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Matching Northeast Biological Samples to Dealer-reported Commercial Landings, 2006-2015

by Brian C Linton

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INTRODUCTION

Length and age samples collected from commercial fisheries provide important information on the size and age structure of managed fish stocks. These biological samples are used with landings data to estimate commercial catch-at-age. Catch-at-age is used in age-structured stock assessment models to help estimate key management quantities like age-specific spawning stock biomass and fishing mortality rates. Length and age samples must be representative of commercial landings to obtain accurate estimates of catch-at-age. If length and age samples are not representative of landings, then bias may be introduced into the catch-at-age estimates and age-structured assessment model results.

In the Northeast and Mid-Atlantic regions, commercial length and age samples are collected by contracted port samplers as part of the Greater Atlantic Regional Fisheries Office Port Biological Sampling Program (PBSP). Port samplers select commercial trips to sample based on biological sampling requests. The sampling requests are made annually by the Northeast Fisheries Science Center's (NEFSC) stock assessment analysts. Sampling requests are stratified by region, species, market category, gear, stock area, and quarter. Samples may be collected at different points along the processing chain: at the dock, fish dealer, or fish exchange. A length sample typically consists of 100 fish of a specific species and market category landed on a single commercial fishing trip, while an age sample typically consists of 25 fish subsampled from a length sample. The target number of fish in a sample can vary based on species and market category, and the realized number of fish in a sample can differ from the target number. Biological sample information is entered into the NEFSC Biological Sample Monitoring Database System (BSMDBS) by the port samplers. Additional details on the PBSP's sampling protocol can be found in GARFO (2017).

Finalized commercial length, age, and dealer-reported landings data reside in the NEFSC's Commercial Fisheries Database System (CFDBS). Since 1994, commercial length data have resided in year-specific Commercial Fisheries Length Data with Area Allocation (CFLEN AA) tables, while commercial age data reside in year-specific Commercial Fisheries Age Data with Area Allocation (CFAGE AA) tables, and dealer-reported landings data reside in year-specific Commercial Fisheries Detail Species Data with Area Allocation (CFDETS AA) tables. Biological samples and dealer-reported landings are allocated to statistical areas by using information from vessel trip reports, which are filed by vessel captains.

Commercial age and length samples generally are assumed to be representative of commercial landings in stock assessments conducted through the Northeast Regional Stock Assessment Workshop process. This study attempts to evaluate if those biological samples are representative of landings. One means of determining if length and age samples are representative is to match those samples to the commercial fishing trips from which they were collected. Therefore, the goals of this study are to (1) match age samples to their associated length samples and (2) match length samples to their associated commercial trips.

METHODS

Length and Age Sample Matching

The first part of this analysis included the 16 fish species assessed by the NEFSC, from which both commercial length and age samples were collected in the most recent 10 years with finalized AA tables (2006-2015; Table 1). Commercial length data were obtained from the 2006 to 2015 CFLEN AA tables in CFDBS. Commercial age data were obtained from the 2006 to 2015

CFAGE AA tables in CFDBS. Length and age data were aggregated at the sample level by using the LINK variable, which uniquely identifies a sample. All database variables used in the following analyses are defined in Table 2. Matching was conducted by using R (R Core Team 2017). The R script for all analyses presented here can be found in Appendix A.

The LINK variable was used to match age samples to length samples. There are other variables common to the age and length samples that should have the same values, when the age and length sample LINK variables match. Four of these variables were compared between the age and length samples, when the age and length sample LINK variables matched: PORT (port, as a proxy for region), NEGEAR (gear), AREA (statistical area, as proxy for stock area), and NESPP4 (species and market category). These 4 variables were chosen, because they represent the biological sampling strata not captured by the LINK variable. If an age sample's LINK, PORT, NEGEAR, AREA, and NESPP4 variables matched those same variables in a length sample, then the age sample was considered a match to that length sample. If an age sample's LINK variable did not match the LINK variable of any length sample, then the age sample was considered an "orphan." If an age sample's LINK variable matched a length sample's LINK variable, but 1 or more of the PORT, NEGEAR, AREA, or NESPP4 variables did not match, then the age sample was considered a partial match to the length sample.

Length Sample and Landings Matching

The second part of this analysis included the 30 fish species assessed by the NEFSC, from which commercial length samples were collected between 2006 and 2015 (Table 1). Commercial length data were obtained from the 2006 to 2015 CFLEN AA tables in CFDBS. Dealer-reported landings data were obtained from the 2006 to 2015 CFDETS AA tables in CFDBS. Length data were aggregated at the sample level using the LINK variable, which uniquely identifies a sample. Dealer-reported landings were aggregated at the commercial fishing trip level using the YEAR, MONTH, DAY, PERMIT (vessel permit number), and NESPP3 (species) variables, which uniquely identify a trip landing a specific species.

The YEAR, MONTH, DAY, PERMIT, and NESPP3 variables were used to match length samples to commercial fishing trips. There are other variables common to the length samples and dealer-reported landings that should have the same values, when length sample and commercial trip YEAR, MONTH, DAY, PERMIT, and NESPP3 variables match. Four of these variables were compared between the length samples and commercial trips, when the length sample and commercial trip YEAR, MONTH, DAY, PERMIT, and NESPP3 variables matched: PORT, NEGEAR, AREA, and NESPP4. If a length sample's YEAR, MONTH, DAY, PERMIT, NESPP3, PORT, NEGEAR, AREA, and NESPP4 variables matched those same variables in a commercial trip, then the length sample was considered a match to that commercial trip. If a length sample's YEAR, MONTH, DAY, PERMIT, and NESPP3 variables did not match those same variables in any commercial trip, then the length sample was considered an orphan. If a length sample's YEAR, MONTH, DAY, PERMIT, and NESPP3 variables matched those same variables in a commercial trip, but 1 or more of the PORT, NEGEAR, AREA, or NESPP4 variables did not match, then the length sample was considered a partial match to that commercial trip.

RESULTS

Length and Age Sample Matching

The species-specific proportions of age samples collected during 2006-2015 that could be matched to length samples were relatively high (Table 3; Figure 1). Atlantic mackerel (*Scomber scombrus*) was the 1 exception to these matching rates, with a matched age sample proportion of 0.66. For the remaining species, the proportions of age samples that could be matched to length samples ranged from 0.93 for anglerfish (*Lophius americanus*) and butterfish (*Peprilus triacanthus*) to 1.00 for bluefish (*Pomatomus saltatrix*) and silver hake (*Merluccius bilinearis*).

The majority of species analyzed had at least 1 orphan age sample (Table 3; Figure 1). Anglerfish, bluefish, American plaice (*Hippoglossoides platessoides*), silver hake, and black sea bass (*Centropristis striata*) were the only species without orphan age samples. For the remaining species, the proportions of age samples that were orphan samples ranged from 0.0009 for pollock to 0.3333 for Atlantic mackerel.

The majority of species analyzed had at least 1 partially matched age sample (Table 3; Figure 1). Bluefish, butterfish, silver hake, and golden tilefish (*Lopholatilus chamaeleonticeps*) were the only species without partially matched age samples. For the remaining species, the proportions of age samples that were partial matches ranged from 0.0017 for Atlantic cod (*Gadus morhua*) to 0.0667 for anglerfish. The majority of partial matches were due to differences in the AREA variable between age and length samples (Table 4; Figure 2). Anglerfish, haddock (*Melanogrammus aeglefinus*), Atlantic mackerel, scup (*Stenotomus chrysops*), winter flounder (*Pseudopleuronectes americanus*), witch flounder (*Glyptocephalus cynoglossus*), and yellowtail flounder (*Limanda ferruginea*) had proportions of partially matched age samples that had different AREA values greater than 0.5.

Length Sample and Landings Matching

The species-specific proportions of length samples, collected during 2006-2015, that could be matched to commercial trips varied by species (Table 5; Figure 3). American shad (*Alosa sapidissima*) and offshore hake (*Merluccius albidus*) were the only species without matched length samples. For the remaining species, the proportions of length samples that could be matched to commercial trips ranged from 0.07 for ocean pout (*Zoarces americanus*) to 0.69 for spiny dogfish (*Squalus acanthias*).

All of the species analyzed had at least 1 orphan length sample (Table 5; Figure 3). The proportions of length samples that were orphan samples ranged from 0.09 for blueline tilefish (*Caulolatilus microps*) to 1.00 for offshore hake.

The majority of species analyzed had at least 1 partially matched age sample (Table 5; Figure 3). Ocean pout, Atlantic herring (*Clupea harengus*), and offshore hake were the only species without partially matched length samples. For the remaining species, the proportions of length samples that were partial matches ranged from 0.03 for red hake to 0.60 for Atlantic halibut (*Hippoglossus hippoglossus*). The majority of partial matches were due to differences in the NESPP4 variable between length samples and commercial trips (Table 6; Figure 4). Bluefish, butterfish, Atlantic halibut, scup, silver hake, white hake (*Urophycis tenuis*), and windowpane flounder (*Scophthalmus aquosus*) had proportions of partially matched length samples that had different NESPP4 values greater than 0.5.

A cursory examination of the dealer data indicates that many of these discrepancies in the NESPP4 variable between length samples and commercial trips are associated with 2-3 fish dealers, though this may be an artifact of the volume of landings handled by those dealers. Further investigation of the dealer data will be required to better understand this issue.

Year- and species-specific proportions of matched, orphan, and partially matched length samples are available in Appendix B for additional details.

DISCUSSION

While the majority of commercial age samples could be matched to length samples, there still were a handful of orphan and partially matched age samples. The existence of the orphan age samples generally can be explained by missing data values associated with the age samples. It is unclear how these missing data values are present in the age sample, but not the associated length sample, because both samples are collected and entered into BSMDBS by the same port sampler. For the same reason, it is difficult to explain how partially matched age samples can occur. The fact that differences in AREA values between age and length samples are the primary cause of these partial matches suggests that there might be issues with the algorithm used to allocate age and length samples to statistical areas. Regardless of the reasons, it should be remembered that only a small number of age samples are orphans or partial matches. In addition, the PBSP is planning to switch from a paper-based data collection system to an electronic data collection system in FY2018, which should help to eliminate orphan and partially matched age samples going forward.

A relatively high proportion of length samples could not be matched completely to a commercial trip, because of differences in variable values between length samples and the commercial trips from which they were collected. These differences in variable values likely arise from the fact that these 2 data streams are reported by different parties. The commercial length samples are reported by the PBSP port samplers, while the commercial landings are reported by fish dealers. These differences could be introduced through errors in reporting, through an actual change in a variable's value, or through a change in the disposition of the landed fish. Errors in reporting could range from unintentional key punch errors to intentional misreporting of catch. Changes in variable values can occur when fish dealers sort unclassified fish into different market categories after biological sampling occurs, or when dealers change market categories after sampling occurs, due to changes in demand or price. In the case of offshore hake, where none of the length samples could be matched to commercial trips, it appears that these fish may have come from mixed landings of silver and offshore hake, which are often reported simply as silver hake. These mixed landings are a known issue in the silver hake assessment (Alade and Traver 2018). Introduction of a universal trip ID variable would improve matching between length samples and commercial trips going forward but would not address problems matching historical length samples and commercial trips.

Partial matches appear to be an important issue when matching length samples to commercial trips. Length samples that are partial matches to commercial trips introduce uncertainty in the representativeness of those samples. For example, if the AREA value differs between the length sample and its trip, then it may not be clear which statistical area is correct. This uncertainty in statistical area assignment may result in uncertainty in stock area assignment, which means the sample may not be representative of landings from the stock area to which it was assigned. In addition, it may mean that the landings from that commercial trip were assigned to the incorrect stock area. If differences in variable values between biological samples and commercial trips cannot be resolved, then consideration must be given to the appropriateness of using partially matched samples in stock assessments.

Orphan samples appear to be an issue when matching length samples to commercial trips. Orphan length samples cannot be matched to a commercial trip, and, therefore, may not be representative of commercial landings. If biological samples cannot be matched to commercial trips, then consideration must be given to the appropriateness of using orphan samples in stock assessments. One option would be to assume that the orphan samples are representative of the landings and include them in stock assessments. This option would maintain the status quo approach. The second option would be to assume that the orphan samples are not representative of the landings and to exclude them from use in stock assessments. The impact of both options on the accuracy and precision of assessment results is unknown but likely would vary by stock. A simulation study could be conducted to determine the possible impacts of including non-representative biological samples in an assessment. In addition, current stock assessments could be rerun excluding orphan (and perhaps partially matched) length and age samples for comparison purposes.

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Table 1. Species for which commercial length and age samples were collected from 2006-2015. Abbreviations are those used in the figures. Length indicates whether or not length samples were collected. Age indicates whether or not age samples were collected.

Species	Abbreviation	Length	Age
ANGLERFISH (*Lophius americanus*)	ANGLER	yes	yes
BLUEFISH (*Pomatomus saltatrix*)	BLUEFISH	yes	yes
BUTTERFISH *(Peprilus triacanthus)*	BUTTRFSH	yes	yes
COD, ATLANTIC *(Gadus morhua)*	COD	yes	yes
CUSK (*Brosme brosme*)	CUSK	yes	no
DOGFISH, SPINY (*Squalus acanthias*)	DOGF SP	yes	no
FLOUNDER, AM. PLAICE (*Hippoglossoides platessoides*)	AMPLAICE	yes	yes
FLOUNDER, SAND-DAB (*Scophthalmus aquosus*)	WINDP FL	yes	no
FLOUNDER, SUMMER (*Paralichthys dentatus*)	SUM FL	yes	yes
FLOUNDER, WINTER (*Pseudopleuronectes americanus*)	WIN FL	yes	yes
FLOUNDER, WITCH (*Glyptocephalus cynoglossus*)	WIT FL	yes	yes
FLOUNDER, YELLOWTAIL (*Limanda ferruginea*)	YEL FL	yes	yes
HADDOCK (*Melanogrammus aeglefinus*)	HADDOCK	yes	yes
HAGFISH (*Myxine glutinosa*)	HAGFISH	yes	no
HAKE, OFFSHORE (*Merluccius albidus*)	OFFSHHAK	yes	no
HAKE, RED (*Urophycis chuss*)	RED HAKE	yes	no
HAKE, SILVER (*Merluccius bilinearis*)	SIL HAKE	yes	yes
HAKE, WHITE (*Urophycis tenuis*)	WH HAKE	yes	no
HALIBUT, ATLANTIC (*Hippoglossus hippoglossus*)	HALIBUT	yes	no
HERRING, ATLANTIC (*Clupea harengus*)	SEA HERR	yes	no
MACKEREL, ATLANTIC (*Scomber scombrus*)	MACKEREL	yes	yes
POLLOCK (*Pollachius virens*)	POLLOCK	yes	yes
POUT, OCEAN (*Zoarces americanus*)	O POUT	yes	no
REDFISH (*Sebastes fasciatus*)	REDFISH	yes	no
SCUP (*Stenotomus chrysops*)	SCUP	yes	yes
SEA BASS, BLACK (*Centropristis striata*)	BLKSBASS	yes	yes
SHAD, AMERICAN (*Alosa sapidissima*)	AM SHAD	yes	no
TILEFISH, BLUELINE (*Caulolatilus microps*)	BLU TILE	yes	no
TILEFISH, GOLDEN (*Lopholatilus chamaeleonticeps*)	GLD TILE	yes	yes
WOLFFISH, ATLANTIC (*Anarhichas lupus*)	WOLFFISH	yes	no

Table 2. Commercial Fisheries Database System (CFDBS) variables used in analyses. Definition explains meaning of variables. Age-Length indicates whether or not variables were used to match commercial age and length samples. Length-Landings indicates whether or not variables were used to match length samples to commercial trips.

Variable	Definition	Age-Length	Length-Landings
AREA	Allocated area in which catch occurred	yes	yes
DAY	Day of vessel landing	no	yes
LINK	Links age and length samples; consists of MONTH, DOCN, TALLYNO, SAMPNO variables	yes	no
MONTH	Month of vessel landing	no	yes
NEGEAR	Gear used by vessel	yes	yes
NESPP3	Species	no	yes
NESPP4	Species and market category	yes	yes
PERMIT	Vessel permit number	no	yes
PORT	Port in which vessel landed catch	yes	yes
YEAR	Year of vessel landing	no	yes

Table 3. Proportion of commercial age samples that could be matched to commercial length samples (Match) by species from 2006 to 2015. No. of Samples is the number of age samples collected. Orphan is the proportion of age samples that could not be matched to length samples. Partial Match is the proportion of age samples that matched some, but not all, variable values between the age and length samples.

