, which have a standard deviation of 10. Therefore, a value of  $S=10$  represents a broad prior for the transformed data. Thus, we use a normal distribution with a center  $M_\mu=0$  and scale  $S_\mu=100$  as our non-informative prior. This is equivalent of distribution centered at 0.5 with data varying from 0 to 1 for non-transformed data, which is justified given the variability of mislabeling studies (see [4]). We also ran the model with prior of a center  $M_\mu=0$  and scale  $S_\mu=10$  to explore any differences in model results. Some argue that a mildly informative prior can improve model estimates [6]. Thus, we re-ran our model using a mildly informative prior with the goal of assessing any influence of our non-informative prior on the results. We used a normal distribution with the center in the naive mean of our data (i.e.,  $M_\mu=0.30$  which equals -0.85 on a logistic scale) and scale  $S_\mu=10$ . Model estimates and HDI intervals for the model did not change with all three models. Thus, the prior has little influence on the posterior distribution. Thus, we carried out the analyses with the non-informative prior.

**$\sigma \sim \text{Unif}(\mathbf{L}_\sigma, \mathbf{H}_\sigma)$ .** The hyper-parameter  $\sigma$  describes the precision of the mean (i.e., scale). The prior on  $\sigma$  can also be whatever is an appropriate description prior knowledge on the dispersion of the data. In our case, prior knowledge is limited, and we use a uniform distribution that is vague and noncommittal, allowing a broad range of values for the scale parameter  $\sigma$  that describes the spread of the normal distribution. We use a lower ( $L_\sigma = 0$ ) and higher value ( $H_\sigma = 100$ ), which allows the model to estimate a posterior distribution of  $\sigma$  according to the spread of mislabeling rates given by the data.

**$\nu \sim \text{Exp}(1/30)$ .** The normality hyper-parameter  $\nu$  is estimated and given a broad exponential prior. It can range from 1 to  $\infty$ . When  $\nu = 1$  the  $t$  distribution has very long tails, while when  $\nu$  approaches  $\infty$ , the  $t$  distribution becomes normal. Values of  $> \sim 30$  indicate a normal distribution, while values  $< \sim 30$  indicate a distribution with heavier tails than a normal distribution. Typically, one is not interested in the exact estimated value of  $\nu$ ; rather, in giving the model flexibility to use heavy tails if the data demand them.

**Model Performance and Diagnostics.** From the Bayesian model, we generated a Markov Chain Monte Carlo (MCMC) sample from the posterior distribution. We ran the model with three parallel chains for 1,000,000 iterations without thinning. The values from the MCMC sample of the posterior distribution must be representative from the true posterior distribution and the parameter estimates must be accurate and stable (i.e., the mean and HDI should not differ significantly when the model is re-run). We carried out a series of diagnostic tests in order to check whether the MCMC sample from the posterior distribution of the model is representative of the true posterior distribution and whether the estimates are accurate and stable.

**Representativeness.** First, we assessed whether the MCMC sample was a representative sample from the posterior distribution via visual examination. *Trace plots* reveal if all chains meander and overlap with each other, indicating they are representative of the posterior distribution (Fig. SI-3; [7]). They also allow for the assessment of convergence and the necessary so-called *burn-in* period (i.e., the number of steps that should be excluded from the MCMC sample). We used a *burn-in* rate of 1,000. *Density plots* are smoothed histograms of the parameter values

<sup>2</sup> We tested a binomial model with beta priors as opposed to logistic-transformed priors. However, the model performed poorly, resulting in issues with convergence and low effective sample sizes.

sampled by each chain, which provide another visual tool to assess overlap (Fig. SI-3). Second, we assess representativeness numerically with the Gelman-Rubin statistic, which is known as the *shrink factor*. We used the heuristic of a Gelman-Rubin statistic  $>1.1$  as a warning that the chains have potentially not converged adequately [7]. In our model, all estimates had a Gelman-Rubin statistic  $<1.1$  (Table SI-2).

**Accuracy.** First, we also assessed visually if MCMC samples were large enough for a stable and accurate numerical estimate of the prior distribution. *Autocorrelation plots* show the degree of autocorrelation between chains (Fig. SI-2; [7]). Second, we assess accuracy numerically with the Effective Sample Size (ESS), which divides the actual sample size by the amount of autocorrelation. We used a heuristic of a ESS  $<10,000$  as a warning that the sample size may not be sufficient with respect to accuracy [7]. In our model, all estimates had an ESS  $>10,000$  (Table SI-2). Last, we also use the Monte Carlo Standard Error (MCSE) as a numerical diagnostic of accuracy. The MCSE indicates the estimated standard deviation of the sample mean in the chain, on the scale of the parameter value. In particular, we use the MCSE to assess the accuracy of the posterior mean, using a heuristic of  $>5\%$  (i.e., % of the standard deviation) as a warning that sample size may not be sufficient with respect to accuracy [7, 8]. In all cases, MCSE was  $<5\%$  (Table SI-2).

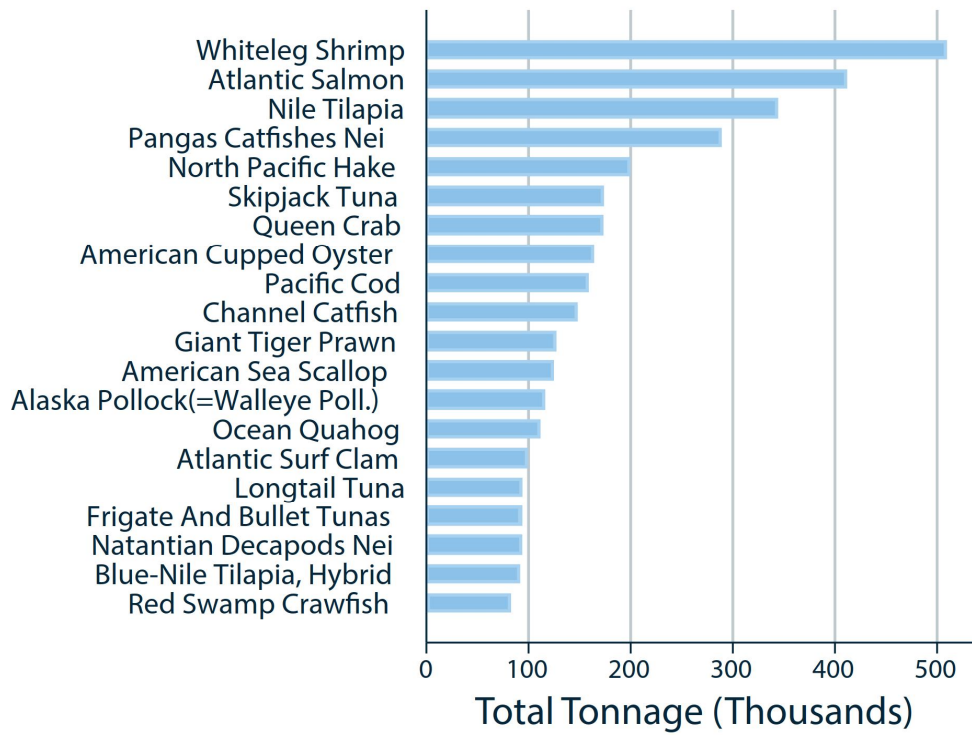
**Posterior Predictive Check.** We also compared the data to the posterior predictions of the model by generating simulated data from the credible parameter values of the model and examining the quality of the simulated data. The simulated data resembled the actual data as it is shown for the central tendency  $\mu$  in Figure SI-4. This constitutes a form of posterior predictive check, by which we check whether the model appears to be a reasonable description of the data.

## Robustness Checks

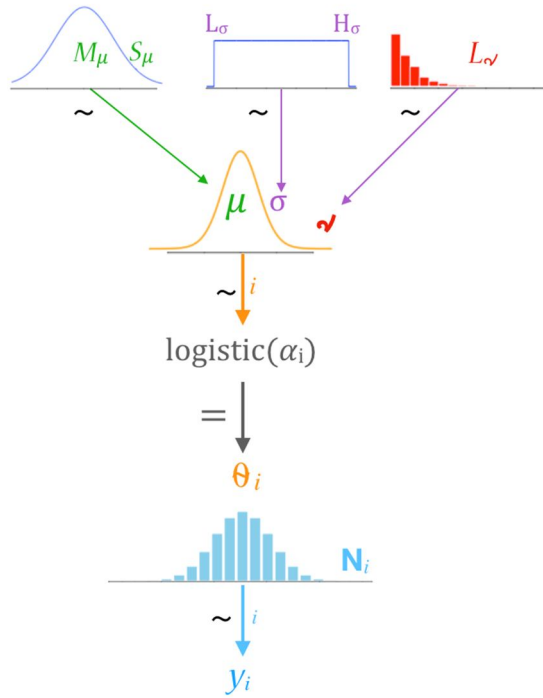
*Results Using Alternative Datasets of Mislabeling Pairs.* We used our two alternative datasets to test the difference in imported percentages between the substitute and expected product, using the bootstrapping procedure described in the Materials and Methods. The first contains product pairs with  $\geq 50$  samples tested globally, but relaxes the assumption that the expected product must have been tested in the U.S. (Global  $\$50+$  pairs; 387 pairs). The second contains all pairs with 100 or more samples tested globally (Global  $\$100+$  pairs; 277 pairs). The results are presented in Table SI-4. We found that substitute products are more likely to be imported than the expected products that they replace, and that the average difference across all pairs is large in magnitude and statistically significant.