Species	No. of Samples	Match	Orphan	Partial Match
ANGLERFISH (*Lophius americanus*)	15	0.9333	0.0000	0.0667
BLUEFISH (*Pomatomus saltatrix*)	138	1.0000	0.0000	0.0000
BUTTERFISH (*Peprilus triacanthus*)	29	0.9310	0.0690	0.0000
COD, ATLANTIC (*Gadus morhua*)	4,822	0.9965	0.0019	0.0017
FLOUNDER, AM. PLAICE (*Hippoglossoides platessoides*)	805	0.9975	0.0000	0.0025
FLOUNDER, SUMMER (*Paralichthys dentatus*)	1,980	0.9904	0.0061	0.0035
FLOUNDER, WINTER (*Pseudopleuronectes americanus*)	1,460	0.9925	0.0021	0.0055
FLOUNDER, WITCH (*Glyptocephalus cynoglossus*)	1,334	0.9963	0.0015	0.0022
FLOUNDER, YELLOWTAIL (*Limanda ferruginea*)	1,705	0.9941	0.0029	0.0029
HADDOCK (*Melanogrammus aeglefinus*)	2,182	0.9991	0.0005	0.0005
HAKE, SILVER (*Merluccius bilinearis*)	188	1.0000	0.0000	0.0000
MACKEREL, ATLANTIC (*Scomber scombrus*)	165	0.6606	0.3333	0.0061
POLLOCK (*Pollachius virens*)	1,120	0.9982	0.0009	0.0009
SCUP (*Stenotomus chrysops*)	1,262	0.9929	0.0040	0.0032
SEA BASS, BLACK (*Centropristis striata*)	556	0.9982	0.0000	0.0018
TILEFISH, GOLDEN (*Lopholatilus chamaeleonticeps*)	258	0.9612	0.0388	0.0000

Table 4. Proportion of commercial age samples that did not completely match to commercial length samples by species from 2006 to 2015 (Partial Match in Table 3; Figure 1). No. of Samples is the number of partially matched age samples. PORT, NEGEAR, AREA, and NESPP4 are the proportion of partially matched age samples where the value of that variable differed between the age and length samples. Multiple variable names (e.g., PORT.NEGEAR) are the proportion of partially matched age samples where the values of those variables differed between the age and length samples.

Species	No. of Samples	PORT	NEGEAR	AREA	NESPP4	PORT. NEGEAR	PORT. AREA	PORT. NESPP4	NEGEAR. AREA	NEGEAR. NESPP4	AREA. NESPP4	PORT. NEGEAR. AREA	PORT. NEGEAR. NESPP4	PORT. AREA. NESPP4	NEGEAR. AREA. NESPP4	PORT. NEGEAR. AREA. NESPP4
ANGLERFISH *Lophius americanus*	1	0.0000	0.0000	1.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
COD, ATLANTIC *Gadus morhua*	8	0.1250	0.2500	0.5000	0.0000	0.1250	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, AM. PLAICE *Hippoglossoides platessoides*	2	0.0000	0.0000	0.5000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.5000	0.0000	0.0000	0.0000
FLOUNDER, SUMMER *Paralichthys dentatus*	7	0.2857	0.4286	0.1429	0.0000	0.1429	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, WINTER *Pseudopleuronectes americanus*	8	0.0000	0.0000	1.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, WITCH *Glyptocephalus cynoglossus*	3	0.0000	0.0000	1.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, YELLOWTAIL *Limanda ferruginea*	5	0.0000	0.0000	1.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HADDOCK *Melanogrammus aeglefinus*	1	0.0000	0.0000	1.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MACKEREL, ATLANTIC *Scomber scombrus*	1	0.0000	0.0000	1.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
POLLOCK *Pollachius virens*	1	0.0000	1.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SCUP *Stenotomus chrysops*	4	0.0000	0.0000	0.7500	0.0000	0.2500	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SEA BASS, BLACK *Centropristis striata*	1	1.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

Table 5. Proportion of commercial length samples that could be matched to commercial trips (Match) by species from 2006 to 2015. No. of Trips is the number of commercial trips sampled. No. of Samples is the number of length samples collected. Orphan is the proportion of length samples that could not be matched to commercial trips. Partial Match is the proportion of length samples that matched some, but not all, variable values between the length samples and commercial trips.

Species	No. of Trips	No. of Samples	Match	Orphan	Partial Match
ANGLERFISH (*Lophius americanus*)	902	1,044	0.5862	0.2443	0.1695
BLUEFISH (*Pomatomus saltatrix*)	765	875	0.3874	0.3006	0.3120
BUTTERFISH (*Peprilus triacanthus*	341	354	0.3418	0.3588	0.2994
COD, ATLANTIC (*Gadus morhua*)	4,020	5,376	0.6475	0.2072	0.1453
CUSK (*Brosme brosme*)	854	861	0.5656	0.2485	0.1858
DOGFISH, SPINY (*Squalus acanthias*)	542	547	0.6947	0.1353	0.1700
FLOUNDER, AM. PLAICE (*Hippoglossoides platessoides*)	688	925	0.5676	0.2822	0.1503
FLOUNDER, SAND-DAB (*Scophthalmus aquosus*)	151	151	0.3841	0.3444	0.2715
FLOUNDER, SUMMER (*Paralichthys dentatus*)	1,596	2,180	0.6147	0.2587	0.1266
FLOUNDER, WINTER (*Pseudopleuronectes americanus*)	1,230	1,642	0.4927	0.3076	0.1998
FLOUNDER, WITCH (*Glyptocephalus cynoglossus*)	1,251	1,539	0.6381	0.2326	0.1293
FLOUNDER, YELLOWTAIL (*Limanda ferruginea*)	1,262	1,804	0.5072	0.3343	0.1585
HADDOCK (*Melanogrammus aeglefinus*)	1,663	2,448	0.6070	0.2471	0.1458
HAGFISH (*Myxine glutinosa*)	192	193	0.4663	0.4249	0.1088
HAKE, OFFSHORE (*Merluccius albidus*)	40	48	0.0000	1.0000	0.0000
HAKE, RED (*Urophycis chuss*)	348	354	0.6554	0.3192	0.0254
HAKE, SILVER (*Merluccius bilinearis*)	1,245	1,619	0.4688	0.2847	0.2464
HAKE, WHITE (*Urophycis tenuis*)	903	1,211	0.4946	0.3047	0.2007
HALIBUT, ATLANTIC (*Hippoglossus hippoglossus*)	873	873	0.1913	0.2119	0.5968
HERRING, ATLANTIC (*Clupea harengus*)	22	23	0.2609	0.7391	0.0000
MACKEREL, ATLANTIC (*Scomber scombrus*)	415	530	0.1868	0.2736	0.5396
POLLOCK (*Pollachius virens*)	1,063	1,275	0.6165	0.1922	0.1914
POUT, OCEAN (*Zoarces americanus*)	15	15	0.0667	0.9333	0.0000
REDFISH (*Sebastes fasciatus*)	187	190	0.6211	0.2368	0.1421
SCUP (*Stenotomus chrysops*)	994	1,362	0.5382	0.3289	0.1329
SEA BASS, BLACK (*Centropristis striata*)	722	978	0.4560	0.3303	0.2137
SHAD, AMERICAN (*Alosa sapidissima*)	3	3	0.0000	0.6667	0.3333
TILEFISH, BLUELINE (*Caulolatilus microps*)	8	11	0.5455	0.0909	0.3636
TILEFISH, GOLDEN (*Lopholatilus chamaeleonticeps*)	520	1,056	0.5095	0.3788	0.1117
WOLFFISH, ATLANTIC (*Anarhichas lupus*)	464	465	0.6301	0.2151	0.1548

Table 6. Proportion of commercial length samples that did not completely match to commercial trips by species from 2006 to 2015 (Partial Match in Table 5; Figure 3). No. of Trips is the number of commercial trips from which partially matched length samples were collected. No. of Samples is the number of partially matched length samples. PORT, NEGEAR, AREA, and NESPP4 are the proportion of partially matched length samples where the value of that variable differed between the length samples and commercial trips. Multiple variable names (e.g., PORT.NEGEAR) are the proportion of partially matched age samples where the values of those variables differed between the length samples and commercial trips.

Species	No. of Trips	No. of Samples	PORT	NEGEAR	AREA	NESPP4	PORT. NEGEAR	PORT. AREA	PORT. NESPP4	NEGEAR. AREA	NEGEAR. NESPP4	AREA. NESPP4	PORT. NEGEAR. AREA	PORT. NEGEAR. NESPP4	PORT. AREA. NESPP4	NEGEAR .AREA. NESPP4	PORT. NEGEAR. AREA. NESPP4
ANGLERFISH																	
Lophius americanus	158	177	0.3220	0.1695	0.2486	0.1864	0.0000	0.0113	0.0113	0.0226	0.0113	0.0056	0.0000	0.0000	0.0000	0.0113	0.0000
BLUEFISH																	
Pomatomus saltatrix	239	273	0.0293	0.2308	0.0293	0.6117	0.0000	0.0037	0.0220	0.0256	0.0073	0.0183	0.0073	0.0037	0.0000	0.0073	0.0037
BUTTERFISH																	
Peprilus triacanthus	104	106	0.0000	0.0189	0.0472	0.8491	0.0000	0.0094	0.0283	0.0000	0.0283	0.0189	0.0000	0.0000	0.0000	0.0000	0.0000
COD, ATLANTIC																	
Gadus morhua	634	781	0.4814	0.2228	0.1549	0.0294	0.0102	0.0179	0.0141	0.0576	0.0013	0.0013	0.0090	0.0000	0.0000	0.0000	0.0000
CUSK																	
Brosme brosme	155	160	0.2063	0.2813	0.0875	0.2750	0.0063	0.0000	0.0063	0.0625	0.0563	0.0125	0.0000	0.0000	0.0000	0.0063	0.0000
DOGFISH, SPINY																	
Squalus acanthias	93	93	0.2903	0.3441	0.1075	0.1398	0.0215	0.0108	0.0108	0.0538	0.0108	0.0000	0.0108	0.0000	0.0000	0.0000	0.0000
FLOUNDER, AM. PLAICE																	
Hippoglossoides platessoides	113	139	0.3022	0.2662	0.2374	0.1223	0.0000	0.0072	0.0144	0.0504	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, SAND-DAB																	
Scophthalmus aquosus	41	41	0.0000	0.0732	0.1463	0.6585	0.0000	0.0244	0.0244	0.0488	0.0000	0.0244	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, SUMMER																	
Paralichthys dentatus	225	276	0.0543	0.2138	0.1812	0.4239	0.0000	0.0000	0.0399	0.0326	0.0109	0.0109	0.0000	0.0000	0.0181	0.0145	0.0000
FLOUNDER, WINTER																	
Pseudopleuronectes americanus	277	328	0.0915	0.1372	0.2165	0.2957	0.0244	0.0091	0.0549	0.0884	0.0244	0.0122	0.0213	0.0030	0.0030	0.0152	0.0030
FLOUNDER, WITCH																	
Glyptocephalus cynoglossus	168	199	0.3367	0.1608	0.3015	0.0352	0.0050	0.0101	0.0503	0.0754	0.0050	0.0050	0.0050	0.0000	0.0101	0.0000	0.0000
FLOUNDER, YELLOWTAIL																	
Limanda ferruginea	237	286	0.1399	0.1224	0.2448	0.3392	0.0140	0.0035	0.0210	0.0734	0.0000	0.0105	0.0280	0.0000	0.0000	0.0035	0.0000
HADDOCK																	
Melanogrammus aeglefinus	259	357	0.0980	0.3193	0.2381	0.1513	0.0084	0.0028	0.0000	0.1457	0.0252	0.0112	0.0000	0.0000	0.0000	0.0000	0.0000

Table 6, continued. Proportion of commercial length samples that did not completely match to commercial trips by species from 2006 to 2015 (Partial Match in Table 5; Figure 3). No. of Trips is the number of commercial trips from which partially matched length samples were collected. No. of Samples is the number of partially matched length samples. PORT, NEGEAR, AREA, and NESPP4 are the proportion of partially matched length samples where the value of that variable differed between the length samples and commercial trips. Multiple variable names (e.g., PORT.NEGEAR) are the proportion of partially matched age samples where the values of those variables differed between the length samples and commercial trips.

Species	No. of Trips	No. of Samples	PORT	NEGEAR	AREA	NESPP4	PORT. NEGEAR	PORT. AREA	PORT. NESPP4	NEGEAR. AREA	NEGEAR. NESPP4	AREA. NESPP4	PORT. NEGEAR. AREA	PORT. NEGEAR. NESPP4	PORT. AREA. NESPP4	NEGEAR .AREA. NESPP4	PORT. NEGEAR. AREA. NESPP4
HAGFISH																	
Myxine glutinosa	21	21	0.0000	0.5238	0.0952	0.0000	0.0000	0.0000	0.0000	0.3810	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, RED																	
Urophycis chuss	9	9	0.2222	0.2222	0.3333	0.0000	0.0000	0.1111	0.0000	0.1111	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, SILVER																	
Merluccius bilinearis	360	399	0.0627	0.0251	0.0376	0.8045	0.0000	0.0025	0.0125	0.0125	0.0075	0.0251	0.0000	0.0000	0.0025	0.0075	0.0000
HAKE, WHITE																	
Urophycis tenuis	217	243	0.1111	0.1111	0.1029	0.6132	0.0123	0.0041	0.0000	0.0247	0.0000	0.0206	0.0000	0.0000	0.0000	0.0000	0.0000
HALIBUT, ATLANTIC																	
Hippoglossus hippoglossus	521	521	0.0096	0.0403	0.0307	0.7889	0.0000	0.0000	0.0422	0.0096	0.0345	0.0345	0.0000	0.0038	0.0000	0.0058	0.0000
MACKEREL, ATLANTIC																	
Scomber scombrus	200	286	0.0140	0.3497	0.0175	0.2657	0.0035	0.0035	0.0140	0.1084	0.1154	0.0210	0.0035	0.0070	0.0035	0.0734	0.0000
POLLOCK																	
Pollachius virens	209	244	0.3566	0.1393	0.1230	0.2172	0.0205	0.0123	0.0041	0.0369	0.0574	0.0205	0.0000	0.0000	0.0000	0.0123	0.0000
REDFISH																	
Sebastes fasciatus	27	27	0.0741	0.1852	0.2963	0.2963	0.0370	0.0000	0.0000	0.0741	0.0000	0.0000	0.0000	0.0000	0.0000	0.0370	0.0000
SCUP																	
Stenotomus chrysops	160	181	0.1215	0.0442	0.1492	0.5304	0.0000	0.0166	0.0331	0.0221	0.0055	0.0552	0.0110	0.0055	0.0000	0.0000	0.0055
SEA BASS, BLACK																	
Centropristis striata	160	209	0.1770	0.1579	0.1962	0.3014	0.0048	0.0239	0.0096	0.0526	0.0239	0.0191	0.0096	0.0048	0.0000	0.0048	0.0144
SHAD, AMERICAN																	
Alosa sapidissima	1	1	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	1.0000
TILEFISH, BLUELINE																	
Caulolatilus microps	3	4	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
TILEFISH, GOLDEN																	
Lopholatilus chamaeleonticeps	84	118	0.3475	0.0593	0.0169	0.4746	0.0000	0.0339	0.0508	0.0085	0.0000	0.0085	0.0000	0.0000	0.0000	0.0000	0.0000
WOLFFISH, ATLANTIC																	
Anarhichas lupus	71	72	0.3333	0.1806	0.3611	0.0000	0.0139	0.0278	0.0000	0.0694	0.0000	0.0000	0.0139	0.0000	0.0000	0.0000	0.0000