We also conducted the analysis of differences in Seafood Watch scores using the two alternative datasets. Table SI-5 and SI-6 shows the results of the test for proportion of substitute products with a higher score using the *Global 50+ pairs* and *Global 100+ pairs* datasets, respectively. Results are generally consistent with results from a primary dataset (*U.S. 50+ pairs*). All tests using bootstrapped distributions of the *Global 50+ pairs* dataset resulted in negative and significant differences in Seafood Watch scores. For the *Global 100+ pairs* dataset, all four differences were negative, with three being statistically significant.

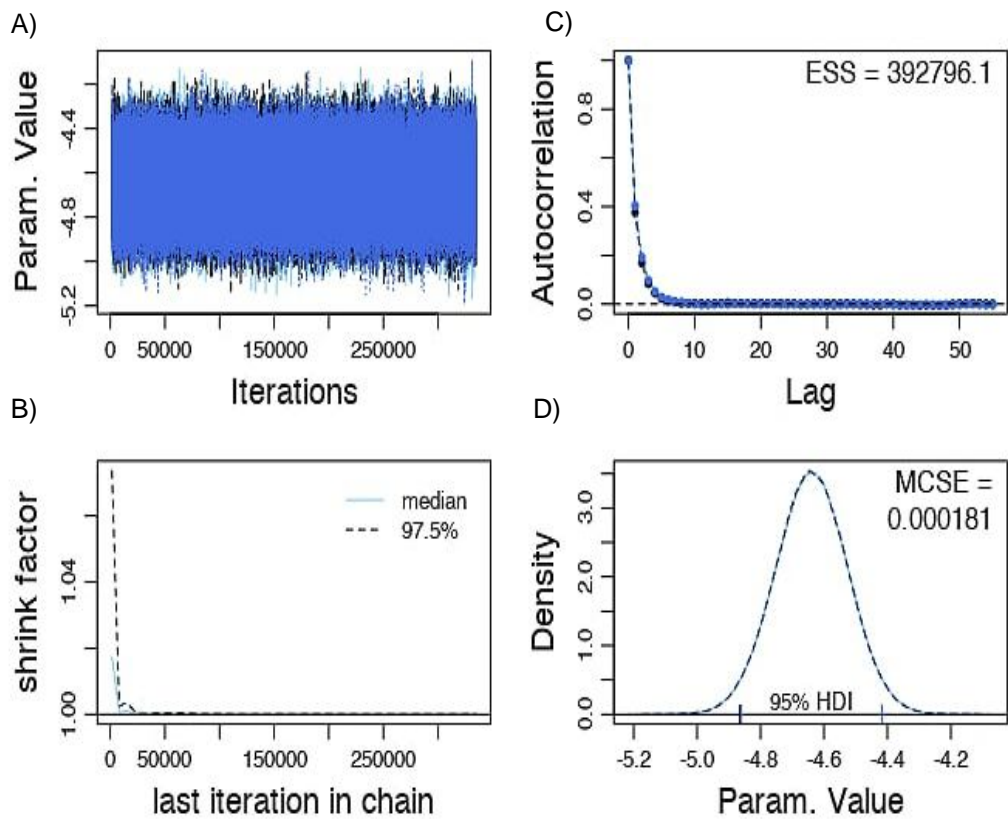
*Seafood Watch Score and Import Percentage Analyses with Product Exclusion.* In the process of aggregating Seafood Watch scores, we discovered that some mislabeled products were missing scores for a large subset of the overall apparent consumption. For example, the product *hake\** contains all of the products in the genus *Merluccius*. However, the vast majority of the apparent consumption for *hake\** is derived from North Pacific Hake (*Merluccius productus*) for which there are no scores available. Another example is the product swordfish (*Xiphias gladius*) for which scores were not available for specific countries that export the product to the U.S. We also perform a test excluding tuna because the fields in the 2016 trade data from the U.S. National Oceanic and Atmospheric Administration's National Marine Fisheries Service we use to identify products – “product group” and “product group species” – do not provide information on the types tuna (e.g. albacore, yellowfin) for many imports in airtight containers. In all of these cases, we calculated the import percent difference and aggregated Seafood Watch scores as described previously. We then re-ran the same analyses, but iteratively excluding each one of these product groups. Our goal was to explore if our results are robust to missing scores. Table SI-7 shows the results, which are qualitatively similar and remain significant.



**Figure SI-1:** U.S. apparent consumption (2016 volume in live-weight equivalents): top 20 seafood products

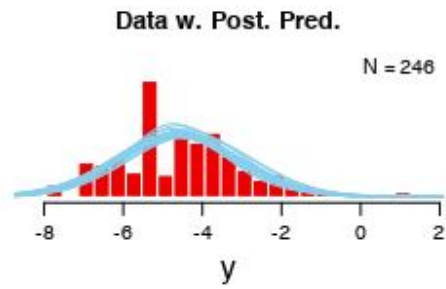


**Figure SI-2.** Robust logistic regression model with one level of hierarchy. Model schematic adopted from [7].



**Figure SI-3.** Visual diagnostics to assess the representativeness and accuracy of MCMC samples. A) Trace plots reveal if all chains meander and overlap with each other, indicating they are representative of the posterior distribution. B) The shrink factor informs if the chains have converged adequately. C) Autocorrelation plots show the degree of autocorrelation between chains, which informs Effective Sample Size. D) Density plot is a smoothed histogram of a parameter value sampled by each chain. We used the function *diagMCMC* from [7] to generate the visual diagnostics.





**Figure SI-4.** Histogram of the data (after the logistic transformation) superimposed with a smattering of  $t$ -distributed curves that have credible  $\mu$  and  $\sigma$  values from the MCMC sample of the posterior predicted distribution.

**Table SI-1.** Seafood mislabeling rate estimates for the expected-substitute pairs included in the meta-analysis. The posterior mean, median, and mode, along with the 95% HDI are shown. Total number of samples included in the meta-analysis for each pair is shown (n). The average 95% HDI interval for the 246 expected-substitute pair rates is 3%. Common names correspond to Fishbase [2] and Sealifebase [3]. Products with an \* represent more than one species.

Expected	Substitute	Posterior Mean	Posterior Median	Posterior Mode	Lower 95% HDI	Higher 95% HDI	n
Albacore	<i>Katsuwonus pelamis</i>	3%	3%	2%	<1%	6%	88
Albacore	<i>Lepidocybium flavobrunneum</i>	2%	2%	1%	<1%	5%	88
Albacore	<i>Thunnus albacares</i>	3%	3%	2%	<1%	6%	88
Albacore	<i>Thunnus obesus</i>	3%	3%	2%	<1%	6%	88
Albacore	<i>Thunnus thynnus</i>	1%	1%	<1%	<1%	3%	88
Amur sturgeon	<i>Huso dauricus</i>	16%	16%	16%	11%	22%	151
Anchovy*	<i>Engraulis encrasicolus</i>	2%	2%	1%	<1%	4%	91
Angler*	<i>Lophius litulon</i>	3%	3%	3%	1%	7%	128
Angler*	<i>Lophius vomerinus</i>	2%	2%	1%	<1%	4%	128
Angler*	<i>Protonibea diacanthus</i>	1%	1%	<1%	<1%	2%	128
Atlantic bluefin tuna	<i>Thunnus alalunga</i>	1%	<1%	<1%	<1%	1%	243
Atlantic bluefin tuna	<i>Thunnus albacares</i>	34%	34%	34%	28%	40%	243
Atlantic bluefin tuna	<i>Thunnus atlanticus</i>	1%	<1%	<1%	<1%	1%	243
Atlantic bluefin tuna	<i>Thunnus obesus</i>	18%	18%	18%	14%	23%	243
Atlantic cod	<i>Brosme brosme</i>	<1%	<1%	<1%	<1%	<1%	2143
Atlantic cod	<i>Gadus chalcogrammus</i>	<1%	<1%	<1%	<1%	1%	2143
Atlantic cod	<i>Gadus*cephalus</i>	1%	1%	1%	1%	2%	2143
Atlantic cod	<i>Melanogrammus aeglefinus</i>	2%	2%	2%	1%	2%	2143
Atlantic cod	<i>Merlangius merlangus</i>	<1%	<1%	<1%	<1%	<1%	2143
Atlantic cod	<i>Merluccius nr</i>	<1%	<1%	<1%	<1%	<1%	2143
Atlantic cod	<i>Molva dypterygia</i>	<1%	<1%	<1%	<1%	<1%	2143
Atlantic cod	<i>Molva molva</i>	<1%	<1%	<1%	<1%	1%	2143
Atlantic cod	<i>Pangasianodon hypophthalmus</i>	<1%	<1%	<1%	<1%	<1%	2143
Atlantic cod	<i>Perca flavescens</i>	<1%	<1%	<1%	<1%	<1%	2143
Atlantic cod	<i>Pollachius pollachius</i>	<1%	<1%	<1%	<1%	<1%	2143
Atlantic cod	<i>Pollachius virens</i>	1%	1%	1%	<1%	1%	2143