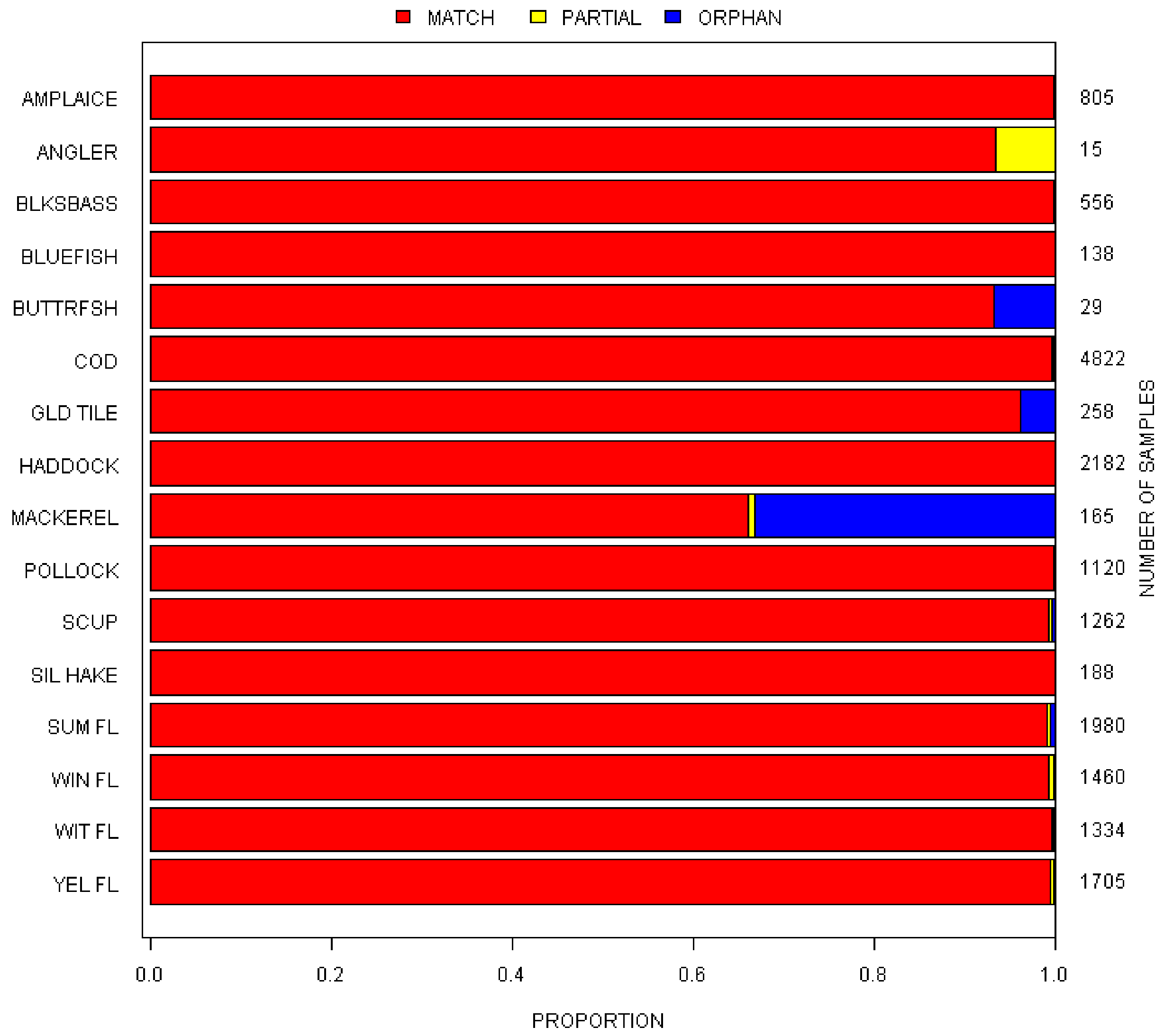

Figure 1. Proportion of commercial age samples that could be matched to commercial length samples (Match) by species from 2006 to 2015. Orphan is the proportion of age samples that could not be matched to length samples. Partial Match is the proportion of age samples that matched some, but not all, variable values between the age and length samples. Number of Samples is the number of age samples collected. Species include anglerfish (*Lophius americanus*, ANGLER), bluefish (*Pomatomus saltatrix*, BLUEFISH), butterfish (*Peprilus triacanthus*, BUTTRFSH), Atlantic cod (*Gadus morhua*, COD), American plaice (*Hippoglossoides platessoides*, AMPLAICE), summer flounder (*Paralichthys dentatus*, SUM FL), winter flounder (*Pseudopleuronectes americanus*, WIN FL), witch flounder (*Glyptocephalus cynoglossus*, WIT FL), yellowtail flounder (*Limanda ferruginea*, YEL FL), haddock (*Melanogrammus aeglefinus*, HADDOCK), silver hake (*Merluccius bilinearis*, SIL HAKE), Atlantic mackerel (*Scomber scombrus*, MACKEREL), pollock (*Pollachius virens*, POLLOCK), scup (*Stenotomus chrysops*, SCUP), black sea bass (*Centropristis striata*, BLKSBASS), golden tilefish (*Lopholatilus chamaeleonticeps*, GLD TILE).

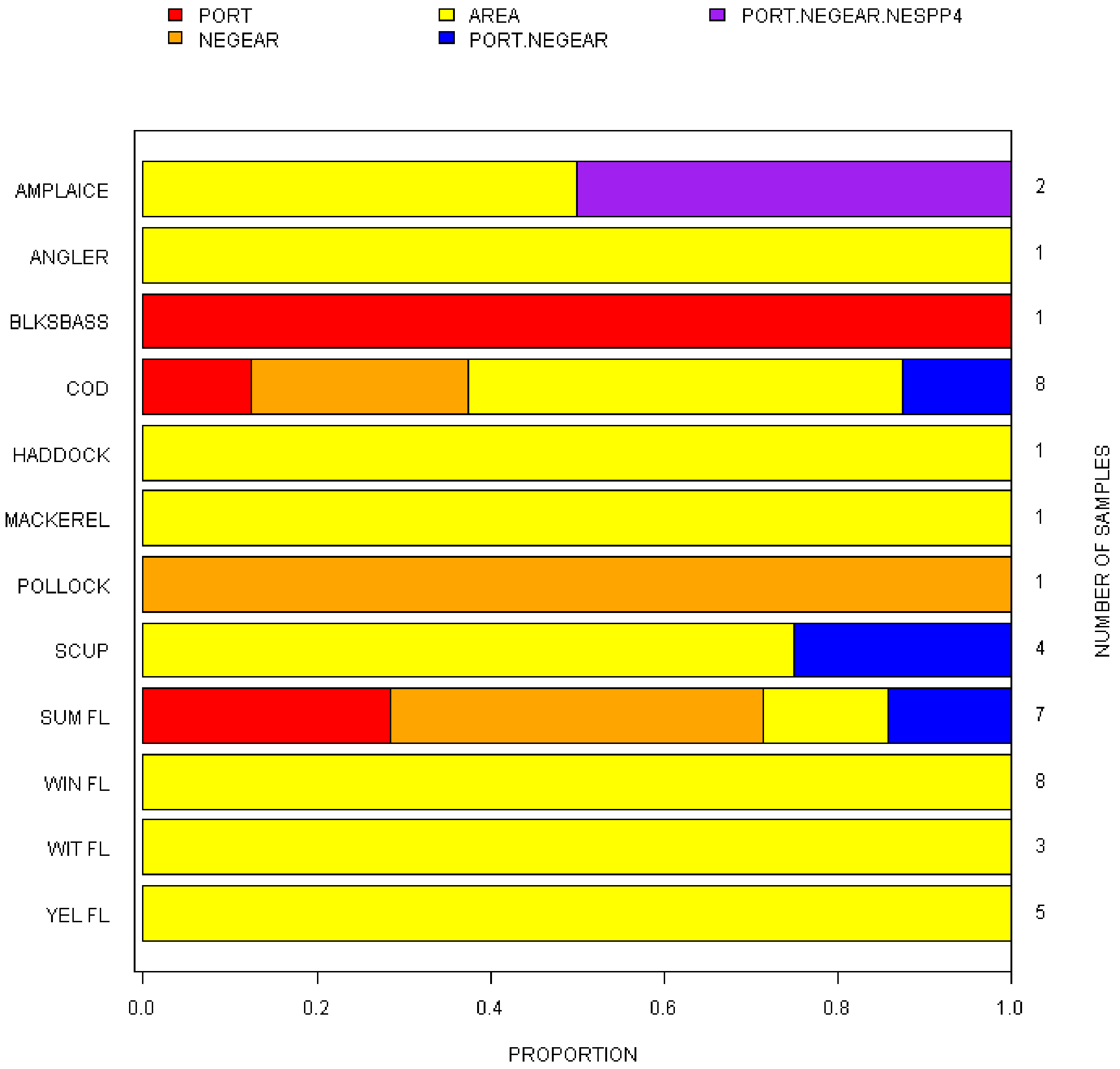

Figure 2. Proportion of commercial age samples that did not completely match to commercial length samples by species from 2006 to 2015 (Partial Match in Table 3; Figure 1). Number of Samples is the number of partially matched age samples. PORT, NEGEAR, AREA, and NESPP4 are the proportion of partially matched age samples where the value of that variable differed between the age and length samples. Multiple variable names (e.g., PORT.NEGEAR) are the proportion of partially matched age samples where the values of those variables differed between the age and length samples. Species include anglerfish (*Lophius americanus*, ANGLER), Atlantic cod (*Gadus morhua*, COD), American plaice (*Hippoglossoides platessoides*, AMPLAICE), summer flounder (*Paralichthys dentatus*, SUM FL), winter flounder (*Pseudopleuronectes americanus*, WIN FL), witch flounder (*Glyptocephalus cynoglossus*, WIT FL), yellowtail flounder (*Limanda ferruginea*, YEL FL), haddock (*Melanogrammus aeglefinus*, HADDOCK), Atlantic mackerel (*Scomber scombrus*, MACKEREL), pollock (*Pollachius virens*, POLLOCK), scup (*Stenotomus chrysops*, SCUP), black sea bass (*Centropristis striata*, BLKSBASS).

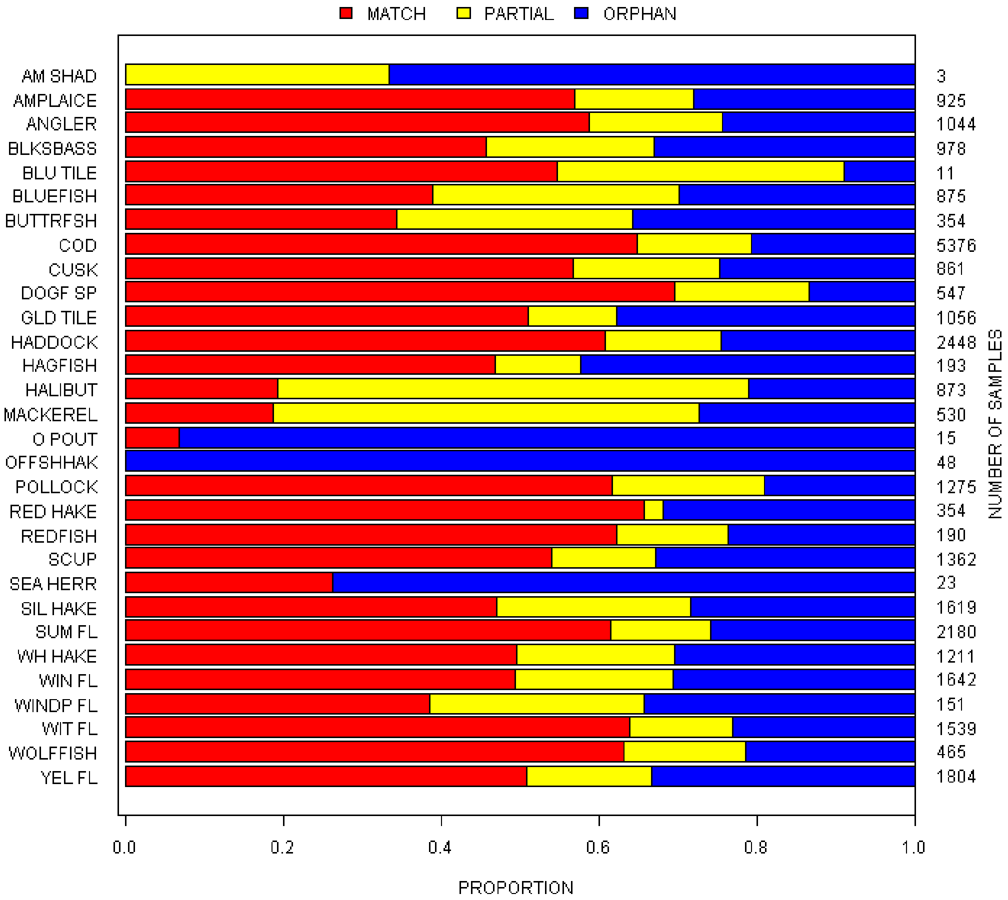

Figure 3. Proportion of commercial length samples that could be matched to commercial trips (Match) by species from 2006 to 2015. Orphan is the proportion of length samples that could not be matched to commercial trips. Partial Match is the proportion of length samples that matched some, but not all, variable values between the length samples and commercial trips. Number of Samples is the number of length samples collected. Species include anglerfish (*Lophius americanus*, ANGLER), bluefish (*Pomatomus saltatrix*, BLUEFISH), butterfish (*Peprilus triacanthus*, BUTTRFSH), Atlantic cod (*Gadus morhua*, COD), cusk (*Brosme brosme*, CUSK), spiny dogfish (*Squalus acanthias*, DOGF SP), American plaice (*Hippoglossoides platessoides*, AMPLAICE), windowpane flounder (*Scophthalmus aquosus*, WINDP FL), summer flounder (*Paralichthys dentatus*, SUM FL), winter flounder (*Pseudopleuronectes americanus*, WIN FL), witch flounder (*Glyptocephalus cynoglossus*, WIT FL), yellowtail flounder (*Limanda ferruginea*, YEL FL), haddock (*Melanogrammus aeglefinus*, HADDOCK), hagfish (*Myxine glutinosa*, HAGFISH), offshore hake (*Merluccius albidus*, OFFSHHAK), red hake (*Urophycis chuss*, RED HAKE), silver hake (*Merluccius bilinearis*, SIL HAKE), white hake (*Urophycis tenuis*, WH HAKE), Atlantic halibut (*Hippoglossus hippoglossus*, HALIBUT), Atlantic herring (*Clupea harengus*, SEA HERR), Atlantic mackerel (*Scomber scombrus*, MACKEREL), pollock (*Pollachius virens*, POLLOCK), ocean pout (*Zoarces americanus*, O POUT), redfish (*Sebastes fasciatus*, REDFISH), scup (*Stenotomus chrysops*, SCUP), black sea bass (*Centropristis striata*, BLKSBASS), American shad (*Alosa sapidissima*, AM SHAD), blueline tilefish (*Caulolatilus microps*, BLU TILE), golden tilefish (*Lopholatilus chamaeleonticeps*, GLD TILE), Atlantic wolffish (*Anarhichas lupus*, WOLFFISH).

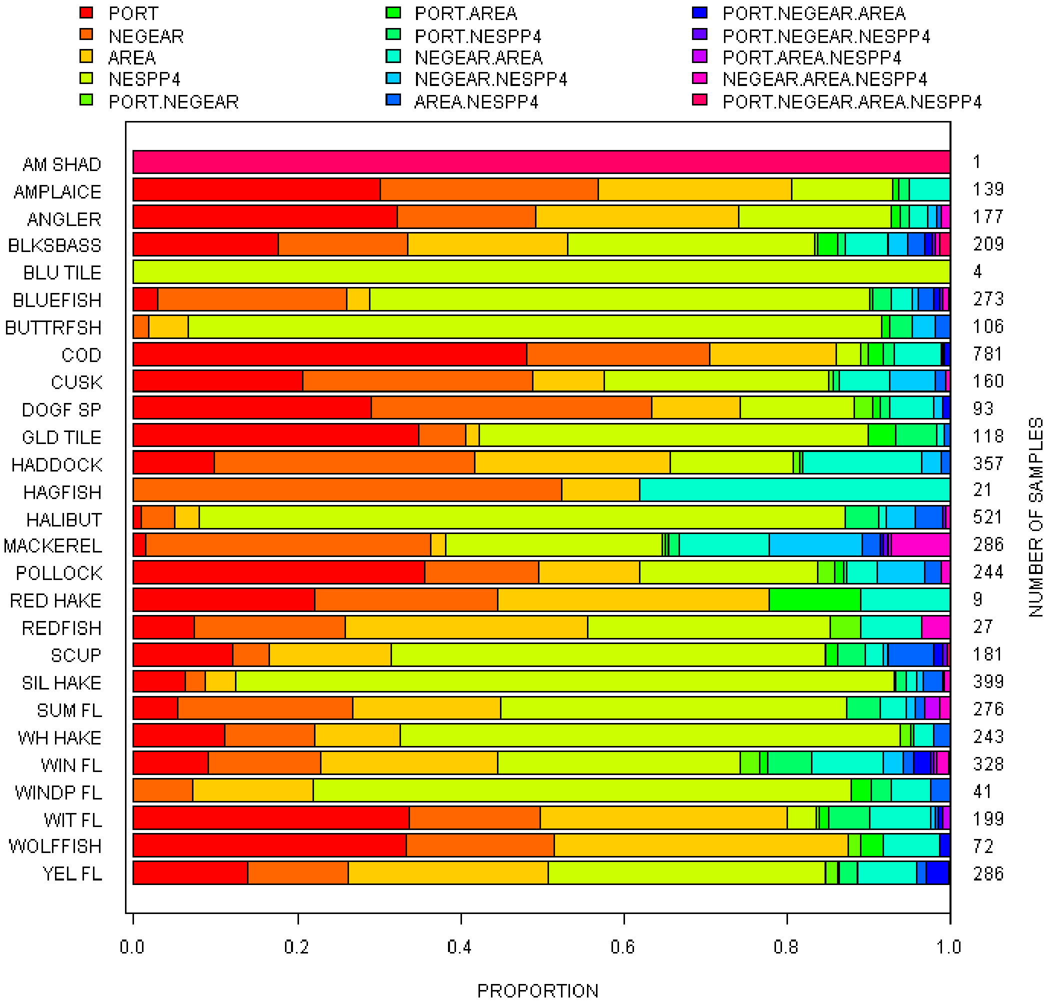

Figure 4. Proportion of commercial length samples that did not completely match to commercial trips by species from 2006 to 2015 (Partial Match in Table 5; Figure 3). Number of Samples is the number of partially matched length samples. PORT, NEGEAR, AREA, and NESPP4 are the proportion of partially matched length samples where the value of that variable differed between the length samples and commercial trips. Multiple variable names (e.g., PORT.NEGEAR) are the proportion of partially matched age samples where the values of those variables differed between the length samples and commercial trips. Species include anglerfish (*Lophius americanus*, ANGLER), bluefish (*Pomatomus saltatrix*, BLUEFISH), butterfish (*Peprilus triacanthus*, BUTTRFSH), Atlantic cod (*Gadus morhua*, COD), cusk (*Brosme brosme*, CUSK), spiny dogfish (*Squalus acanthias*, DOGF SP), American plaice (*Hippoglossoides platessoides*, AMPLAICE), windowpane flounder (*Scophthalmus aquosus*, WINDP FL), summer flounder (*Paralichthys dentatus*, SUM FL), winter flounder (*Pseudopleuronectes americanus*, WIN FL), witch flounder (*Glyptocephalus cynoglossus*, WIT FL), yellowtail flounder (*Limanda ferruginea*, YEL FL), haddock (*Melanogrammus aeglefinus*, HADDOCK), hagfish (*Myxine glutinosa*, HAGFISH), red hake (*Urophycis chuss*, RED HAKE), silver hake (*Merluccius bilinearis*, SIL HAKE), white hake (*Urophycis tenuis*, WH HAKE), Atlantic halibut (*Hippoglossus hippoglossus*, HALIBUT), Atlantic mackerel (*Scomber scombrus*, MACKEREL), pollock (*Pollachius virens*, POLLOCK), redfish (*Sebastes fasciatus*, REDFISH), scup (*Stenotomus chrysops*, SCUP), black sea bass (*Centropristis striata*, BLKSBASS), American shad (*Alosa sapidissima*, AM SHAD), blueline tilefish (*Caulolatilus microps*, BLU TILE), golden tilefish (*Lopholatilus chamaeleonticeps*, GLD TILE), Atlantic wolffish (*Anarhichas lupus*, WOLFFISH).