Expected	Substitute	Posterior Mean	Posterior Median	Posterior Mode	Lower 95% HDI	Higher 95% HDI	n
Atlantic cod	<i>Ruvettus pretiosus</i>	<1%	<1%	<1%	<1%	1%	2143
Atlantic salmon	<i>Oncorhynchus keta</i>	1%	1%	1%	<1%	2%	256
Atlantic salmon	<i>Oncorhynchus mykiss</i>	3%	2%	2%	1%	4%	256
Atlantic salmon	<i>Oncorhynchus nerka</i>	1%	<1%	<1%	<1%	1%	256
Atlantic salmon	<i>Salmo trutta</i>	1%	<1%	<1%	<1%	1%	256
Barramundi	<i>Lates niloticus</i>	5%	4%	4%	1%	9%	93
Barramundi	<i>Lates nr</i>	11%	10%	10%	5%	17%	93
Barramundi	<i>Seriolella brama</i>	5%	4%	4%	1%	9%	93
Beluga	<i>Acipenser baerii</i>	1%	1%	1%	<1%	1%	701
Beluga	<i>Acipenser baerii x naccaraii x persicus</i>	<1%	<1%	<1%	<1%	1%	701
Beluga	<i>Acipenser gueldenstaedtii</i>	3%	2%	2%	1%	4%	701
Beluga	<i>Acipenser gueldenstaedtii x naccaraii</i>	<1%	<1%	<1%	<1%	1%	701
Beluga	<i>Acipenser persicus</i>	<1%	<1%	<1%	<1%	1%	701
Beluga	<i>Acipenser sinensis</i>	<1%	<1%	<1%	<1%	1%	701
Beluga	<i>Acipenser stellatus</i>	1%	1%	1%	<1%	1%	701
Beluga	<i>Acipenser transmontanus</i>	<1%	<1%	<1%	<1%	1%	701
Beluga	<i>Huso dauricus</i>	<1%	<1%	<1%	<1%	1%	701
Blue crab	<i>Callinectes bellicosus</i>	2%	2%	1%	<1%	5%	90
Blue crab	<i>Charybdis nr</i>	2%	2%	1%	<1%	5%	90
Blue crab	<i>Portunus nr</i>	4%	3%	3%	1%	8%	90
Blue crab	<i>Portunus pelagicus</i>	23%	23%	22%	15%	32%	90
Blue crab	<i>Portunus pseudoargentatus</i>	2%	2%	1%	<1%	5%	90
Blue crab	<i>Portunus sanguinolentus</i>	2%	2%	1%	<1%	5%	90
Blue crab	<i>Portunus trituberculatus</i>	2%	2%	1%	<1%	5%	90
Chinook salmon	<i>Oncorhynchus keta</i>	14%	14%	13%	7%	22%	70
Chinook salmon	<i>Oncorhynchus kisutch</i>	2%	2%	1%	<1%	6%	70
Chinook salmon	<i>Salmo salar</i>	11%	11%	10%	5%	19%	70
Cod*	<i>Albatrossia pectoralis</i>	1%	1%	1%	<1%	1%	1007
Cod*	<i>Anarhichas minor</i>	<1%	<1%	<1%	<1%	<1%	1007

Expected	Substitute	Posterior Mean	Posterior Median	Posterior Mode	Lower 95% HDI	Higher 95% HDI	n
Cod*	<i>Anoplopoma fimbria</i>	<1%	<1%	<1%	<1%	<1%	1007
Cod*	<i>Argentina silus</i>	1%	1%	1%	1%	2%	1007
Cod*	<i>Atheresthes evermanni</i>	<1%	<1%	<1%	<1%	<1%	1007
Cod*	<i>Atheresthes stomias</i>	<1%	<1%	<1%	<1%	<1%	1007
Cod*	<i>Dissostichus eleginoides</i>	<1%	<1%	<1%	<1%	<1%	1007
Cod*	<i>Gadus chalcogrammus</i>	2%	2%	2%	1%	2%	1007
Cod*	<i>Lagocephalus spadiceus</i>	1%	1%	1%	<1%	1%	1007
Cod*	<i>Lagocephalus wheeleri</i>	<1%	<1%	<1%	<1%	<1%	1007
Cod*	<i>Lates niloticus</i>	<1%	<1%	<1%	<1%	<1%	1007
Cod*	<i>Macrourus carinatus</i>	<1%	<1%	<1%	<1%	1%	1007
Cod*	<i>Melanogrammus aeglefinus</i>	2%	2%	2%	1%	3%	1007
Cod*	<i>Merluccius angustimanus</i>	<1%	<1%	<1%	<1%	1%	1007
Cod*	<i>Merluccius capensis</i>	<1%	<1%	<1%	<1%	<1%	1007
Cod*	<i>Merluccius hubbsi</i>	1%	<1%	<1%	<1%	1%	1007
Cod*	<i>Merluccius merluccius</i>	<1%	<1%	<1%	<1%	1%	1007
Cod*	<i>Merluccius paradoxus</i>	<1%	<1%	<1%	<1%	1%	1007
Cod*	<i>Merluccius productus</i>	<1%	<1%	<1%	<1%	1%	1007
Cod*	<i>Micromesistius australis</i>	<1%	<1%	<1%	<1%	1%	1007
Cod*	<i>Molva dypterygia</i>	<1%	<1%	<1%	<1%	<1%	1007
Cod*	<i>Molva molva</i>	1%	1%	1%	<1%	1%	1007
Cod*	<i>Oreochromis nr</i>	<1%	<1%	<1%	<1%	1%	1007
Cod*	<i>Pangasianodon hypophthalmus</i>	1%	<1%	<1%	<1%	1%	1007
Cod*	<i>Pollachius pollachius</i>	1%	1%	1%	1%	2%	1007
Cod*	<i>Pollachius virens</i>	5%	5%	5%	4%	7%	1007
Cod*	<i>Reinhardtius hippoglossoides</i>	1%	1%	1%	1%	2%	1007
Cod*	<i>Ruvettus pretiosus</i>	1%	1%	1%	<1%	1%	1007
Common dolphinfish	<i>Argyrozona argyrozona</i>	2%	1%	1%	<1%	4%	59
Common dolphinfish	<i>Brachyplatystoma platynemum</i>	2%	1%	1%	<1%	4%	59
Common dolphinfish	<i>Seriola lalandi</i>	7%	7%	6%	2%	13%	59

Expected	Substitute	Posterior Mean	Posterior Median	Posterior Mode	Lower 95% HDI	Higher 95% HDI	n
Danube sturgeon	<i>Acipenser baerii</i>	<1%	<1%	<1%	<1%	<1%	2528
Danube sturgeon	<i>Acipenser baerii x naccaraii x persicus</i>	<1%	<1%	<1%	<1%	<1%	2528
Danube sturgeon	<i>Acipenser nudiventris</i>	<1%	<1%	<1%	<1%	1%	2528
Danube sturgeon	<i>Acipenser persicus</i>	<1%	<1%	<1%	<1%	<1%	2528
Danube sturgeon	<i>Acipenser schrenckii</i>	<1%	<1%	<1%	<1%	1%	2528
Danube sturgeon	<i>Acipenser stellatus</i>	1%	1%	1%	1%	1%	2528
Danube sturgeon	<i>Acipenser transmontanus</i>	<1%	<1%	<1%	<1%	<1%	2528
Danube sturgeon	<i>Huso dauricus</i>	<1%	<1%	<1%	<1%	<1%	2528
Danube sturgeon	<i>Huso huso</i>	2%	2%	2%	1%	2%	2528
Flounder*	<i>Atheresthes stomias</i>	7%	7%	6%	2%	14%	56
Flounder*	<i>Cynoscion guatucupa</i>	3%	2%	2%	<1%	7%	56
Flounder*	<i>Isopisthus parvipinnis</i>	2%	1%	1%	<1%	4%	56
Flounder*	<i>Micropogonias furnieri</i>	3%	2%	2%	<1%	7%	56
Flounder*	<i>Pangasianodon hypophthalmus</i>	2%	1%	1%	<1%	4%	56
Flounder*	<i>Pangasianodon nr</i>	2%	1%	1%	<1%	4%	56
Flounder*	<i>Paralichthys patagonicus</i>	3%	2%	1%	<1%	7%	56
Fringebarbel sturgeon	<i>Acipenser stellatus</i>	8%	8%	7%	2%	15%	64
Fringebarbel sturgeon	<i>Huso huso</i>	4%	3%	2%	1%	8%	64
Grouper*	<i>Acanthistius brasiliensis</i>	1%	1%	<1%	<1%	2%	189
Grouper*	<i>Aprion virescens</i>	2%	2%	2%	1%	5%	189
Grouper*	<i>Brotula barbata</i>	2%	2%	1%	<1%	4%	189
Grouper*	<i>Caulolatilus nr</i>	1%	1%	<1%	<1%	2%	189
Grouper*	<i>Chelidonichthys capensis</i>	1%	1%	<1%	<1%	2%	189
Grouper*	<i>Cynoscion albus</i>	1%	1%	<1%	<1%	2%	189
Grouper*	<i>Cynoscion guatucupa</i>	1%	1%	<1%	<1%	2%	189
Grouper*	<i>Cynoscion virescens</i>	2%	2%	1%	<1%	4%	189
Grouper*	<i>Gadus chalcogrammus</i>	1%	1%	<1%	<1%	2%	189
Grouper*	<i>Hyporthodus nr</i>	1%	1%	<1%	<1%	2%	189
Grouper*	<i>Lobotes surinamensis</i>	1%	1%	<1%	<1%	2%	189

Expected	Substitute	Posterior Mean	Posterior Median	Posterior Mode	Lower 95% HDI	Higher 95% HDI	n
Grouper*	<i>Merluccius merluccius</i>	1%	1%	<1%	<1%	2%	189
Grouper*	<i>Micropogonias furnieri</i>	1%	1%	<1%	<1%	2%	189
Grouper*	<i>Oreochromis niloticus</i>	1%	1%	<1%	<1%	2%	189
Grouper*	<i>Oreochromis nr</i>	1%	1%	<1%	<1%	2%	189
Grouper*	<i>Pangasianodon hypophthalmus</i>	2%	2%	2%	1%	5%	189
Grouper*	<i>Pangasius bocourti</i>	1%	1%	1%	<1%	2%	189
Grouper*	<i>Scarus nr</i>	1%	1%	<1%	<1%	2%	189
Grouper*	<i>Scomberomorus cavalla</i>	1%	1%	<1%	<1%	2%	189
Haddock	<i>Gadus*cephalus</i>	<1%	<1%	<1%	<1%	1%	626
Haddock	<i>Gadus morhua</i>	3%	3%	3%	1%	4%	626
Haddock	<i>Gadus nr</i>	<1%	<1%	<1%	<1%	1%	626
Haddock	<i>Lepidocybium flavobrunneum</i>	<1%	<1%	<1%	<1%	1%	626
Haddock	<i>Merlangius merlangus</i>	1%	<1%	<1%	<1%	1%	626
Haddock	<i>Pollachius pollachius</i>	<1%	<1%	<1%	<1%	1%	626
Haddock	<i>Pollachius virens</i>	1%	<1%	<1%	<1%	1%	626
Humphead snapper	<i>Lutjanus erythropterus</i>	22%	21%	21%	12%	33%	54
Humphead snapper	<i>Lutjanus malabaricus</i>	51%	51%	51%	38%	64%	54
Humphead snapper	<i>Lutjanus nr</i>	2%	1%	1%	<1%	5%	54
Humphead snapper	<i>Lutjanus sebae</i>	2%	1%	1%	<1%	5%	54
Kaluga	<i>Acipenser gueldenstaedtii</i>	1%	<1%	<1%	<1%	1%	237
Kaluga	<i>Acipenser schrenckii</i>	11%	10%	10%	7%	15%	237
Northern red snapper	<i>Gadus morhua</i>	1%	<1%	<1%	<1%	2%	219
Northern red snapper	<i>Lates niloticus</i>	1%	<1%	<1%	<1%	2%	219
Northern red snapper	<i>Lutjanus analis</i>	1%	1%	1%	<1%	3%	219
Northern red snapper	<i>Lutjanus erythropterus</i>	1%	1%	1%	<1%	2%	219
Northern red snapper	<i>Lutjanus griseus</i>	3%	3%	3%	1%	5%	219
Northern red snapper	<i>Lutjanus malabaricus</i>	2%	2%	1%	<1%	3%	219
Northern red snapper	<i>Lutjanus novemfasiatus</i>	1%	<1%	<1%	<1%	2%	219
Northern red snapper	<i>Lutjanus sanguineus</i>	12%	12%	12%	8%	17%	219

Expected	Substitute	Posterior Mean	Posterior Median	Posterior Mode	Lower 95% HDI	Higher 95% HDI	n
Northern red snapper	<i>Lutjanus synagris</i>	6%	6%	6%	3%	10%	219
Northern red snapper	<i>Lutjanus vivanus</i>	1%	<1%	<1%	<1%	2%	219
Northern red snapper	<i>Ocyurus chrysurus</i>	1%	1%	1%	<1%	2%	219
Northern red snapper	<i>Oreochromis nr</i>	7%	7%	7%	4%	11%	219
Northern red snapper	<i>Pagrus major</i>	5%	5%	5%	3%	8%	219
Northern red snapper	<i>Pangasianodon hypophthalmus</i>	1%	<1%	<1%	<1%	1%	219
Northern red snapper	<i>Pinjalo lewisi</i>	1%	<1%	<1%	<1%	1%	219
Northern red snapper	<i>Pristipomoides sieboldii</i>	1%	1%	1%	<1%	2%	219
Northern red snapper	<i>Rhomboplites aurorubens</i>	2%	2%	2%	1%	4%	219
Northern red snapper	<i>Sebastes fasciatus</i>	1%	1%	1%	<1%	2%	219
Northern red snapper	<i>Sebastes nr</i>	1%	1%	1%	<1%	2%	219
Pacific bluefin tuna	<i>Thunnus albacares</i>	68%	68%	68%	56%	79%	61
Pacific bluefin tuna	<i>Thunnus obesus</i>	19%	19%	18%	10%	29%	61
Pacific bluefin tuna	<i>Xiphias gladius</i>	2%	1%	1%	<1%	4%	61
Pacific cod	<i>Gadus morhua</i>	6%	6%	5%	3%	10%	169
Pacific cod	<i>Liparis nr</i>	2%	1%	1%	<1%	3%	169
Pacific cod	<i>Melanogrammus aeglefinus</i>	1%	1%	1%	<1%	3%	169
Pacific salmon*	<i>Oncorhynchus mykiss</i>	1%	<1%	<1%	<1%	1%	235
Pacific salmon*	<i>Salmo salar</i>	26%	26%	25%	20%	32%	235
Pacific snapper*	<i>Oreochromis nr</i>	8%	8%	7%	3%	14%	77
Salmon*	<i>Cynoscion guatucupa</i>	1%	1%	1%	<1%	2%	204
Salmon*	<i>Micropogonias furnieri</i>	1%	1%	<1%	<1%	2%	204
Salmon*	<i>Oncorhynchus mykiss</i>	1%	1%	1%	<1%	2%	204
Salmon*	<i>Prionace glauca</i>	1%	1%	<1%	<1%	2%	204
Salmon*	<i>Salmo trutta</i>	1%	1%	<1%	<1%	2%	204
Salmon*	<i>Seriola zonata</i>	1%	1%	<1%	<1%	2%	204
Salmon*	<i>Thunnus alalunga</i>	1%	1%	<1%	<1%	2%	204
Sardine*	<i>Brevoortia aurea</i>	19%	18%	18%	13%	24%	193
Sardine*	<i>Centengraulis edentulus</i>	5%	5%	5%	2%	8%	193