APPENDIX A

```
#Match biosamples to commercial landings
#Define connection to Sole server
library(RODBC)

sole <- odbcDriverConnect('case=nochange;SERVER=sole;DBQ=sole;DRIVER={Oracle in
OraClient11g_home1};UID=****;PWD=****')

##### Start of user specifications #####

#Specify save file directory
direct <- 'C:\\[directory path name]\\'

#Specify year
year <- seq(2006,2015,by = 1)

#Nespp3 species code list
nespp3.list <-
"('012','023','051','081','096','120','121','122','123','124','125','147','150','152','153','154','159','168','170'
,'212','240','250','269','305','329','335','347','352','418','420','422','444','446','508','509','512')"

##### End of user specifications #####

#Number of years
n.yr <- length(year)

for(j in 1:n.yr) {  #Loop over years
 #Query CFDBS.CFLENyyyyAA
 cflen.query <- paste("select
u.link,u.port,u.year,u.month,u.docn,u.day,u.permit,u.hullnum,u.negear,u.area,u.nespp4,u.nespp3,v.spp
nm,v.sppnm8,u.utilcd,u.length,u.numlen,u.alevel,u.tallyno,u.sampno from cfdbs.cflen",year[j],"aa
u,cfdbs.cfspp v where u.nespp3 IN ",nespp3.list," and u.nespp4 = v.nespp4",sep="")
 cflen.raw <- sqlQuery(sole,cflen.query,stringsAsFactors = FALSE,as.is = TRUE)
 cflen.raw[,c('LENGTH')] <- as.numeric(cflen.raw[,c('LENGTH')])
 cflen.raw[,c('NUMLEN')] <- as.numeric(cflen.raw[,c('NUMLEN')])
 cflen <- cflen.raw

 #Query CFDBS.CFAGEyyyyAA
 cfage.query <- paste("select
u.link,u.port,u.year,u.month,u.docn,u.negear,u.area,u.subtrip,u.nespp4,u.nespp3,v.sppnm,v.sppnm8,u.l
ength,u.age,u.numage,u.alevel,u.no_len_match,u.tallyno,u.sampno from cfdbs.cfage",year[j],"aa
u,cfdbs.cfspp v where u.nespp3 IN ",nespp3.list," and u.nespp4 = v.nespp4",sep="")
 cfage.raw <- sqlQuery(sole,cfage.query,stringsAsFactors = FALSE,as.is = TRUE)
 cfage.raw[,c('LENGTH')] <- as.numeric(cfage.raw[,c('LENGTH')])
 cfage.raw[,c('AGE')] <- as.numeric(cfage.raw[,c('AGE')])
 cfage.raw[,c('NUMAGE')] <- as.numeric(cfage.raw[,c('NUMAGE')])
 cfage <- cfage.raw
#Replace NAs with 0s for later aggregation
```

```
 cfage[is.na(cfage$NO_LEN_MATCH),c('NO_LEN_MATCH')] <- 0
 cfage[,c('NO_LEN_MATCH')] <- as.numeric(cfage.raw[,c('NO_LEN_MATCH')])
 cfage[is.na(cfage$NEGEAR),c('NEGEAR')] <- '999'

 #Query CFDBS.CFDETSyyyyAA
 cfdets.query <- paste("select
u.link,u.port,u.year,u.dlrtrpid,u.month,u.docn,u.day,u.dealnum,u.permit,u.hullnum,u.negear,u.area,u.su
btrip,u.nespp4,u.nespp3,v.sppnm,v.sppnm8,u.spplivlb,u.utilcd,u.vserial,u.alevel from
cfdbs.cfdets",year[j],"aa u,cfdbs.cfspp v where u.nespp3 IN ",nespp3.list," and u.nespp4 =
v.nespp4",sep="")
 cfdets <- sqlQuery(sole,cfdets.query,stringsAsFactors = FALSE,as.is = TRUE)
 cfdets[,c('DEALNUM')] <- as.numeric(cfdets[,c('DEALNUM')])
 cfdets[,c('SPPLIVLB')] <- as.numeric(cfdets[,c('SPPLIVLB')])

 #Differentiate species abbreviations for golden and blueline tilefish
 cfdets[cfdets$NESPP3==446,c('SPPNM8')] <- 'GLD TILE'
 cfdets[cfdets$NESPP3==444,c('SPPNM8')] <- 'BLU TILE'

#Sum number of lengths measured by sample
 cflen.samp <-
aggregate(cflen$NUMLEN,cflen[,c('LINK','PORT','YEAR','MONTH','DOCN','DAY','PERMIT','NEGEAR','AREA',
'NESPP4','NESPP3','SPPNM','SPPNM8','UTILCD','TALLYNO','SAMPNO')],FUN = sum,na.rm = TRUE)
 names(cflen.samp)[names(cflen.samp)=='x'] <- 'NUMLEN'

 #Differentiate species abbreviations for golden and blueline tilefish
 cflen.samp[cflen.samp$NESPP3==446,c('SPPNM8')] <- 'GLD TILE'
 cflen.samp[cflen.samp$NESPP3==444,c('SPPNM8')] <- 'BLU TILE'

 #Check to make sure that length samples and individual lengths aren't lost when aggregating
 cflen.samp.check <-
nrow(aggregate(cflen$NUMLEN,cflen[,c('MONTH','DOCN','TALLYNO','SAMPNO')],FUN = sum,na.rm =
TRUE)) - nrow(cflen.samp)
 cflen.num.check <- sum(cflen$NUMLEN) - sum(cflen.samp$NUMLEN)

 #Sum number of age structures collected by sample
 cfage.samp <-
aggregate(cfage[,c('NUMAGE','NO_LEN_MATCH')],cfage[,c('LINK','PORT','YEAR','MONTH','DOCN','NEGEA
R','AREA','NESPP4','NESPP3','SPPNM','SPPNM8','TALLYNO','SAMPNO')],FUN = sum,na.rm = TRUE)
 cfage.samp$LEN_MATCH <- cfage.samp$NUMAGE - cfage.samp$NO_LEN_MATCH

 #Differentiate species abbreviations for golden and blueline tilefish
 cfage.samp[cfage.samp$NESPP3==446,c('SPPNM8')] <- 'GLD TILE'
 cfage.samp[cfage.samp$NESPP3==444,c('SPPNM8')] <- 'BLU TILE'

 #Check to make sure that age samples and individual age structures aren't lost when aggregating
 cfage.samp.check <-
nrow(aggregate(cfage[,c('NUMAGE','NO_LEN_MATCH')],cfage[,c('LINK','YEAR')],FUN = sum,na.rm =
TRUE)) - nrow(cfage.samp)
```

```
 cfage.num.check <- sum(cfage$NUMAGE) - sum(cfage.samp$NUMAGE)

 ####################################################
 ### BEGIN MATCHING LENGTH SAMPLES TO AGE SAMPLES ###
 ####################################################

#Merge age and length samples
 #bio.samp <- merge(cflen.samp,cfage.samp,by = c('MONTH','DOCN','TALLYNO','SAMPNO'),all = TRUE)
 bio.samp <- merge(cflen.samp,cfage.samp,by = c('LINK'),all = TRUE)

 #Rename variables
 names(bio.samp)[names(bio.samp) == 'YEAR.x'] <- 'YEAR'
 names(bio.samp)[names(bio.samp) == 'MONTH.x'] <- 'MONTH'
 names(bio.samp)[names(bio.samp) == 'DOCN.x'] <- 'DOCN'
 names(bio.samp)[names(bio.samp) == 'NESPP4.x'] <- 'NESPP4'
 names(bio.samp)[names(bio.samp) == 'NESPP3.x'] <- 'NESPP3'
 names(bio.samp)[names(bio.samp) == 'SPPNM.x'] <- 'SPPNM'
 names(bio.samp)[names(bio.samp) == 'SPPNM8.x'] <- 'SPPNM8'
 names(bio.samp)[names(bio.samp) == 'PORT.x'] <- 'PORT'
 names(bio.samp)[names(bio.samp) == 'NEGEAR.x'] <- 'NEGEAR'
 names(bio.samp)[names(bio.samp) == 'AREA.x'] <- 'AREA'
 names(bio.samp)[names(bio.samp) == 'TALLYNO.x'] <- 'TALLYNO'
 names(bio.samp)[names(bio.samp) == 'SAMPNO.x'] <- 'SAMPNO'

 names(bio.samp)[names(bio.samp) == 'YEAR.y'] <- 'YEAR.AGE'
 names(bio.samp)[names(bio.samp) == 'MONTH.y'] <- 'MONTH.AGE'
 names(bio.samp)[names(bio.samp) == 'DOCN.y'] <- 'DOCN.AGE'
 names(bio.samp)[names(bio.samp) == 'NESPP4.y'] <- 'NESPP4.AGE'
 names(bio.samp)[names(bio.samp) == 'NESPP3.y'] <- 'NESPP3.AGE'
 names(bio.samp)[names(bio.samp) == 'SPPNM.y'] <- 'SPPNM.AGE'
 names(bio.samp)[names(bio.samp) == 'SPPNM8.y'] <- 'SPPNM8.AGE'
 names(bio.samp)[names(bio.samp) == 'PORT.y'] <- 'PORT.AGE'
 names(bio.samp)[names(bio.samp) == 'NEGEAR.y'] <- 'NEGEAR.AGE'
 names(bio.samp)[names(bio.samp) == 'AREA.y'] <- 'AREA.AGE'
 names(bio.samp)[names(bio.samp) == 'TALLYNO.y'] <- 'TALLYNO.AGE'
 names(bio.samp)[names(bio.samp) == 'SAMPNO.y'] <- 'SAMPNO.AGE'

#Use SPPNM.AGE and SPPNM8.AGE when SPPNM and SPPNM8 are NA (i.e., age samples with no
matching length samples)
 bio.samp[is.na(bio.samp$SPPNM) & !is.na(bio.samp$SPPNM.AGE),c('SPPNM')] <-
bio.samp[is.na(bio.samp$SPPNM) & !is.na(bio.samp$SPPNM.AGE),c('SPPNM.AGE')]
bio.samp[is.na(bio.samp$SPPNM8) & !is.na(bio.samp$SPPNM8.AGE),c('SPPNM8')] <-
bio.samp[is.na(bio.samp$SPPNM8) & !is.na(bio.samp$SPPNM8.AGE),c('SPPNM8.AGE')]

 #Check that age and length samples were not lost
 biosamp.length.check <- nrow(bio.samp[!is.na(bio.samp$NUMLEN),]) - nrow(cflen.samp)
 biosamp.age.check <- nrow(bio.samp[!is.na(bio.samp$NUMAGE),]) - nrow(cfage.samp)
```

```
 #Flag matched biosamples with different PORT between length and age samples
 bio.samp$PORT.FLAG <- NA
 if(nrow(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) & bio.samp$PORT !=
bio.samp$PORT.AGE,]) > 0) {
  bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) & bio.samp$PORT !=
bio.samp$PORT.AGE,c('PORT.FLAG')] <- 1
 }
 #Flag matched biosamples with different NEGEAR between length and age samples
 bio.samp$NEGEAR.FLAG <- NA
 if(nrow(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) & bio.samp$NEGEAR !=
bio.samp$NEGEAR.AGE,]) > 0) {
  bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) & bio.samp$NEGEAR !=
bio.samp$NEGEAR.AGE,c('NEGEAR.FLAG')] <- 1
 }
 #Flag matched biosamples with different AREA between length and age samples
 bio.samp$AREA.FLAG <- NA
 if(nrow(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) & bio.samp$AREA !=
bio.samp$AREA.AGE,]) > 0) {
  bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) & bio.samp$AREA !=
bio.samp$AREA.AGE,c('AREA.FLAG')] <- 1
 }
#Flag matched biosamples with different NESPP4 between length and age samples
 bio.samp$NESPP4.FLAG <- NA
 if(nrow(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) & bio.samp$NESPP4 !=
bio.samp$NESPP4.AGE,]) > 0) {
bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) & bio.samp$NESPP4 !=
bio.samp$NESPP4.AGE,c('NESPP4.FLAG')] <- 1
 }

#Calculate total number of age samples by species
 total.samp.spp <- aggregate(cfage.samp$YEAR,cfage.samp[,c('SPPNM','SPPNM8')],FUN = length)
 names(total.samp.spp)[names(total.samp.spp)=='x'] <- 'TOTAL.N'

#Calculate number of age samples that match to length samples by species
 if(nrow(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) &
is.na(bio.samp$PORT.FLAG) & is.na(bio.samp$NEGEAR.FLAG) & is.na(bio.samp$AREA.FLAG) &
is.na(bio.samp$NESPP4.FLAG),]) > 0) {
  match.samp.spp <- aggregate(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) &
is.na(bio.samp$PORT.FLAG) & is.na(bio.samp$NEGEAR.FLAG) & is.na(bio.samp$AREA.FLAG) &
is.na(bio.samp$NESPP4.FLAG),c('YEAR')],bio.samp[!is.na(bio.samp$NUMLEN) &
!is.na(bio.samp$NUMAGE) & is.na(bio.samp$PORT.FLAG) & is.na(bio.samp$NEGEAR.FLAG) &
is.na(bio.samp$AREA.FLAG) & is.na(bio.samp$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  match.samp.spp <- total.samp.spp[,c('SPPNM','SPPNM8')]
  match.samp.spp$x <- 0
 }
 names(match.samp.spp)[names(match.samp.spp)=='x'] <- year[j]
```

```
 #Calculate number of age samples that don't match to length samples by species
 if(nrow(bio.samp[is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) & is.na(bio.samp$PORT.FLAG)
& is.na(bio.samp$NEGEAR.FLAG) & is.na(bio.samp$AREA.FLAG) & is.na(bio.samp$NESPP4.FLAG),]) > 0) {
  nomatch.samp.spp <- aggregate(bio.samp[is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) &
is.na(bio.samp$PORT.FLAG) & is.na(bio.samp$NEGEAR.FLAG) & is.na(bio.samp$AREA.FLAG) &
is.na(bio.samp$NESPP4.FLAG),c('YEAR')],bio.samp[is.na(bio.samp$NUMLEN) &
!is.na(bio.samp$NUMAGE) & is.na(bio.samp$PORT.FLAG) & is.na(bio.samp$NEGEAR.FLAG) &
is.na(bio.samp$AREA.FLAG) & is.na(bio.samp$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  nomatch.samp.spp <- total.samp.spp[,c('SPPNM','SPPNM8')]
  nomatch.samp.spp$x <- 0
}
 names(nomatch.samp.spp)[names(nomatch.samp.spp)=='x'] <- year[j]

 #Calculate number of age samples that match to length samples but have different PORT by species
 if(nrow(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) &
!is.na(bio.samp$PORT.FLAG) & is.na(bio.samp$NEGEAR.FLAG) & is.na(bio.samp$AREA.FLAG) &
is.na(bio.samp$NESPP4.FLAG),]) > 0) {
  port.samp.spp <- aggregate(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) &
!is.na(bio.samp$PORT.FLAG) & is.na(bio.samp$NEGEAR.FLAG) & is.na(bio.samp$AREA.FLAG) &
is.na(bio.samp$NESPP4.FLAG),c('YEAR')],bio.samp[!is.na(bio.samp$NUMLEN) &
!is.na(bio.samp$NUMAGE) & !is.na(bio.samp$PORT.FLAG) & is.na(bio.samp$NEGEAR.FLAG) &
is.na(bio.samp$AREA.FLAG) & is.na(bio.samp$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  port.samp.spp <- total.samp.spp[,c('SPPNM','SPPNM8')]
  port.samp.spp$x <- 0
 }
 names(port.samp.spp)[names(port.samp.spp)=='x'] <- year[j]

 #Calculate number of age samples that match to length samples but have different NEGEAR by species
 if(nrow(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) &
is.na(bio.samp$PORT.FLAG) & !is.na(bio.samp$NEGEAR.FLAG) & is.na(bio.samp$AREA.FLAG) &
is.na(bio.samp$NESPP4.FLAG),]) > 0) {
  negear.samp.spp <- aggregate(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) &
is.na(bio.samp$PORT.FLAG) & !is.na(bio.samp$NEGEAR.FLAG) & is.na(bio.samp$AREA.FLAG) &
is.na(bio.samp$NESPP4.FLAG),c('YEAR')],bio.samp[!is.na(bio.samp$NUMLEN) &
!is.na(bio.samp$NUMAGE) & is.na(bio.samp$PORT.FLAG) & !is.na(bio.samp$NEGEAR.FLAG) &
is.na(bio.samp$AREA.FLAG) & is.na(bio.samp$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  negear.samp.spp <- total.samp.spp[,c('SPPNM','SPPNM8')]
  negear.samp.spp$x <- 0
 }
 names(negear.samp.spp)[names(negear.samp.spp)=='x'] <- year[j]

 #Calculate number of age samples that match to length samples but have different AREA by species
 if(nrow(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) &
is.na(bio.samp$PORT.FLAG) & is.na(bio.samp$NEGEAR.FLAG) & !is.na(bio.samp$AREA.FLAG) &
is.na(bio.samp$NESPP4.FLAG),]) > 0) {
```

```
  area.samp.spp <- aggregate(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) &
is.na(bio.samp$PORT.FLAG) & is.na(bio.samp$NEGEAR.FLAG) & !is.na(bio.samp$AREA.FLAG) &
is.na(bio.samp$NESPP4.FLAG),c('YEAR')],bio.samp[!is.na(bio.samp$NUMLEN) &
!is.na(bio.samp$NUMAGE) & is.na(bio.samp$PORT.FLAG) & is.na(bio.samp$NEGEAR.FLAG) &
!is.na(bio.samp$AREA.FLAG) & is.na(bio.samp$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  area.samp.spp <- total.samp.spp[,c('SPPNM','SPPNM8')]
  area.samp.spp$x <- 0
 }
 names(area.samp.spp)[names(area.samp.spp)=='x'] <- year[j]

 #Calculate number of age samples that match to length samples but have different NESPP4 by species
 if(nrow(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) &
is.na(bio.samp$PORT.FLAG) & is.na(bio.samp$NEGEAR.FLAG) & is.na(bio.samp$AREA.FLAG) &
!is.na(bio.samp$NESPP4.FLAG),]) > 0) {
  nespp4.samp.spp <- aggregate(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) &
is.na(bio.samp$PORT.FLAG) & is.na(bio.samp$NEGEAR.FLAG) & !is.na(bio.samp$AREA.FLAG) &
!is.na(bio.samp$NESPP4.FLAG),c('YEAR')],bio.samp[!is.na(bio.samp$NUMLEN) &
!is.na(bio.samp$NUMAGE) & is.na(bio.samp$PORT.FLAG) & is.na(bio.samp$NEGEAR.FLAG) &
is.na(bio.samp$AREA.FLAG) & !is.na(bio.samp$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  nespp4.samp.spp <- total.samp.spp[,c('SPPNM','SPPNM8')]
  nespp4.samp.spp$x <- 0
 }