Expected	Substitute	Posterior Mean	Posterior Median	Posterior Mode	Lower 95% HDI	Higher 95% HDI	n
Sardine*	<i>Clupea harengus</i>	4%	4%	3%	1%	7%	193
Sardine*	<i>Rastrelliger faughni</i>	1%	1%	<1%	<1%	2%	193
Sardine*	<i>Scomber japonicus</i>	6%	6%	6%	3%	10%	193
Sardine*	<i>Trachurus lathami</i>	1%	1%	<1%	<1%	2%	193
Seabass*	<i>Lateolabrax japonicus</i>	3%	3%	2%	<1%	7%	51
Seabass*	<i>Morone chrysops</i>	2%	1%	1%	<1%	5%	51
Seabass*	<i>Morone saxatilis</i>	2%	1%	1%	<1%	5%	51
Seabass*	<i>Oreochromis niloticus</i>	2%	1%	1%	<1%	5%	51
Seabass*	<i>Pagrus major</i>	3%	3%	2%	<1%	7%	51
Seabass*	<i>Paralichthys dentatus</i>	2%	1%	1%	<1%	5%	51
Seabass*	<i>Sciaenops ocellatus</i>	2%	1%	1%	<1%	5%	51
Seabass*	<i>Sparus aurata</i>	3%	3%	2%	<1%	7%	51
Shrimp*	<i>Litopenaeus vannamei</i>	1%	1%	<1%	<1%	3%	85
Shrimp*	<i>Pleoticus robustus</i>	3%	3%	2%	<1%	6%	85
Snapper*	<i>Lutjanus argentimaculatus</i>	2%	2%	2%	<1%	5%	114
Snapper*	<i>Lutjanus kasmira</i>	1%	1%	<1%	<1%	3%	114
Snapper*	<i>Lutjanus sanguineus</i>	1%	1%	<1%	<1%	3%	114
Snapper*	<i>Oreochromis aureus</i>	2%	1%	1%	<1%	4%	114
Snapper*	<i>Oreochromis mossambicus</i>	2%	1%	1%	<1%	4%	114
Snapper*	<i>Oreochromis niloticus</i>	12%	12%	12%	7%	18%	114
Snapper*	<i>Oreochromis nr</i>	6%	5%	5%	2%	10%	114
Snapper*	<i>Oreochromis urolepis</i>	1%	1%	<1%	<1%	3%	114
Snapper*	<i>Pagrus major</i>	1%	1%	<1%	<1%	3%	114
Snapper*	<i>Sebastes alutus</i>	2%	1%	1%	<1%	4%	114
Snapper*	<i>Sebastes babcocki</i>	1%	1%	<1%	<1%	3%	114
Snapper*	<i>Sebastes entomelas</i>	2%	2%	2%	<1%	5%	114
Snapper*	<i>Sebastes flavidus</i>	3%	3%	2%	1%	6%	114
Snapper*	<i>Seriola quinqueradiata</i>	1%	1%	<1%	<1%	3%	114
Snapper*	<i>Sparus aurata</i>	1%	1%	<1%	<1%	3%	114



Expected	Substitute	Posterior Mean	Posterior Median	Posterior Mode	Lower 95% HDI	Higher 95% HDI	n
Sockeye salmon	<i>Oncorhynchus kisutch</i>	2%	2%	1%	<1%	4%	92
Squid*	<i>Doryteuthis gahi</i>	4%	3%	3%	1%	8%	91
Squid*	<i>Lagocephalus spadiceus</i>	6%	5%	5%	2%	10%	91
Squid*	<i>Sepia pharaonis</i>	10%	10%	9%	4%	16%	91
Squid*	<i>Upeneus japonicus</i>	2%	2%	1%	<1%	5%	91
Squid*	<i>Uroteuthis duvaucelii</i>	5%	4%	4%	1%	9%	91
Starry sturgeon	<i>Acipenser baerii</i>	<1%	<1%	<1%	<1%	1%	1183
Starry sturgeon	<i>Acipenser baerii x naccaraii x persicus</i>	<1%	<1%	<1%	<1%	<1%	1183
Starry sturgeon	<i>Acipenser gueldenstaedtii</i>	1%	1%	1%	1%	2%	1183
Starry sturgeon	<i>Acipenser gueldenstaedtii x naccarii</i>	<1%	<1%	<1%	<1%	<1%	1183
Starry sturgeon	<i>Acipenser nudiventris</i>	4%	4%	4%	3%	5%	1183
Starry sturgeon	<i>Acipenser persicus</i>	<1%	<1%	<1%	<1%	<1%	1183
Starry sturgeon	<i>Acipenser ruthenus</i>	<1%	<1%	<1%	<1%	<1%	1183
Starry sturgeon	<i>Huso dauricus</i>	<1%	<1%	<1%	<1%	<1%	1183
Starry sturgeon	<i>Huso huso</i>	<1%	<1%	<1%	<1%	<1%	1183
Starry sturgeon	<i>Polyodon spathula</i>	<1%	<1%	<1%	<1%	1%	1183
Striped catfish	<i>Coryphaena hippurus</i>	1%	1%	<1%	<1%	2%	194
Striped catfish	<i>Micropogonias furnieri</i>	1%	1%	<1%	<1%	2%	194
Striped catfish	<i>Nemipterus japonicus</i>	1%	1%	<1%	<1%	2%	194
Swordfish	<i>Istiompax indica</i>	1%	<1%	<1%	<1%	1%	222
Swordfish	<i>Isurus oxyrinchus</i>	5%	5%	4%	2%	7%	222
Swordfish	<i>Makaira nigricans</i>	1%	<1%	<1%	<1%	1%	222
Swordfish	<i>Prionace glauca</i>	11%	11%	11%	7%	15%	222
Swordfish	<i>Thunnus obesus</i>	9%	8%	8%	5%	12%	222
Tilapia*	<i>Pangasianodon hypophthalmus</i>	1%	1%	1%	<1%	4%	69
Tilapia*	<i>Pangasianodon nr</i>	1%	1%	<1%	<1%	4%	69
Tuna*	<i>Auxis rochei</i>	<1%	<1%	<1%	<1%	1%	547
Tuna*	<i>Katsuwonus pelamis</i>	<1%	<1%	<1%	<1%	1%	547
Tuna*	<i>Lepidocybium flavobrunneum</i>	3%	3%	3%	2%	5%	547

Expected	Substitute	Posterior Mean	Posterior Median	Posterior Mode	Lower 95% HDI	Higher 95% HDI	n
Tuna*	<i>Oreochromis mossambicus</i>	<1%	<1%	<1%	<1%	1%	547
Tuna*	<i>Salmo salar</i>	1%	1%	<1%	<1%	1%	547
Tuna*	<i>Seriola lalandi</i>	1%	1%	<1%	<1%	1%	547
Tuna*	<i>Seriola quinqueradiata</i>	<1%	<1%	<1%	<1%	1%	547
Tuna*	<i>Seriola zonata</i>	<1%	<1%	<1%	<1%	1%	547
Whiteleg shrimp	<i>Parapenaeopsis nr</i>	1%	1%	<1%	<1%	3%	111
Whiteleg shrimp	<i>Penaeus monodon</i>	5%	5%	4%	1%	9%	111
Whiteleg shrimp	<i>Xystreureys rasile</i>	1%	1%	<1%	<1%	3%	111
Yellowfin tuna	<i>Euthynnus alletteratus</i>	<1%	<1%	<1%	<1%	1%	392
Yellowfin tuna	<i>Katsuwonus pelamis</i>	1%	1%	<1%	<1%	1%	392
Yellowfin tuna	<i>Sarda sarda</i>	<1%	<1%	<1%	<1%	1%	392
Yellowfin tuna	<i>Seriola quinqueradiata</i>	<1%	<1%	<1%	<1%	1%	392
Yellowfin tuna	<i>Thunnus alalunga</i>	1%	1%	1%	<1%	3%	392
Yellowfin tuna	<i>Thunnus atlanticus</i>	<1%	<1%	<1%	<1%	1%	392
Yellowfin tuna	<i>Thunnus obesus</i>	11%	11%	11%	8%	14%	392
Yellowfin tuna	<i>Thunnus thynnus</i>	2%	2%	2%	1%	4%	392
Yellowtail amberjack	<i>Seriola quinqueradiata</i>	74%	75%	75%	64%	84%	76

**Table SI-2.** Diagnostics for expected-substitute pair mislabeling rate estimates. Effective sample size (ESS), Markov chain standard error (MCSE) and the Gelman-Rubin shrink reduction factor (Shrink factor) for the  $\alpha$  estimates for each pair. Diagnostics indicate converged chains (i.e., Shrink Factor <1.1), ESS > 10,000, and MCSE as a % of the standard deviation <5% for all factors. Common names correspond to Fishbase [2] and Sealifebase [2]. Products with an \* represent more than one species.

<b>Expected</b>	<b>Substitute</b>	<b>ESS</b>	<b>MCSE</b>	<b>Shrink factor</b>
Albacore	<i>Katsuwonus pelamis</i>	604,974	0.4	1.000
Albacore	<i>Lepidocybium flavobrunneum</i>	651,635	0.4	1.000
Albacore	<i>Thunnus albacares</i>	629,973	0.4	1.000
Albacore	<i>Thunnus obesus</i>	625,857	0.4	1.000
Albacore	<i>Thunnus thynnus</i>	638,760	0.4	1.000
Amur sturgeon	<i>Huso dauricus</i>	614,346	0.4	1.000
Anchovy*	<i>Engraulis encrasicolus</i>	627,932	0.4	1.000
Angler*	<i>Lophius litulon</i>	609,959	0.4	1.000
Angler*	<i>Lophius vomerinus</i>	618,636	0.4	1.000
Angler*	<i>Protonibea diacanthus</i>	627,364	0.4	1.000
Atlantic bluefin tuna	<i>Thunnus alalunga</i>	632,255	0.4	1.000
Atlantic bluefin tuna	<i>Thunnus albacares</i>	625,030	0.4	1.000
Atlantic bluefin tuna	<i>Thunnus atlanticus</i>	630,264	0.4	1.000
Atlantic bluefin tuna	<i>Thunnus obesus</i>	619,793	0.4	1.000
Atlantic cod	<i>Brosme brosme</i>	635,320	0.4	1.000
Atlantic cod	<i>Gadus chalcogrammus</i>	627,504	0.4	1.000
Atlantic cod	<i>Gadus*cephalus</i>	616,008	0.4	1.000
Atlantic cod	<i>Melanogrammus aeglefinus</i>	595,508	0.4	1.000
Atlantic cod	<i>Merlangius merlangus</i>	619,410	0.4	1.000
Atlantic cod	<i>Merluccius nr</i>	623,213	0.4	1.000
Atlantic cod	<i>Molva dypterygia</i>	658,255	0.4	1.000
Atlantic cod	<i>Molva molva</i>	634,717	0.4	1.000
Atlantic cod	<i>Pangasianodon hypophthalmus</i>	600,698	0.4	1.000

<b>Expected</b>	<b>Substitute</b>	<b>ESS</b>	<b>MCSE</b>	<b>Shrink factor</b>
Atlantic cod	<i>Perca flavescens</i>	640,742	0.4	1.000
Atlantic cod	<i>Pollachius pollachius</i>	612,982	0.4	1.000
Atlantic cod	<i>Pollachius virens</i>	622,447	0.4	1.000
Atlantic cod	<i>Ruvettus pretiosus</i>	639,077	0.4	1.000
Atlantic salmon	<i>Oncorhynchus keta</i>	633,893	0.4	1.000
Atlantic salmon	<i>Oncorhynchus mykiss</i>	626,611	0.4	1.000
Atlantic salmon	<i>Oncorhynchus nerka</i>	649,063	0.4	1.000
Atlantic salmon	<i>Salmo trutta</i>	633,790	0.4	1.000
Barramundi	<i>Lates niloticus</i>	613,034	0.4	1.000
Barramundi	<i>Lates nr</i>	607,074	0.4	1.000
Barramundi	<i>Serirolella brama</i>	636,720	0.4	1.000
Beluga	<i>Acipenser baerii</i>	639,415	0.4	1.000
Beluga	<i>Acipenser baerii x naccarii x persicus</i>	625,196	0.4	1.000
Beluga	<i>Acipenser gueldenstaedtii</i>	609,098	0.4	1.000
Beluga	<i>Acipenser gueldenstaedtii x naccarii</i>	614,922	0.4	1.000
Beluga	<i>Acipenser persicus</i>	644,383	0.4	1.000
Beluga	<i>Acipenser sinensis</i>	635,218	0.4	1.000
Beluga	<i>Acipenser stellatus</i>	609,765	0.4	1.000
Beluga	<i>Acipenser transmontanus</i>	637,686	0.4	1.000
Beluga	<i>Huso dauricus</i>	644,302	0.4	1.000
Blue crab	<i>Callinectes bellicosus</i>	628,757	0.4	1.000
Blue crab	<i>Charybdis nr</i>	645,025	0.4	1.000
Blue crab	<i>Portunus nr</i>	635,903	0.4	1.000
Blue crab	<i>Portunus pelagicus</i>	622,913	0.4	1.000
Blue crab	<i>Portunus pseudoargentatus</i>	622,992	0.4	1.000
Blue crab	<i>Portunus sanguinolentus</i>	662,358	0.4	1.000
Blue crab	<i>Portunus trituberculatus</i>	625,402	0.4	1.000
Chinook salmon	<i>Oncorhynchus keta</i>	612,000	0.4	1.000
Chinook salmon	<i>Oncorhynchus kisutch</i>	638,862	0.4	1.000

<b>Expected</b>	<b>Substitute</b>	<b>ESS</b>	<b>MCSE</b>	<b>Shrink factor</b>
Chinook salmon	<i>Salmo salar</i>	615,442	0.4	1.000
Cod*	<i>Albatrossia pectoralis</i>	632,044	0.4	1.000
Cod*	<i>Anarhichas minor</i>	646,508	0.4	1.000
Cod*	<i>Anoplopoma fimbria</i>	611,717	0.4	1.000
Cod*	<i>Argentina silus</i>	627,959	0.4	1.000
Cod*	<i>Atheresthes evermanni</i>	656,415	0.4	1.000
Cod*	<i>Atheresthes stomias</i>	630,544	0.4	1.000
Cod*	<i>Dissostichus eleginoides</i>	614,203	0.4	1.000
Cod*	<i>Gadus chalcogrammus</i>	637,083	0.4	1.000
Cod*	<i>Lagocephalus spadiceus</i>	621,730	0.4	1.000
Cod*	<i>Lagocephalus wheeleri</i>	631,184	0.4	1.000
Cod*	<i>Lates niloticus</i>	617,780	0.4	1.000
Cod*	<i>Macrourus carinatus</i>	622,233	0.4	1.000
Cod*	<i>Melanogrammus aeglefinus</i>	620,014	0.4	1.000
Cod*	<i>Merluccius angustimanus</i>	627,712	0.4	1.000
Cod*	<i>Merluccius capensis</i>	637,487	0.4	1.000
Cod*	<i>Merluccius hubbsi</i>	609,666	0.4	1.000
Cod*	<i>Merluccius merluccius</i>	623,645	0.4	1.000
Cod*	<i>Merluccius paradoxus</i>	614,560	0.4	1.000
Cod*	<i>Merluccius productus</i>	644,420	0.4	1.000
Cod*	<i>Micromesistius australis</i>	632,384	0.4	1.000
Cod*	<i>Molva dypterygia</i>	630,589	0.4	1.000
Cod*	<i>Molva molva</i>	629,223	0.4	1.000
Cod*	<i>Oreochromis nr</i>	643,975	0.4	1.000
Cod*	<i>Pangasianodon hypophthalmus</i>	635,059	0.4	1.000
Cod*	<i>Pollachius pollachius</i>	624,391	0.4	1.000
Cod*	<i>Pollachius virens</i>	634,100	0.4	1.000
Cod*	<i>Reinhardtius hippoglossoides</i>	651,458	0.4	1.000
Cod*	<i>Ruvettus pretiosus</i>	629,912	0.4	1.000

<b>Expected</b>	<b>Substitute</b>	<b>ESS</b>	<b>MCSE</b>	<b>Shrink factor</b>
Common dolphinfish	<i>Argyrozona argyrozona</i>	623,829	0.4	1.000
Common dolphinfish	<i>Brachyplatystoma platynemum</i>	647,530	0.4	1.000
Common dolphinfish	<i>Seriola lalandi</i>	628,307	0.4	1.000
Danube sturgeon	<i>Acipenser baerii</i>	637,830	0.4	1.000
Danube sturgeon	<i>Acipenser baerii x naccaraii x persicus</i>	605,952	0.4	1.000
Danube sturgeon	<i>Acipenser nudiventris</i>	623,625	0.4	1.000
Danube sturgeon	<i>Acipenser persicus</i>	629,512	0.4	1.000
Danube sturgeon	<i>Acipenser schrenckii</i>	619,298	0.4	1.000
Danube sturgeon	<i>Acipenser stellatus</i>	610,092	0.4	1.000
Danube sturgeon	<i>Acipenser transmontanus</i>	640,972	0.4	1.000
Danube sturgeon	<i>Huso dauricus</i>	637,722	0.4	1.000
Danube sturgeon	<i>Huso huso</i>	617,145	0.4	1.000
Flounder*	<i>Atheresthes stomias</i>	609,590	0.4	1.000
Flounder*	<i>Cynoscion guatucupa</i>	618,590	0.4	1.000
Flounder*	<i>Isopisthus parvipinnis</i>	637,935	0.4	1.000
Flounder*	<i>Micropogonias furnieri</i>	646,736	0.4	1.000
Flounder*	<i>Pangasianodon hypophthalmus</i>	627,748	0.4	1.000
Flounder*	<i>Pangasianodon nr</i>	636,811	0.4	1.000
Flounder*	<i>Paralichthys patagonicus</i>	619,612	0.4	1.000
Fringebarbel sturgeon	<i>Acipenser stellatus</i>	632,619	0.4	1.000
Fringebarbel sturgeon	<i>Huso huso</i>	625,040	0.4	1.000
Grouper*	<i>Acanthistius brasilianus</i>	631,120	0.4	1.000
Grouper*	<i>Aprion virescens</i>	639,407	0.4	1.000
Grouper*	<i>Brotula barbata</i>	617,729	0.4	1.000
Grouper*	<i>Caulolatilus nr</i>	640,586	0.4	1.000
Grouper*	<i>Chelidonichthys capensis</i>	653,528	0.4	1.000