 names(nespp4.samp.spp)[names(nespp4.samp.spp)=='x'] <- year[j]

 #Calculate number of age samples that match to length samples but have different PORT and NEGEAR
by species
 if(nrow(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) &
!is.na(bio.samp$PORT.FLAG) & !is.na(bio.samp$NEGEAR.FLAG) & is.na(bio.samp$AREA.FLAG) &
is.na(bio.samp$NESPP4.FLAG),]) > 0) {
  port.negear.samp.spp <- aggregate(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE)
& !is.na(bio.samp$PORT.FLAG) & !is.na(bio.samp$NEGEAR.FLAG) & is.na(bio.samp$AREA.FLAG) &
is.na(bio.samp$NESPP4.FLAG),c('YEAR')],bio.samp[!is.na(bio.samp$NUMLEN) &
!is.na(bio.samp$NUMAGE) & !is.na(bio.samp$PORT.FLAG) & !is.na(bio.samp$NEGEAR.FLAG) &
is.na(bio.samp$AREA.FLAG) & is.na(bio.samp$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  port.negear.samp.spp <- total.samp.spp[,c('SPPNM','SPPNM8')]
  port.negear.samp.spp$x <- 0
 }
 names(port.negear.samp.spp)[names(port.negear.samp.spp)=='x'] <- year[j]

 #Calculate number of age samples that match to length samples but have different PORT and AREA by
species
 if(nrow(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) &
!is.na(bio.samp$PORT.FLAG) & is.na(bio.samp$NEGEAR.FLAG) & !is.na(bio.samp$AREA.FLAG) &
is.na(bio.samp$NESPP4.FLAG),]) > 0) {
```

```
  port.area.samp.spp <- aggregate(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) &
!is.na(bio.samp$PORT.FLAG) & is.na(bio.samp$NEGEAR.FLAG) & !is.na(bio.samp$AREA.FLAG) &
is.na(bio.samp$NESPP4.FLAG),c('YEAR')],bio.samp[!is.na(bio.samp$NUMLEN) &
!is.na(bio.samp$NUMAGE) & !is.na(bio.samp$PORT.FLAG) & is.na(bio.samp$NEGEAR.FLAG) &
!is.na(bio.samp$AREA.FLAG) & is.na(bio.samp$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  port.area.samp.spp <- total.samp.spp[,c('SPPNM','SPPNM8')]
  port.area.samp.spp$x <- 0
 }
 names(port.area.samp.spp)[names(port.area.samp.spp)=='x'] <- year[j]

 #Calculate number of age samples that match to length samples but have different PORT and NESPP4
by species
 if(nrow(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) &
!is.na(bio.samp$PORT.FLAG) & is.na(bio.samp$NEGEAR.FLAG) & is.na(bio.samp$AREA.FLAG) &
!is.na(bio.samp$NESPP4.FLAG),]) > 0) {
  port.nespp4.samp.spp <- aggregate(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE)
& !is.na(bio.samp$PORT.FLAG) & is.na(bio.samp$NEGEAR.FLAG) & !is.na(bio.samp$AREA.FLAG) &
!is.na(bio.samp$NESPP4.FLAG),c('YEAR')],bio.samp[!is.na(bio.samp$NUMLEN) &
!is.na(bio.samp$NUMAGE) & !is.na(bio.samp$PORT.FLAG) & is.na(bio.samp$NEGEAR.FLAG) &
is.na(bio.samp$AREA.FLAG) & !is.na(bio.samp$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  port.nespp4.samp.spp <- total.samp.spp[,c('SPPNM','SPPNM8')]
  port.nespp4.samp.spp$x <- 0
 }
 names(port.nespp4.samp.spp)[names(port.nespp4.samp.spp)=='x'] <- year[j]

 #Calculate number of age samples that match to length samples but have different NEGEAR and AREA
by species
 if(nrow(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) &
is.na(bio.samp$PORT.FLAG) & !is.na(bio.samp$NEGEAR.FLAG) & !is.na(bio.samp$AREA.FLAG) &
is.na(bio.samp$NESPP4.FLAG),]) > 0) {
  negear.area.samp.spp <- aggregate(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE)
& is.na(bio.samp$PORT.FLAG) & !is.na(bio.samp$NEGEAR.FLAG) & !is.na(bio.samp$AREA.FLAG) &
is.na(bio.samp$NESPP4.FLAG),c('YEAR')],bio.samp[!is.na(bio.samp$NUMLEN) &
!is.na(bio.samp$NUMAGE) & is.na(bio.samp$PORT.FLAG) & !is.na(bio.samp$NEGEAR.FLAG) &
!is.na(bio.samp$AREA.FLAG) & is.na(bio.samp$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  negear.area.samp.spp <- total.samp.spp[,c('SPPNM','SPPNM8')]
  negear.area.samp.spp$x <- 0
 }
 names(negear.area.samp.spp)[names(negear.area.samp.spp)=='x'] <- year[j]

 #Calculate number of age samples that match to length samples but have different NEGEAR and
NESPP4 by species
 if(nrow(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) &
is.na(bio.samp$PORT.FLAG) & !is.na(bio.samp$NEGEAR.FLAG) & is.na(bio.samp$AREA.FLAG) &
!is.na(bio.samp$NESPP4.FLAG),]) > 0) {
```

```
  negear.nespp4.samp.spp <- aggregate(bio.samp[!is.na(bio.samp$NUMLEN) &
!is.na(bio.samp$NUMAGE) & is.na(bio.samp$PORT.FLAG) & !is.na(bio.samp$NEGEAR.FLAG) &
!is.na(bio.samp$AREA.FLAG) &
!is.na(bio.samp$NESPP4.FLAG),c('YEAR')],bio.samp[!is.na(bio.samp$NUMLEN) &
!is.na(bio.samp$NUMAGE) & is.na(bio.samp$PORT.FLAG) & !is.na(bio.samp$NEGEAR.FLAG) &
is.na(bio.samp$AREA.FLAG) & !is.na(bio.samp$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  negear.nespp4.samp.spp <- total.samp.spp[,c('SPPNM','SPPNM8')]
  negear.nespp4.samp.spp$x <- 0
 }
 names(negear.nespp4.samp.spp)[names(negear.nespp4.samp.spp)=='x'] <- year[j]

 #Calculate number of age samples that match to length samples but have different AREA and NESPP4
by species
 if(nrow(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) &
is.na(bio.samp$PORT.FLAG) & is.na(bio.samp$NEGEAR.FLAG) & !is.na(bio.samp$AREA.FLAG) &
!is.na(bio.samp$NESPP4.FLAG),]) > 0) {
  area.nespp4.samp.spp <- aggregate(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE)
& is.na(bio.samp$PORT.FLAG) & !is.na(bio.samp$NEGEAR.FLAG) & !is.na(bio.samp$AREA.FLAG) &
!is.na(bio.samp$NESPP4.FLAG),c('YEAR')],bio.samp[!is.na(bio.samp$NUMLEN) &
!is.na(bio.samp$NUMAGE) & is.na(bio.samp$PORT.FLAG) & is.na(bio.samp$NEGEAR.FLAG) &
!is.na(bio.samp$AREA.FLAG) & !is.na(bio.samp$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  area.nespp4.samp.spp <- total.samp.spp[,c('SPPNM','SPPNM8')]
  area.nespp4.samp.spp$x <- 0
 }
 names(area.nespp4.samp.spp)[names(area.nespp4.samp.spp)=='x'] <- year[j]

 #Calculate number of age samples that match to length samples but have different PORT, NEGEAR and
AREA by species
 if(nrow(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) &
!is.na(bio.samp$PORT.FLAG) & !is.na(bio.samp$NEGEAR.FLAG) & !is.na(bio.samp$AREA.FLAG) &
is.na(bio.samp$NESPP4.FLAG),]) > 0) {
  port.negear.area.samp.spp <- aggregate(bio.samp[!is.na(bio.samp$NUMLEN) &
!is.na(bio.samp$NUMAGE) & !is.na(bio.samp$PORT.FLAG) & !is.na(bio.samp$NEGEAR.FLAG) &
!is.na(bio.samp$AREA.FLAG) &
is.na(bio.samp$NESPP4.FLAG),c('YEAR')],bio.samp[!is.na(bio.samp$NUMLEN) &
!is.na(bio.samp$NUMAGE) & !is.na(bio.samp$PORT.FLAG) & !is.na(bio.samp$NEGEAR.FLAG) &
!is.na(bio.samp$AREA.FLAG) & is.na(bio.samp$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  port.negear.area.samp.spp <- total.samp.spp[,c('SPPNM','SPPNM8')]
  port.negear.area.samp.spp$x <- 0
 }
 names(port.negear.area.samp.spp)[names(port.negear.area.samp.spp)=='x'] <- year[j]

 #Calculate number of age samples that don't match to length samples due to different PORT, NEGEAR
and NESPP4 by species
```

```
 if(nrow(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) &
!is.na(bio.samp$PORT.FLAG) & !is.na(bio.samp$NEGEAR.FLAG) & is.na(bio.samp$AREA.FLAG) &
!is.na(bio.samp$NESPP4.FLAG),]) > 0) {
  port.negear.nespp4.samp.spp <- aggregate(bio.samp[!is.na(bio.samp$NUMLEN) &
!is.na(bio.samp$NUMAGE) & !is.na(bio.samp$PORT.FLAG) & !is.na(bio.samp$NEGEAR.FLAG) &
is.na(bio.samp$AREA.FLAG) &
!is.na(bio.samp$NESPP4.FLAG),c('YEAR')],bio.samp[!is.na(bio.samp$NUMLEN) &
!is.na(bio.samp$NUMAGE) & !is.na(bio.samp$PORT.FLAG) & !is.na(bio.samp$NEGEAR.FLAG) &
is.na(bio.samp$AREA.FLAG) & !is.na(bio.samp$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  port.negear.nespp4.samp.spp <- total.samp.spp[,c('SPPNM','SPPNM8')]
  port.negear.nespp4.samp.spp$x <- 0
 }
 names(port.negear.nespp4.samp.spp)[names(port.negear.nespp4.samp.spp)=='x'] <- year[j]

 #Calculate number of age samples that match to length samples but have different PORT, AREA and
NESPP4 by species
 if(nrow(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) &
!is.na(bio.samp$PORT.FLAG) & is.na(bio.samp$NEGEAR.FLAG) & !is.na(bio.samp$AREA.FLAG) &
!is.na(bio.samp$NESPP4.FLAG),]) > 0) {
  port.area.nespp4.samp.spp <- aggregate(bio.samp[!is.na(bio.samp$NUMLEN) &
!is.na(bio.samp$NUMAGE) & !is.na(bio.samp$PORT.FLAG) & is.na(bio.samp$NEGEAR.FLAG) &
!is.na(bio.samp$AREA.FLAG) &
!is.na(bio.samp$NESPP4.FLAG),c('YEAR')],bio.samp[!is.na(bio.samp$NUMLEN) &
!is.na(bio.samp$NUMAGE) & !is.na(bio.samp$PORT.FLAG) & is.na(bio.samp$NEGEAR.FLAG) &
!is.na(bio.samp$AREA.FLAG) & !is.na(bio.samp$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  port.area.nespp4.samp.spp <- total.samp.spp[,c('SPPNM','SPPNM8')]
  port.area.nespp4.samp.spp$x <- 0
 }
 names(port.area.nespp4.samp.spp)[names(port.area.nespp4.samp.spp)=='x'] <- year[j]

 #Calculate number of age samples that match to length samples but have different NEGEAR, AREA and
NESPP4 by species
 if(nrow(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) &
is.na(bio.samp$PORT.FLAG) & !is.na(bio.samp$NEGEAR.FLAG) & !is.na(bio.samp$AREA.FLAG) &
!is.na(bio.samp$NESPP4.FLAG),]) > 0) {
  negear.area.nespp4.samp.spp <- aggregate(bio.samp[!is.na(bio.samp$NUMLEN) &
!is.na(bio.samp$NUMAGE) & is.na(bio.samp$PORT.FLAG) & !is.na(bio.samp$NEGEAR.FLAG) &
!is.na(bio.samp$AREA.FLAG) &
!is.na(bio.samp$NESPP4.FLAG),c('YEAR')],bio.samp[!is.na(bio.samp$NUMLEN) &
!is.na(bio.samp$NUMAGE) & is.na(bio.samp$PORT.FLAG) & !is.na(bio.samp$NEGEAR.FLAG) &
!is.na(bio.samp$AREA.FLAG) & !is.na(bio.samp$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  negear.area.nespp4.samp.spp <- total.samp.spp[,c('SPPNM','SPPNM8')]
  negear.area.nespp4.samp.spp$x <- 0
 }
 names(negear.area.nespp4.samp.spp)[names(negear.area.nespp4.samp.spp)=='x'] <- year[j]
```

```
 #Calculate number of age samples that match to length samples but have different PORT, NEGEAR,
AREA and NESPP4 by species
 if(nrow(bio.samp[!is.na(bio.samp$NUMLEN) & !is.na(bio.samp$NUMAGE) &
!is.na(bio.samp$PORT.FLAG) & !is.na(bio.samp$NEGEAR.FLAG) & !is.na(bio.samp$AREA.FLAG) &
!is.na(bio.samp$NESPP4.FLAG),]) > 0) {
  port.negear.area.samp.spp <- aggregate(bio.samp[!is.na(bio.samp$NUMLEN) &
!is.na(bio.samp$NUMAGE) & !is.na(bio.samp$PORT.FLAG) & !is.na(bio.samp$NEGEAR.FLAG) &
!is.na(bio.samp$AREA.FLAG) &
!is.na(bio.samp$NESPP4.FLAG),c('YEAR')],bio.samp[!is.na(bio.samp$NUMLEN) &
!is.na(bio.samp$NUMAGE) & !is.na(bio.samp$PORT.FLAG) & !is.na(bio.samp$NEGEAR.FLAG) &
!is.na(bio.samp$AREA.FLAG) & !is.na(bio.samp$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  port.negear.area.nespp4.samp.spp <- total.samp.spp[,c('SPPNM','SPPNM8')]
  port.negear.area.nespp4.samp.spp$x <- 0
 }
 names(port.negear.area.nespp4.samp.spp)[names(port.negear.area.nespp4.samp.spp)=='x'] <- year[j]

 #Append age samples by species from different matching categories
 if(nrow(match.samp.spp) > 0) {
  names(match.samp.spp)[names(match.samp.spp)==year[j]] <- 'MATCH.N'
  temp1 <- merge(total.samp.spp,match.samp.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
 } else {
  temp1 <- total.samp.spp
  temp1$MATCH.N <- 0
 }
 if(nrow(nomatch.samp.spp) > 0) {
  names(nomatch.samp.spp)[names(nomatch.samp.spp)==year[j]] <- 'NOMATCH.N'
  temp2 <- merge(temp1,nomatch.samp.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
 } else {
  temp2 <- temp1
  temp2$NOMATCH.N <- 0
 }
 if(nrow(port.samp.spp) > 0) {
  names(port.samp.spp)[names(port.samp.spp)==year[j]] <- 'PORT.N'
  temp3 <- merge(temp2,port.samp.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
 } else {
  temp3 <- temp2
  temp3$PORT.N <- 0
 }
 if(nrow(negear.samp.spp) > 0) {
  names(negear.samp.spp)[names(negear.samp.spp)==year[j]] <- 'NEGEAR.N'
  temp4 <- merge(temp3,negear.samp.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
 } else {
  temp4 <- temp3
  temp4$NEGEAR.N <- 0
 }
 if(nrow(area.samp.spp) > 0) {
```

```
 names(area.samp.spp)[names(area.samp.spp)==year[j]] <- 'AREA.N'
 temp5 <- merge(temp4,area.samp.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
} else {
 temp5 <- temp4
 temp5$AREA.N <- 0
}
if(nrow(nespp4.samp.spp) > 0) {
 names(nespp4.samp.spp)[names(nespp4.samp.spp)==year[j]] <- 'NESPP4.N'
 temp5.1 <- merge(temp5,nespp4.samp.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
} else {
 temp5.1 <- temp5
 temp5.1$NESPP4.N <- 0
}
if(nrow(port.negear.samp.spp) > 0) {
 names(port.negear.samp.spp)[names(port.negear.samp.spp)==year[j]] <- 'PORT.NEGEAR.N'
 temp6 <- merge(temp5.1,port.negear.samp.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
} else {
 temp6 <- temp5.1
 temp6$PORT.NEGEAR.N <- 0
}
if(nrow(port.area.samp.spp) > 0) {
 names(port.area.samp.spp)[names(port.area.samp.spp)==year[j]] <- 'PORT.AREA.N'
 temp7 <- merge(temp6,port.area.samp.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
} else {
 temp7 <- temp6
 temp7$PORT.AREA.N <- 0
}
if(nrow(port.nespp4.samp.spp) > 0) {
 names(port.nespp4.samp.spp)[names(port.nespp4.samp.spp)==year[j]] <- 'PORT.NESPP4.N'
 temp7.1 <- merge(temp7,port.nespp4.samp.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
} else {
 temp7.1 <- temp7
 temp7.1$PORT.NESPP4.N <- 0
}
if(nrow(negear.area.samp.spp) > 0) {
 names(negear.area.samp.spp)[names(negear.area.samp.spp)==year[j]] <- 'NEGEAR.AREA.N'
 temp8 <- merge(temp7.1,negear.area.samp.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
} else {
 temp8 <- temp7.1
 temp8$NEGEAR.AREA.N <- 0
}
if(nrow(negear.nespp4.samp.spp) > 0) {
 names(negear.nespp4.samp.spp)[names(negear.nespp4.samp.spp)==year[j]] <- 'NEGEAR.NESPP4.N'
 temp8.1 <- merge(temp8,negear.nespp4.samp.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
} else {
 temp8.1 <- temp8
 temp8.1$NEGEAR.NESPP4.N <- 0
}
```

```
 if(nrow(area.nespp4.samp.spp) > 0) {
  names(area.nespp4.samp.spp)[names(area.nespp4.samp.spp)==year[j]] <- 'AREA.NESPP4.N'
  temp8.2 <- merge(temp8.1,area.nespp4.samp.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
 } else {
  temp8.2 <- temp8.1
  temp8.2$AREA.NESPP4.N <- 0
 }
 if(nrow(port.negear.area.samp.spp) > 0) {
  names(port.negear.area.samp.spp)[names(port.negear.area.samp.spp)==year[j]] <-
'PORT.NEGEAR.AREA.N'
  temp9 <- merge(temp8.2,port.negear.area.samp.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
 } else {
  temp9 <- temp8.2
  temp9$PORT.NEGEAR.AREA.N <- 0
 }
  if(nrow(port.negear.nespp4.samp.spp) > 0) {
  names(port.negear.nespp4.samp.spp)[names(port.negear.nespp4.samp.spp)==year[j]] <-
'PORT.NEGEAR.NESPP4.N'
  temp10 <- merge(temp9,port.negear.nespp4.samp.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
 } else {
  temp10 <- temp9
  temp10$PORT.NEGEAR.NESPP4.N <- 0
 }
 if(nrow(port.area.nespp4.samp.spp) > 0) {
  names(port.area.nespp4.samp.spp)[names(port.area.nespp4.samp.spp)==year[j]] <-
'PORT.AREA.NESPP4.N'
  temp11 <- merge(temp10,port.area.nespp4.samp.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
 } else {
  temp11 <- temp10
  temp11$PORT.AREA.NESPP4.N <- 0
 }
 if(nrow(negear.area.nespp4.samp.spp) > 0) {
  names(negear.area.nespp4.samp.spp)[names(negear.area.nespp4.samp.spp)==year[j]] <-
'NEGEAR.AREA.NESPP4.N'
  temp12 <- merge(temp11,negear.area.nespp4.samp.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
 } else {
  temp12 <- temp11
  temp12$NEGEAR.AREA.NESPP4.N <- 0
 }
 if(nrow(port.negear.area.nespp4.samp.spp) > 0) {
  names(port.negear.area.nespp4.samp.spp)[names(port.negear.area.nespp4.samp.spp)==year[j]] <-
'PORT.NEGEAR.AREA.NESPP4.N'
  temp13 <- merge(temp12,port.negear.area.nespp4.samp.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
 } else {
  temp13 <- temp12
  temp13$PORT.NEGEAR.AREA.NESPP4.N <- 0
 }
 #Replace NAs with 0s to calculate proportions
```

```
 temp13[is.na(temp13)] <- 0

#Calculate proportions of age samples matched
 biosamp.p <- temp13
 biosamp.p$MATCH.P <- biosamp.p$MATCH.N/biosamp.p$TOTAL.N
 biosamp.p$NOMATCH.P <- biosamp.p$NOMATCH.N/biosamp.p$TOTAL.N
 biosamp.p$PORT.P <- biosamp.p$PORT.N/biosamp.p$TOTAL.N
 biosamp.p$NEGEAR.P <- biosamp.p$NEGEAR.N/biosamp.p$TOTAL.N
 biosamp.p$AREA.P <- biosamp.p$AREA.N/biosamp.p$TOTAL.N
 biosamp.p$NESPP4.P <- biosamp.p$NESPP4.N/biosamp.p$TOTAL.N
 biosamp.p$PORT.NEGEAR.P <- biosamp.p$PORT.NEGEAR.N/biosamp.p$TOTAL.N
 biosamp.p$PORT.AREA.P <- biosamp.p$PORT.AREA.N/biosamp.p$TOTAL.N
 biosamp.p$PORT.NESPP4.P <- biosamp.p$PORT.NESPP4.N/biosamp.p$TOTAL.N
 biosamp.p$NEGEAR.AREA.P <- biosamp.p$NEGEAR.AREA.N/biosamp.p$TOTAL.N
 biosamp.p$NEGEAR.NESPP4.P <- biosamp.p$NEGEAR.NESPP4.N/biosamp.p$TOTAL.N
 biosamp.p$AREA.NESPP4.P <- biosamp.p$AREA.NESPP4.N/biosamp.p$TOTAL.N
 biosamp.p$PORT.NEGEAR.AREA.P <- biosamp.p$PORT.NEGEAR.AREA.N/biosamp.p$TOTAL.N
 biosamp.p$PORT.NEGEAR.NESPP4.P <- biosamp.p$PORT.NEGEAR.NESPP4.N/biosamp.p$TOTAL.N
 biosamp.p$PORT.AREA.NESPP4.P <- biosamp.p$PORT.AREA.NESPP4.N/biosamp.p$TOTAL.N
 biosamp.p$NEGEAR.AREA.NESPP4.P <- biosamp.p$NEGEAR.AREA.NESPP4.N/biosamp.p$TOTAL.N
 biosamp.p$PORT.NEGEAR.AREA.NESPP4.P <-
biosamp.p$PORT.NEGEAR.AREA.NESPP4.N/biosamp.p$TOTAL.N
 biosamp.p$TOTAL.P <-
rowSums(biosamp.p[,c('MATCH.P','NOMATCH.P','PORT.P','NEGEAR.P','AREA.P','NESPP4.P','PORT.NEGEA
R.P','PORT.AREA.P','PORT.NESPP4.P','NEGEAR.AREA.P','NEGEAR.NESPP4.P','AREA.NESPP4.P','PORT.NEGE
AR.AREA.P','PORT.NEGEAR.NESPP4.P','PORT.AREA.NESPP4.P','NEGEAR.AREA.NESPP4.P','PORT.NEGEAR.A
REA.NESPP4.P')])

 #Proportions of age samples matched for output
 biosamp.out <-
biosamp.p[,c('SPPNM','SPPNM8','TOTAL.N','MATCH.P','NOMATCH.P','PORT.P','NEGEAR.P','AREA.P','NESP
P4.P','PORT.NEGEAR.P','PORT.AREA.P','PORT.NESPP4.P','NEGEAR.AREA.P','NEGEAR.NESPP4.P','AREA.NES
PP4.P','PORT.NEGEAR.AREA.P','PORT.NEGEAR.NESPP4.P','PORT.AREA.NESPP4.P','NEGEAR.AREA.NESPP4.
P','PORT.NEGEAR.AREA.NESPP4.P','TOTAL.P')]

 #Calculate total proportion of ages samples that partially match length samples
 biosamp.sum <-
cbind(biosamp.out[,c('SPPNM','SPPNM8','TOTAL.N','MATCH.P','NOMATCH.P')],rowSums(biosamp.out[,c(
'PORT.P','NEGEAR.P','AREA.P','NESPP4.P','PORT.NEGEAR.P','PORT.AREA.P','PORT.NESPP4.P','NEGEAR.AR
EA.P','NEGEAR.NESPP4.P','AREA.NESPP4.P','PORT.NEGEAR.AREA.P','PORT.NEGEAR.NESPP4.P','PORT.ARE
A.NESPP4.P','NEGEAR.AREA.NESPP4.P','PORT.NEGEAR.AREA.NESPP4.P')]))
 names(biosamp.sum)[6] <- 'PARTMATCH.P'
 biosamp.sum$TOTAL.P <- rowSums(biosamp.sum[,c('MATCH.P','NOMATCH.P','PARTMATCH.P')])
 names(biosamp.sum)[which(names(biosamp.sum) %in% c('TOTAL.N'))] <- paste(year[j],'.TOTAL.N',sep =
"")
 names(biosamp.sum)[which(names(biosamp.sum) %in% c('MATCH.P'))] <- paste(year[j],'.MATCH.P',sep
= "")
```

```
 names(biosamp.sum)[which(names(biosamp.sum) %in% c('NOMATCH.P'))] <-
paste(year[j],'.NOMATCH.P',sep = "")
 names(biosamp.sum)[which(names(biosamp.sum) %in% c('PARTMATCH.P'))] <-
paste(year[j],'.PARTMATCH.P',sep = "")

 ############################################################
 ### BEGIN MATCHING LENGTH SAMPLES TO COMMERCIAL LANDINGS ###
 ############################################################

#Length samples to be matched to landings
 biosamp.match <- cflen.samp

#Aggregate landings at trip level
 cfdets.mktcat <-
aggregate(cfdets[,c('SPPLIVLB')],cfdets[,c('YEAR','MONTH','DAY','PERMIT','NESPP4','NESPP3','SPPNM','SP
PNM8','NEGEAR','AREA','PORT')],FUN = sum)
 names(cfdets.mktcat)[names(cfdets.mktcat)=='x'] <- 'SPPLIVLB'

 #Match length samples to landings
 bio.land <- merge(biosamp.match,cfdets.mktcat,by = c('YEAR','MONTH','DAY','PERMIT','NESPP3'),all.x =
TRUE)

 #Rename variables
 names(bio.land)[names(bio.land) == 'LINK.x'] <- 'LINK'
 names(bio.land)[names(bio.land) == 'PORT.x'] <- 'PORT'
 names(bio.land)[names(bio.land) == 'DOCN.x'] <- 'DOCN'
 names(bio.land)[names(bio.land) == 'NEGEAR.x'] <- 'NEGEAR'
 names(bio.land)[names(bio.land) == 'AREA.x'] <- 'AREA'
 names(bio.land)[names(bio.land) == 'NESPP4.x'] <- 'NESPP4'
 names(bio.land)[names(bio.land) == 'SPPNM.x'] <- 'SPPNM'
 names(bio.land)[names(bio.land) == 'SPPNM8.x'] <- 'SPPNM8'
 names(bio.land)[names(bio.land) == 'UTILCD.x'] <- 'UTILCD'

 names(bio.land)[names(bio.land) == 'LINK.y'] <- 'LINK.LND'
 names(bio.land)[names(bio.land) == 'PORT.y'] <- 'PORT.LND'
 names(bio.land)[names(bio.land) == 'DOCN.y'] <- 'DOCN.LND'
 names(bio.land)[names(bio.land) == 'NEGEAR.y'] <- 'NEGEAR.LND'
 names(bio.land)[names(bio.land) == 'AREA.y'] <- 'AREA.LND'
 names(bio.land)[names(bio.land) == 'NESPP4.y'] <- 'NESPP4.LND'
 names(bio.land)[names(bio.land) == 'SPPNM.y'] <- 'SPPNM.LND'
 names(bio.land)[names(bio.land) == 'SPPNM8.y'] <- 'SPPNM8.LND'
 names(bio.land)[names(bio.land) == 'UTILCD.y'] <- 'UTILCD.LND'

 #Flag different PORT between length samples and landings
 bio.land$PORT.FLAG <- NA
 if(nrow(bio.land[!is.na(bio.land$SPPLIVLB) & bio.land$PORT != bio.land$PORT.LND,]) > 0) {
  bio.land[!is.na(bio.land$SPPLIVLB) & bio.land$PORT != bio.land$PORT.LND,c('PORT.FLAG')] <- 1
 }
```

```
 #Flag different NEGEAR between length samples and landings
 bio.land$NEGEAR.FLAG <- NA
 if(nrow(bio.land[!is.na(bio.land$SPPLIVLB) & bio.land$NEGEAR != bio.land$NEGEAR.LND,]) > 0) {
  bio.land[!is.na(bio.land$SPPLIVLB) & bio.land$NEGEAR != bio.land$NEGEAR.LND,c('NEGEAR.FLAG')] <-
1
 }

 #Flag different AREA between length samples and landings
 bio.land$AREA.FLAG <- NA
 if(nrow(bio.land[!is.na(bio.land$SPPLIVLB) & bio.land$AREA != bio.land$AREA.LND,]) > 0) {
  bio.land[!is.na(bio.land$SPPLIVLB) & bio.land$AREA != bio.land$AREA.LND,c('AREA.FLAG')] <- 1
 }

 #Flag different NESPP4 between length samples and landings
 bio.land$NESPP4.FLAG <- NA
 if(nrow(bio.land[!is.na(bio.land$SPPLIVLB) & bio.land$NESPP4 != bio.land$NESPP4.LND,]) > 0) {
  bio.land[!is.na(bio.land$SPPLIVLB) & bio.land$NESPP4 != bio.land$NESPP4.LND,c('NESPP4.FLAG')] <- 1
 }

 #Sum up flags
 bio.land$TOTAL.FLAG <-
rowSums(bio.land[,c('PORT.FLAG','NEGEAR.FLAG','AREA.FLAG','NESPP4.FLAG')],na.rm = TRUE)

 #Sort so that "best" match is first
 bioland.sort <- bio.land[order(bio.land$LINK,bio.land$TOTAL.FLAG),]
 #Drop duplicate matches, keeping best match
 bioland.new <- bioland.sort[!duplicated(bioland.sort$LINK),]

 #Check that length samples were not lost
 bioland.check <- nrow(bioland.new) - nrow(biosamp.match)

 #Calculate total number of length samples by species
 total.bioland.spp <- aggregate(biosamp.match$YEAR,biosamp.match[,c('SPPNM','SPPNM8')],FUN =
length)
 names(total.bioland.spp)[names(total.bioland.spp)=='x'] <- 'TOTAL.N'

 #Calculate total number of fishing trips by species
 total.trip <- unique(biosamp.match[,c('YEAR','MONTH','DAY','PERMIT','SPPNM','SPPNM8')])
 total.trip.spp <- aggregate(total.trip$YEAR,total.trip[,c('SPPNM','SPPNM8')],FUN = length)
 names(total.trip.spp)[names(total.trip.spp)=='x'] <- 'TRIP.N'

 #Calculate number of fishing trips associated with partial matches by species
 part.trip <- unique(bioland.new[bioland.new$TOTAL.FLAG >
0,c('YEAR','MONTH','DAY','PERMIT','SPPNM','SPPNM8')])
 part.trip.spp <- aggregate(part.trip$YEAR,part.trip[,c('SPPNM','SPPNM8')],FUN = length)
 names(part.trip.spp)[names(part.trip.spp)=='x'] <- paste(year[j],'.PART.N',sep = "")
```

```
 #Calculate number of length samples that match to landings by species
 if(nrow(bioland.new[!is.na(bioland.new$SPPLIVLB) & is.na(bioland.new$PORT.FLAG) &
is.na(bioland.new$NEGEAR.FLAG) & is.na(bioland.new$AREA.FLAG) &
is.na(bioland.new$NESPP4.FLAG),]) > 0) {
  match.bioland.spp <- aggregate(bioland.new[!is.na(bioland.new$SPPLIVLB) &
is.na(bioland.new$PORT.FLAG) & is.na(bioland.new$NEGEAR.FLAG) & is.na(bioland.new$AREA.FLAG) &
is.na(bioland.new$NESPP4.FLAG),c('YEAR')],bioland.new[!is.na(bioland.new$SPPLIVLB) &
is.na(bioland.new$PORT.FLAG) & is.na(bioland.new$NEGEAR.FLAG) & is.na(bioland.new$AREA.FLAG) &
is.na(bioland.new$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  match.bioland.spp <- total.bioland.spp[,c('SPPNM','SPPNM8')]
  match.bioland.spp$x <- 0
 }
 names(match.bioland.spp)[names(match.bioland.spp)=='x'] <- year[j]

 #Calculate number of length samples that don't match to landings by species
 if(nrow(bioland.new[is.na(bioland.new$SPPLIVLB) & is.na(bioland.new$PORT.FLAG) &
is.na(bioland.new$NEGEAR.FLAG) & is.na(bioland.new$AREA.FLAG) &
is.na(bioland.new$NESPP4.FLAG),]) > 0) {
  nomatch.bioland.spp <- aggregate(bioland.new[is.na(bioland.new$SPPLIVLB) &
is.na(bioland.new$PORT.FLAG) & is.na(bioland.new$NEGEAR.FLAG) & is.na(bioland.new$AREA.FLAG) &
is.na(bioland.new$NESPP4.FLAG),c('YEAR')],bioland.new[is.na(bioland.new$SPPLIVLB) &
is.na(bioland.new$PORT.FLAG) & is.na(bioland.new$NEGEAR.FLAG) & is.na(bioland.new$AREA.FLAG) &
is.na(bioland.new$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  nomatch.bioland.spp <- total.bioland.spp[,c('SPPNM','SPPNM8')]
  nomatch.bioland.spp$x <- 0
 }
 names(nomatch.bioland.spp)[names(nomatch.bioland.spp)=='x'] <- year[j]

 #Calculate number of length samples that match to landings but have different PORT by species
 if(nrow(bioland.new[!is.na(bioland.new$SPPLIVLB) & !is.na(bioland.new$PORT.FLAG) &
is.na(bioland.new$NEGEAR.FLAG) & is.na(bioland.new$AREA.FLAG) &
is.na(bioland.new$NESPP4.FLAG),]) > 0) {
  port.bioland.spp <- aggregate(bioland.new[!is.na(bioland.new$SPPLIVLB) &
!is.na(bioland.new$PORT.FLAG) & is.na(bioland.new$NEGEAR.FLAG) & is.na(bioland.new$AREA.FLAG) &
is.na(bioland.new$NESPP4.FLAG),c('YEAR')],bioland.new[!is.na(bioland.new$SPPLIVLB) &
!is.na(bioland.new$PORT.FLAG) & is.na(bioland.new$NEGEAR.FLAG) & is.na(bioland.new$AREA.FLAG) &
is.na(bioland.new$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  port.bioland.spp <- total.bioland.spp[,c('SPPNM','SPPNM8')]
  port.bioland.spp$x <- 0
 }
 names(port.bioland.spp)[names(port.bioland.spp)=='x'] <- year[j]

 #Calculate number of length samples that match to landings but have different NEGEAR by species
```

```
 if(nrow(bioland.new[!is.na(bioland.new$SPPLIVLB) & is.na(bioland.new$PORT.FLAG) &
!is.na(bioland.new$NEGEAR.FLAG) & is.na(bioland.new$AREA.FLAG) &
is.na(bioland.new$NESPP4.FLAG),]) > 0) {
  negear.bioland.spp <- aggregate(bioland.new[!is.na(bioland.new$SPPLIVLB) &
is.na(bioland.new$PORT.FLAG) & !is.na(bioland.new$NEGEAR.FLAG) & is.na(bioland.new$AREA.FLAG) &
is.na(bioland.new$NESPP4.FLAG),c('YEAR')],bioland.new[!is.na(bioland.new$SPPLIVLB) &
is.na(bioland.new$PORT.FLAG) & !is.na(bioland.new$NEGEAR.FLAG) & is.na(bioland.new$AREA.FLAG) &
is.na(bioland.new$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  negear.bioland.spp <- total.bioland.spp[,c('SPPNM','SPPNM8')]
  negear.bioland.spp$x <- 0
 }
 names(negear.bioland.spp)[names(negear.bioland.spp)=='x'] <- year[j]

 #Calculate number of length samples that match to landings but have different AREA by species
 if(nrow(bioland.new[!is.na(bioland.new$SPPLIVLB) & is.na(bioland.new$PORT.FLAG) &
is.na(bioland.new$NEGEAR.FLAG) & !is.na(bioland.new$AREA.FLAG) &
is.na(bioland.new$NESPP4.FLAG),]) > 0) {
  area.bioland.spp <- aggregate(bioland.new[!is.na(bioland.new$SPPLIVLB) &
is.na(bioland.new$PORT.FLAG) & is.na(bioland.new$NEGEAR.FLAG) & !is.na(bioland.new$AREA.FLAG) &
is.na(bioland.new$NESPP4.FLAG),c('YEAR')],bioland.new[!is.na(bioland.new$SPPLIVLB) &
is.na(bioland.new$PORT.FLAG) & is.na(bioland.new$NEGEAR.FLAG) & !is.na(bioland.new$AREA.FLAG) &
is.na(bioland.new$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  area.bioland.spp <- total.bioland.spp[,c('SPPNM','SPPNM8')]
  area.bioland.spp$x <- 0
 }
 names(area.bioland.spp)[names(area.bioland.spp)=='x'] <- year[j]

 #Calculate number of length samples that match to landings but have different NESPP4 by species
 if(nrow(bioland.new[!is.na(bioland.new$SPPLIVLB) & is.na(bioland.new$PORT.FLAG) &
is.na(bioland.new$NEGEAR.FLAG) & is.na(bioland.new$AREA.FLAG) &
!is.na(bioland.new$NESPP4.FLAG),]) > 0) {
  nespp4.bioland.spp <- aggregate(bioland.new[!is.na(bioland.new$SPPLIVLB) &
is.na(bioland.new$PORT.FLAG) & is.na(bioland.new$NEGEAR.FLAG) & is.na(bioland.new$AREA.FLAG) &
!is.na(bioland.new$NESPP4.FLAG),c('YEAR')],bioland.new[!is.na(bioland.new$SPPLIVLB) &
is.na(bioland.new$PORT.FLAG) & is.na(bioland.new$NEGEAR.FLAG) & is.na(bioland.new$AREA.FLAG) &