<b>Expected</b>	<b>Substitute</b>	<b>ESS</b>	<b>MCSE</b>	<b>Shrink factor</b>
Grouper*	<i>Cynoscion albus</i>	626,003	0.4	1.000
Grouper*	<i>Cynoscion guatucupa</i>	647,566	0.4	1.000
Grouper*	<i>Cynoscion virescens</i>	650,222	0.4	1.000
Grouper*	<i>Gadus chalcogrammus</i>	643,003	0.4	1.000
Grouper*	<i>Hyporthodus nr</i>	627,223	0.4	1.000
Grouper*	<i>Lobotes surinamensis</i>	641,673	0.4	1.000
Grouper*	<i>Merluccius merluccius</i>	649,107	0.4	1.000
Grouper*	<i>Micropogonias furnieri</i>	657,483	0.4	1.000
Grouper*	<i>Oreochromis niloticus</i>	631,787	0.4	1.000
Grouper*	<i>Oreochromis nr</i>	658,557	0.4	1.000
Grouper*	<i>Pangasianodon hypophthalmus</i>	637,404	0.4	1.000
Grouper*	<i>Pangasius bocourti</i>	645,830	0.4	1.000
Grouper*	<i>Scarus nr</i>	666,977	0.4	1.000
Grouper*	<i>Scomberomorus cavalla</i>	649,970	0.4	1.000
Haddock	<i>Gadus*cephalus</i>	622,886	0.4	1.000
Haddock	<i>Gadus morhua</i>	624,397	0.4	1.000
Haddock	<i>Gadus nr</i>	633,823	0.4	1.000
Haddock	<i>Lepidocybium flavobrunneum</i>	638,279	0.4	1.000
Haddock	<i>Merlangius merlangus</i>	647,843	0.4	1.000
Haddock	<i>Pollachius pollachius</i>	638,367	0.4	1.000
Haddock	<i>Pollachius virens</i>	625,015	0.4	1.000
Humphead snapper	<i>Lutjanus erythropterus</i>	617,591	0.4	1.000
Humphead snapper	<i>Lutjanus malabaricus</i>	597,735	0.4	1.000
Humphead snapper	<i>Lutjanus nr</i>	651,535	0.4	1.000
Humphead snapper	<i>Lutjanus sebae</i>	630,145	0.4	1.000
Kaluga	<i>Acipenser gueldenstaedtii</i>	634,267	0.4	1.000
Kaluga	<i>Acipenser schrenckii</i>	626,241	0.4	1.000

<b>Expected</b>	<b>Substitute</b>	<b>ESS</b>	<b>MCSE</b>	<b>Shrink factor</b>
Northern red snapper	<i>Gadus morhua</i>	630,075	0.4	1.000
Northern red snapper	<i>Lates niloticus</i>	657,332	0.4	1.000
Northern red snapper	<i>Lutjanus analis</i>	650,991	0.4	1.000
Northern red snapper	<i>Lutjanus erythropterus</i>	639,239	0.4	1.000
Northern red snapper	<i>Lutjanus griseus</i>	603,397	0.4	1.000
Northern red snapper	<i>Lutjanus malabaricus</i>	620,819	0.4	1.000
Northern red snapper	<i>Lutjanus novemfasiatus</i>	639,114	0.4	1.000
Northern red snapper	<i>Lutjanus sanguineus</i>	643,542	0.4	1.000
Northern red snapper	<i>Lutjanus synagris</i>	611,302	0.4	1.000
Northern red snapper	<i>Lutjanus vivanus</i>	627,832	0.4	1.000
Northern red snapper	<i>Ocyurus chrysurus</i>	648,581	0.4	1.000
Northern red snapper	<i>Oreochromis nr</i>	625,257	0.4	1.000
Northern red snapper	<i>Pagrus major</i>	648,568	0.4	1.000
Northern red snapper	<i>Pangasianodon hypophthalmus</i>	631,884	0.4	1.000
Northern red snapper	<i>Pinjalo lewisi</i>	625,036	0.4	1.000
Northern red snapper	<i>Pristipomoides sieboldii</i>	631,573	0.4	1.000
Northern red snapper	<i>Rhomboplites aurorubens</i>	612,277	0.4	1.000
Northern red snapper	<i>Sebastes fasciatus</i>	642,730	0.4	1.000
Northern red snapper	<i>Sebastes nr</i>	631,595	0.4	1.000



<b>Expected</b>	<b>Substitute</b>	<b>ESS</b>	<b>MCSE</b>	<b>Shrink factor</b>
Pacific bluefin tuna	<i>Thunnus albacares</i>	589,796	0.4	1.000
Pacific bluefin tuna	<i>Thunnus obesus</i>	598,775	0.4	1.000
Pacific bluefin tuna	<i>Xiphias gladius</i>	635,436	0.4	1.000
Pacific cod	<i>Gadus morhua</i>	625,960	0.4	1.000
Pacific cod	<i>Liparis nr</i>	615,977	0.4	1.000
Pacific cod	<i>Melanogrammus aeglefinus</i>	626,688	0.4	1.000
Pacific salmon*	<i>Oncorhynchus mykiss</i>	633,844	0.4	1.000
Pacific salmon*	<i>Salmo salar</i>	601,939	0.4	1.000
Pacific snapper*	<i>Oreochromis nr</i>	627,060	0.4	1.000
Salmon*	<i>Cynoscion guatucupa</i>	654,136	0.4	1.000
Salmon*	<i>Micropogonias furnieri</i>	647,156	0.4	1.000
Salmon*	<i>Oncorhynchus mykiss</i>	619,672	0.4	1.000
Salmon*	<i>Prionace glauca</i>	642,766	0.4	1.000
Salmon*	<i>Salmo trutta</i>	650,003	0.4	1.000
Salmon*	<i>Seriola zonata</i>	643,108	0.4	1.000
Salmon*	<i>Thunnus alalunga</i>	638,441	0.4	1.000
Sardine*	<i>Brevoortia aurea</i>	627,805	0.4	1.000
Sardine*	<i>Centengraulis edentulus</i>	610,138	0.4	1.000
Sardine*	<i>Clupea harengus</i>	625,059	0.4	1.000
Sardine*	<i>Rastrelliger faughni</i>	646,329	0.4	1.000
Sardine*	<i>Scomber japonicus</i>	641,773	0.4	1.000
Sardine*	<i>Trachurus lathami</i>	628,257	0.4	1.000
Seabass*	<i>Lateolabrax japonicus</i>	628,877	0.4	1.000
Seabass*	<i>Morone chrysops</i>	638,820	0.4	1.000
Seabass*	<i>Morone saxatilis</i>	643,728	0.4	1.000
Seabass*	<i>Oreochromis niloticus</i>	654,975	0.4	1.000
Seabass*	<i>Pagrus major</i>	628,406	0.4	1.000
Seabass*	<i>Paralichthys dentatus</i>	649,173	0.4	1.000

<b>Expected</b>	<b>Substitute</b>	<b>ESS</b>	<b>MCSE</b>	<b>Shrink factor</b>
Seabass*	<i>Sciaenops ocellatus</i>	647,636	0.4	1.000
Seabass*	<i>Sparus aurata</i>	634,594	0.4	1.000
Shrimp*	<i>Litopenaeus vannamei</i>	642,882	0.4	1.000
Shrimp*	<i>Pleoticus robustus</i>	623,891	0.4	1.000
Snapper*	<i>Lutjanus argentimaculatus</i>	623,864	0.4	1.000
Snapper*	<i>Lutjanus kasmira</i>	636,416	0.4	1.000
Snapper*	<i>Lutjanus sanguineus</i>	649,620	0.4	1.000
Snapper*	<i>Oreochromis aureus</i>	638,884	0.4	1.000
Snapper*	<i>Oreochromis mossambicus</i>	624,786	0.4	1.000
Snapper*	<i>Oreochromis niloticus</i>	630,445	0.4	1.000
Snapper*	<i>Oreochromis nr</i>	636,995	0.4	1.000
Snapper*	<i>Oreochromis urolepis</i>	655,432	0.4	1.000
Snapper*	<i>Pagrus major</i>	662,327	0.4	1.000
Snapper*	<i>Sebastes alutus</i>	632,270	0.4	1.000
Snapper*	<i>Sebastes babcocki</i>	665,227	0.4	1.000
Snapper*	<i>Sebastes entomelas</i>	630,875	0.4	1.000
Snapper*	<i>Sebastes flavidus</i>	643,771	0.4	1.000
Snapper*	<i>Seriola quinqueradiata</i>	648,597	0.4	1.000
Snapper*	<i>Sparus aurata</i>	638,635	0.4	1.000
Sockeye salmon	<i>Oncorhynchus kisutch</i>	632,192	0.4	1.000
Squid*	<i>Doryteuthis gahi</i>	605,700	0.4	1.000
Squid*	<i>Lagocephalus spadiceus</i>	630,402	0.4	1.000
Squid*	<i>Sepia pharaonis</i>	614,290	0.4	1.000
Squid*	<i>Upeneus japonicus</i>	629,960	0.4	1.000
Squid*	<i>Uroteuthis duvaucelii</i>	613,937	0.4	1.000
Starry sturgeon	<i>Acipenser baerii</i>	614,292	0.4	1.000
Starry sturgeon	<i>Acipenser baerii x naccarii x persicus</i>	623,861	0.4	1.000
Starry sturgeon	<i>Acipenser gueldenstaedtii</i>	626,354	0.4	1.000
Starry sturgeon	<i>Acipenser gueldenstaedtii x naccarii</i>	631,744	0.4	1.000

<b>Expected</b>	<b>Substitute</b>	<b>ESS</b>	<b>MCSE</b>	<b>Shrink factor</b>
Starry sturgeon	<i>Acipenser nudiiventris</i>	620,015	0.4	1.000
Starry sturgeon	<i>Acipenser persicus</i>	626,022	0.4	1.000
Starry sturgeon	<i>Acipenser ruthenus</i>	635,761	0.4	1.000
Starry sturgeon	<i>Huso dauricus</i>	619,253	0.4	1.000
Starry sturgeon	<i>Huso huso</i>	594,126	0.4	1.000
Starry sturgeon	<i>Polyodon spathula</i>	628,556	0.4	1.000
Striped catfish	<i>Coryphaena hippurus</i>	651,213	0.4	1.000
Striped catfish	<i>Micropogonias furnieri</i>	655,506	0.4	1.000
Striped catfish	<i>Nemipterus japonicus</i>	634,809	0.4	1.000
Swordfish	<i>Istiompax indica</i>	630,080	0.4	1.000
Swordfish	<i>Isurus oxyrinchus</i>	620,511	0.4	1.000
Swordfish	<i>Makaira nigricans</i>	657,479	0.4	1.000
Swordfish	<i>Prionace glauca</i>	629,522	0.4	1.000
Swordfish	<i>Thunnus obesus</i>	609,050	0.4	1.000
Tilapia*	<i>Pangasianodon hypophthalmus</i>	646,412	0.4	1.000
Tilapia*	<i>Pangasianodon nr</i>	631,118	0.4	1.000
Tuna*	<i>Auxis rochei</i>	608,491	0.4	1.000
Tuna*	<i>Katsuwonus pelamis</i>	649,813	0.4	1.000
Tuna*	<i>Lepidocybium flavobrunneum</i>	630,804	0.4	1.000
Tuna*	<i>Oreochromis mossambicus</i>	627,047	0.4	1.000
Tuna*	<i>Salmo salar</i>	633,087	0.4	1.000
Tuna*	<i>Seriola lalandi</i>	637,153	0.4	1.000
Tuna*	<i>Seriola quinqueradiata</i>	629,611	0.4	1.000
Tuna*	<i>Seriola zonata</i>	627,995	0.4	1.000
Whiteleg shrimp	<i>Parapenaeopsis nr</i>	646,225	0.4	1.000
Whiteleg shrimp	<i>Penaeus monodon</i>	630,460	0.4	1.000
Whiteleg shrimp	<i>Xystreuryx rasile</i>	644,147	0.4	1.000
Yellowfin tuna	<i>Euthynnus alletteratus</i>	648,716	0.4	1.000
Yellowfin tuna	<i>Katsuwonus pelamis</i>	627,840	0.4	1.000

<b>Expected</b>	<b>Substitute</b>	<b>ESS</b>	<b>MCSE</b>	<b>Shrink factor</b>
Yellowfin tuna	<i>Sarda sarda</i>	635,122	0.4	1.000
Yellowfin tuna	<i>Seriola quinqueradiata</i>	643,166	0.4	1.000
Yellowfin tuna	<i>Thunnus alalunga</i>	636,225	0.4	1.000
Yellowfin tuna	<i>Thunnus atlanticus</i>	642,423	0.4	1.000
Yellowfin tuna	<i>Thunnus obesus</i>	616,969	0.4	1.000
Yellowfin tuna	<i>Thunnus thynnus</i>	632,906	0.4	1.000
Yellowtail amberjack	<i>Seriola quinqueradiata</i>	588,426	0.4	1.000

**Table SI-3:** Bootstrapping Results for Seafood Watch Score Tests (*U.S. 50+ Pairs*)

	<b>Target Species</b>	<b>Other Species</b>	<b>Management Effectiveness</b>	<b>Habitat and Ecosystem</b>
Percentage point difference from 50%	-35.705***	-35.795***	-27.852***	-20.449**
P-value	0.000	0.000	0.000	0.040

N=39

Statistical significance levels: \* 10-percent, \*\* 5-percent, \*\*\* 1-percent

**Table SI-4:** Bootstrapping Results Examining Differences in Import Percentages for *U.S. 50+ Pairs*, *Global 50+ Pairs* and *Global 100+ Pairs* Datasets

	<b>US 50+</b>	<b>Global 50+</b>	<b>Global 100+</b>
Average percentage-point difference in imports	27.842**	30.88***	26.896***
P-value	.014	0.000	0.008
Observations	144	217	167

Statistical significance levels: \* 10-percent, \*\* 5-percent, \*\*\* 1-percent

**Table SI-5:** Bootstrapping Results for Seafood Watch Score Tests: *Global 50+ Pairs*

	<b>Target Species</b>	<b>Other Species</b>	<b>Management Effectiveness</b>	<b>Habitat and Ecosystem</b>
Percentage point difference from 50%	-38.136***	-28.845***	-30.664***	-19.204**
P-value	0.000	0.000	0.000	.030

N=55

Statistical significance levels: \* 10-percent, \*\* 5-percent, \*\*\* 1-percent

**Table SI-6:** Bootstrapping Results for Seafood Watch Score Tests: *Global 100+ Pairs*

	<b>Target Species</b>	<b>Other Species</b>	<b>Management Effectiveness</b>	<b>Habitat and Ecosystem</b>
Percentage point difference from 50%	-35.171***	-22.058***	-27.477***	-10.727
P-value	0.000	0.005	0.000	0.416

N=44

Statistical significance levels: \* 10-percent, \*\* 5-percent, \*\*\* 1-percent



**Table SI-7:** Bootstrapping Results Excluding Species Groups: *U.S. 50+ Pairs*

	Import Percentages	Seafood Watch Scores			
		Target Species	Other Species	Management Effectiveness	Habitat and Ecosystem
Excluding Anchovy Imports N = 143 SW Score N = 38	27.816** (0.047)	-35.797*** (0.000)	-35.887*** (0.000)	-27.924*** (0.000)	-20.501** (0.039)
Excluding Grouper Imports N = 137 SW Score N = 47	27.864** (0.046)	-35.739*** (0.000)	-35.877*** (0.000)	-27.927*** (0.000)	-20.468** (0.040)
Excluding Haddock Imports N = 138 SW Score N = 35	28.046** (0.046)	-35.512*** (0.000)	-35.681*** (0.000)	-28.460*** (0.000)	-20.043* (0.054)
Excluding Hake macro Imports N = 144 SW Score N = 39	27.842** (0.046)	-35.705*** (0.000)	-35.795*** (0.000)	-27.852*** (0.000)	-20.449** (0.040)
Excluding Octopus Imports N = 144 SW Score N = 39	27.842** (0.046)	-35.705*** (0.000)	-35.795*** (0.000)	-27.852*** (0.000)	-20.449** (0.040)
Excluding Sardine Imports N = 141 SW Score N = 38	28.372** (0.042)	-36.416*** (0.000)	-36.506*** (0.000)	-27.498*** (0.000)	-20.204** (0.046)
Excluding Swordfish Imports N = 141 SW Score N = 36	28.924** (0.038)	-34.879*** (0.000)	-34.974*** (0.000)	-29.650*** (0.000)	-23.476*** (0.002)
Excluding Tuna Imports N = 130 SW Score N = 31	30.340** (0.034)	-36.378*** (0.000)	-43.438*** (0.000)	-35.960*** (0.000)	-28.229*** (0.000)

P-values are in parentheses.

Statistical significance levels: \* 10-percent, \*\* 5-percent, \*\*\* 1-percent

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