!is.na(bioland.new$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  nespp4.bioland.spp <- total.bioland.spp[,c('SPPNM','SPPNM8')]
  nespp4.bioland.spp$x <- 0
 }
 names(nespp4.bioland.spp)[names(nespp4.bioland.spp)=='x'] <- year[j]

 #Calculate number of length samples that match to landings but have different PORT and NEGEAR by
species
```

```
 if(nrow(bioland.new[!is.na(bioland.new$SPPLIVLB) & !is.na(bioland.new$PORT.FLAG) &
!is.na(bioland.new$NEGEAR.FLAG) & is.na(bioland.new$AREA.FLAG) &
is.na(bioland.new$NESPP4.FLAG),]) > 0) {
  port.negear.bioland.spp <- aggregate(bioland.new[!is.na(bioland.new$SPPLIVLB) &
!is.na(bioland.new$PORT.FLAG) & !is.na(bioland.new$NEGEAR.FLAG) & is.na(bioland.new$AREA.FLAG)
& is.na(bioland.new$NESPP4.FLAG),c('YEAR')],bioland.new[!is.na(bioland.new$SPPLIVLB) &
!is.na(bioland.new$PORT.FLAG) & !is.na(bioland.new$NEGEAR.FLAG) & is.na(bioland.new$AREA.FLAG)
& is.na(bioland.new$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  port.negear.bioland.spp <- total.bioland.spp[,c('SPPNM','SPPNM8')]
  port.negear.bioland.spp$x <- 0
 }
 names(port.negear.bioland.spp)[names(port.negear.bioland.spp)=='x'] <- year[j]

 #Calculate number of length samples that match to landings but have different PORT and AREA by
species
 if(nrow(bioland.new[!is.na(bioland.new$SPPLIVLB) & !is.na(bioland.new$PORT.FLAG) &
is.na(bioland.new$NEGEAR.FLAG) & !is.na(bioland.new$AREA.FLAG) &
is.na(bioland.new$NESPP4.FLAG),]) > 0) {
  port.area.bioland.spp <- aggregate(bioland.new[!is.na(bioland.new$SPPLIVLB) &
!is.na(bioland.new$PORT.FLAG) & is.na(bioland.new$NEGEAR.FLAG) & !is.na(bioland.new$AREA.FLAG)
& is.na(bioland.new$NESPP4.FLAG),c('YEAR')],bioland.new[!is.na(bioland.new$SPPLIVLB) &
!is.na(bioland.new$PORT.FLAG) & is.na(bioland.new$NEGEAR.FLAG) & !is.na(bioland.new$AREA.FLAG)
& is.na(bioland.new$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  port.area.bioland.spp <- total.bioland.spp[,c('SPPNM','SPPNM8')]
  port.area.bioland.spp$x <- 0
 }
 names(port.area.bioland.spp)[names(port.area.bioland.spp)=='x'] <- year[j]

 #Calculate number of length samples that match to landings but have different PORT and NESPP4 by
species
 if(nrow(bioland.new[!is.na(bioland.new$SPPLIVLB) & !is.na(bioland.new$PORT.FLAG) &
is.na(bioland.new$NEGEAR.FLAG) & is.na(bioland.new$AREA.FLAG) &
!is.na(bioland.new$NESPP4.FLAG),]) > 0) {
  port.nespp4.bioland.spp <- aggregate(bioland.new[!is.na(bioland.new$SPPLIVLB) &
!is.na(bioland.new$PORT.FLAG) & is.na(bioland.new$NEGEAR.FLAG) & is.na(bioland.new$AREA.FLAG) &
!is.na(bioland.new$NESPP4.FLAG),c('YEAR')],bioland.new[!is.na(bioland.new$SPPLIVLB) &
!is.na(bioland.new$PORT.FLAG) & is.na(bioland.new$NEGEAR.FLAG) & is.na(bioland.new$AREA.FLAG) &
!is.na(bioland.new$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  port.nespp4.bioland.spp <- total.bioland.spp[,c('SPPNM','SPPNM8')]
  port.nespp4.bioland.spp$x <- 0
 }
 names(port.nespp4.bioland.spp)[names(port.nespp4.bioland.spp)=='x'] <- year[j]

 #Calculate number of length samples that match to landings but have different NEGEAR and AREA by
species
```

```
 if(nrow(bioland.new[!is.na(bioland.new$SPPLIVLB) & is.na(bioland.new$PORT.FLAG) &
!is.na(bioland.new$NEGEAR.FLAG) & !is.na(bioland.new$AREA.FLAG) &
is.na(bioland.new$NESPP4.FLAG),]) > 0) {
  negear.area.bioland.spp <- aggregate(bioland.new[!is.na(bioland.new$SPPLIVLB) &
is.na(bioland.new$PORT.FLAG) & !is.na(bioland.new$NEGEAR.FLAG) & !is.na(bioland.new$AREA.FLAG)
& is.na(bioland.new$NESPP4.FLAG),c('YEAR')],bioland.new[!is.na(bioland.new$SPPLIVLB) &
is.na(bioland.new$PORT.FLAG) & !is.na(bioland.new$NEGEAR.FLAG) & !is.na(bioland.new$AREA.FLAG)
& is.na(bioland.new$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  negear.area.bioland.spp <- total.bioland.spp[,c('SPPNM','SPPNM8')]
  negear.area.bioland.spp$x <- 0
 }
 names(negear.area.bioland.spp)[names(negear.area.bioland.spp)=='x'] <- year[j]

 #Calculate number of length samples that match to landings but have different NEGEAR and NESPP4 by
species
 if(nrow(bioland.new[!is.na(bioland.new$SPPLIVLB) & is.na(bioland.new$PORT.FLAG) &
!is.na(bioland.new$NEGEAR.FLAG) & is.na(bioland.new$AREA.FLAG) &
!is.na(bioland.new$NESPP4.FLAG),]) > 0) {
  negear.nespp4.bioland.spp <- aggregate(bioland.new[!is.na(bioland.new$SPPLIVLB) &
is.na(bioland.new$PORT.FLAG) & !is.na(bioland.new$NEGEAR.FLAG) & is.na(bioland.new$AREA.FLAG) &
!is.na(bioland.new$NESPP4.FLAG),c('YEAR')],bioland.new[!is.na(bioland.new$SPPLIVLB) &
is.na(bioland.new$PORT.FLAG) & !is.na(bioland.new$NEGEAR.FLAG) & is.na(bioland.new$AREA.FLAG) &
!is.na(bioland.new$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  negear.nespp4.bioland.spp <- total.bioland.spp[,c('SPPNM','SPPNM8')]
  negear.nespp4.bioland.spp$x <- 0
 }
 names(negear.nespp4.bioland.spp)[names(negear.nespp4.bioland.spp)=='x'] <- year[j]

 #Calculate number of length samples that match to landings but have different AREA and NESPP4 by
species
 if(nrow(bioland.new[!is.na(bioland.new$SPPLIVLB) & is.na(bioland.new$PORT.FLAG) &
is.na(bioland.new$NEGEAR.FLAG) & !is.na(bioland.new$AREA.FLAG) &
!is.na(bioland.new$NESPP4.FLAG),]) > 0) {
  area.nespp4.bioland.spp <- aggregate(bioland.new[!is.na(bioland.new$SPPLIVLB) &
is.na(bioland.new$PORT.FLAG) & is.na(bioland.new$NEGEAR.FLAG) & !is.na(bioland.new$AREA.FLAG) &
!is.na(bioland.new$NESPP4.FLAG),c('YEAR')],bioland.new[!is.na(bioland.new$SPPLIVLB) &
is.na(bioland.new$PORT.FLAG) & is.na(bioland.new$NEGEAR.FLAG) & !is.na(bioland.new$AREA.FLAG) &
!is.na(bioland.new$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  area.nespp4.bioland.spp <- total.bioland.spp[,c('SPPNM','SPPNM8')]
  area.nespp4.bioland.spp$x <- 0
 }
 names(area.nespp4.bioland.spp)[names(area.nespp4.bioland.spp)=='x'] <- year[j]

 #Calculate number of length samples that match to landings but have different PORT, NEGEAR and
AREA by species
```

```
 if(nrow(bioland.new[!is.na(bioland.new$SPPLIVLB) & !is.na(bioland.new$PORT.FLAG) &
!is.na(bioland.new$NEGEAR.FLAG) & !is.na(bioland.new$AREA.FLAG) &
is.na(bioland.new$NESPP4.FLAG),]) > 0) {
  port.negear.area.bioland.spp <- aggregate(bioland.new[!is.na(bioland.new$SPPLIVLB) &
!is.na(bioland.new$PORT.FLAG) & !is.na(bioland.new$NEGEAR.FLAG) & !is.na(bioland.new$AREA.FLAG)
& is.na(bioland.new$NESPP4.FLAG),c('YEAR')],bioland.new[!is.na(bioland.new$SPPLIVLB) &
!is.na(bioland.new$PORT.FLAG) & !is.na(bioland.new$NEGEAR.FLAG) & !is.na(bioland.new$AREA.FLAG)
& is.na(bioland.new$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  port.negear.area.bioland.spp <- total.bioland.spp[,c('SPPNM','SPPNM8')]
  port.negear.area.bioland.spp$x <- 0
 }
 names(port.negear.area.bioland.spp)[names(port.negear.area.bioland.spp)=='x'] <- year[j]

 #Calculate number of length samples that match to landings but have different PORT, NEGEAR and
NESPP4 by species
 if(nrow(bioland.new[!is.na(bioland.new$SPPLIVLB) & !is.na(bioland.new$PORT.FLAG) &
!is.na(bioland.new$NEGEAR.FLAG) & is.na(bioland.new$AREA.FLAG) &
!is.na(bioland.new$NESPP4.FLAG),]) > 0) {
  port.negear.nespp4.bioland.spp <- aggregate(bioland.new[!is.na(bioland.new$SPPLIVLB) &
!is.na(bioland.new$PORT.FLAG) & !is.na(bioland.new$NEGEAR.FLAG) & is.na(bioland.new$AREA.FLAG)
& !is.na(bioland.new$NESPP4.FLAG),c('YEAR')],bioland.new[!is.na(bioland.new$SPPLIVLB) &
!is.na(bioland.new$PORT.FLAG) & !is.na(bioland.new$NEGEAR.FLAG) & is.na(bioland.new$AREA.FLAG)
& !is.na(bioland.new$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  port.negear.nespp4.bioland.spp <- total.bioland.spp[,c('SPPNM','SPPNM8')]
  port.negear.nespp4.bioland.spp$x <- 0
 }
 names(port.negear.nespp4.bioland.spp)[names(port.negear.nespp4.bioland.spp)=='x'] <- year[j]

 #Calculate number of length samples that match to landings but have different PORT, AREA and NESPP4
by species
 if(nrow(bioland.new[!is.na(bioland.new$SPPLIVLB) & !is.na(bioland.new$PORT.FLAG) &
is.na(bioland.new$NEGEAR.FLAG) & !is.na(bioland.new$AREA.FLAG) &
!is.na(bioland.new$NESPP4.FLAG),]) > 0) {
  port.area.nespp4.bioland.spp <- aggregate(bioland.new[!is.na(bioland.new$SPPLIVLB) &
!is.na(bioland.new$PORT.FLAG) & is.na(bioland.new$NEGEAR.FLAG) & !is.na(bioland.new$AREA.FLAG)
& !is.na(bioland.new$NESPP4.FLAG),c('YEAR')],bioland.new[!is.na(bioland.new$SPPLIVLB) &
!is.na(bioland.new$PORT.FLAG) & is.na(bioland.new$NEGEAR.FLAG) & !is.na(bioland.new$AREA.FLAG)
& !is.na(bioland.new$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  port.area.nespp4.bioland.spp <- total.bioland.spp[,c('SPPNM','SPPNM8')]
  port.area.nespp4.bioland.spp$x <- 0
 }
 names(port.area.nespp4.bioland.spp)[names(port.area.nespp4.bioland.spp)=='x'] <- year[j]

 #Calculate number of length samples that match to landings but have different NEGEAR, AREA and
NESPP4 by species
```

```
 if(nrow(bioland.new[!is.na(bioland.new$SPPLIVLB) & is.na(bioland.new$PORT.FLAG) &
!is.na(bioland.new$NEGEAR.FLAG) & !is.na(bioland.new$AREA.FLAG) &
!is.na(bioland.new$NESPP4.FLAG),]) > 0) {
  negear.area.nespp4.bioland.spp <- aggregate(bioland.new[!is.na(bioland.new$SPPLIVLB) &
is.na(bioland.new$PORT.FLAG) & !is.na(bioland.new$NEGEAR.FLAG) & !is.na(bioland.new$AREA.FLAG)
& !is.na(bioland.new$NESPP4.FLAG),c('YEAR')],bioland.new[!is.na(bioland.new$SPPLIVLB) &
is.na(bioland.new$PORT.FLAG) & !is.na(bioland.new$NEGEAR.FLAG) & !is.na(bioland.new$AREA.FLAG)
& !is.na(bioland.new$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  negear.area.nespp4.bioland.spp <- total.bioland.spp[,c('SPPNM','SPPNM8')]
  negear.area.nespp4.bioland.spp$x <- 0
 }
 names(negear.area.nespp4.bioland.spp)[names(negear.area.nespp4.bioland.spp)=='x'] <- year[j]

 #Calculate number of length samples that match to landings but have different PORT, NEGEAR, AREA
and NESPP4 by species
 if(nrow(bioland.new[!is.na(bioland.new$SPPLIVLB) & !is.na(bioland.new$PORT.FLAG) &
!is.na(bioland.new$NEGEAR.FLAG) & !is.na(bioland.new$AREA.FLAG) &
!is.na(bioland.new$NESPP4.FLAG),]) > 0) {
  port.negear.area.nespp4.bioland.spp <- aggregate(bioland.new[!is.na(bioland.new$SPPLIVLB) &
!is.na(bioland.new$PORT.FLAG) & !is.na(bioland.new$NEGEAR.FLAG) & !is.na(bioland.new$AREA.FLAG)
& !is.na(bioland.new$NESPP4.FLAG),c('YEAR')],bioland.new[!is.na(bioland.new$SPPLIVLB) &
!is.na(bioland.new$PORT.FLAG) & !is.na(bioland.new$NEGEAR.FLAG) & !is.na(bioland.new$AREA.FLAG)
& !is.na(bioland.new$NESPP4.FLAG),c('SPPNM','SPPNM8')],FUN = length)
 } else {
  port.negear.area.nespp4.bioland.spp <- total.bioland.spp[,c('SPPNM','SPPNM8')]
  port.negear.area.nespp4.bioland.spp$x <- 0
 }
 names(port.negear.area.nespp4.bioland.spp)[names(port.negear.area.nespp4.bioland.spp)=='x'] <-
year[j]

 #Append length samples by species from different matching categories
 temp14a <- merge(total.trip.spp,total.bioland.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
 if(nrow(match.bioland.spp) > 0) {
  names(match.bioland.spp)[names(match.bioland.spp)==year[j]] <- 'MATCH.N'
  temp14 <- merge(temp14a,match.bioland.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
 } else {
  temp14 <- temp14a
  temp14$MATCH.N <- 0
 }
 if(nrow(nomatch.bioland.spp) > 0) {
  names(nomatch.bioland.spp)[names(nomatch.bioland.spp)==year[j]] <- 'NOMATCH.N'
  temp15 <- merge(temp14,nomatch.bioland.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
 } else {
  temp15 <- temp14
  temp15$NOMATCH.N <- 0
 }
 if(nrow(port.bioland.spp) > 0) {
```

```
 names(port.bioland.spp)[names(port.bioland.spp)==year[j]] <- 'PORT.N'
 temp16 <- merge(temp15,port.bioland.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
} else {
 temp16 <- temp15
 temp16$PORT.N <- 0
}
if(nrow(negear.bioland.spp) > 0) {
 names(negear.bioland.spp)[names(negear.bioland.spp)==year[j]] <- 'NEGEAR.N'
 temp17 <- merge(temp16,negear.bioland.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
} else {
 temp17 <- temp16
 temp17$NEGEAR.N <- 0
}
if(nrow(area.bioland.spp) > 0) {
 names(area.bioland.spp)[names(area.bioland.spp)==year[j]] <- 'AREA.N'
 temp18 <- merge(temp17,area.bioland.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
} else {
 temp18 <- temp17
 temp18$AREA.N <- 0
}
if(nrow(nespp4.bioland.spp) > 0) {
 names(nespp4.bioland.spp)[names(nespp4.bioland.spp)==year[j]] <- 'NESPP4.N'
 temp19 <- merge(temp18,nespp4.bioland.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
} else {
 temp19 <- temp18
 temp19$NESPP4.N <- 0
}
if(nrow(port.negear.bioland.spp) > 0) {
 names(port.negear.bioland.spp)[names(port.negear.bioland.spp)==year[j]] <- 'PORT.NEGEAR.N'
 temp20 <- merge(temp19,port.negear.bioland.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
} else {
 temp20 <- temp19
 temp20$PORT.NEGEAR.N <- 0
}
if(nrow(port.area.bioland.spp) > 0) {
 names(port.area.bioland.spp)[names(port.area.bioland.spp)==year[j]] <- 'PORT.AREA.N'
 temp21 <- merge(temp20,port.area.bioland.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
} else {
 temp21 <- temp20
 temp21$PORT.AREA.N <- 0
}
if(nrow(port.nespp4.bioland.spp) > 0) {
 names(port.nespp4.bioland.spp)[names(port.nespp4.bioland.spp)==year[j]] <- 'PORT.NESPP4.N'
 temp22 <- merge(temp21,port.nespp4.bioland.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
} else {
 temp22 <- temp21
 temp22$PORT.NESPP4.N <- 0
}
```

```
 if(nrow(negear.area.bioland.spp) > 0) {
  names(negear.area.bioland.spp)[names(negear.area.bioland.spp)==year[j]] <- 'NEGEAR.AREA.N'
  temp23 <- merge(temp22,negear.area.bioland.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
 } else {
  temp23 <- temp22
  temp23$NEGEAR.AREA.N <- 0
 }
 if(nrow(negear.nespp4.bioland.spp) > 0) {
  names(negear.nespp4.bioland.spp)[names(negear.nespp4.bioland.spp)==year[j]] <-
'NEGEAR.NESPP4.N'
  temp24 <- merge(temp23,negear.nespp4.bioland.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
 } else {
  temp24 <- temp23
  temp24$NEGEAR.NESPP4.N <- 0
 }
 if(nrow(area.nespp4.bioland.spp) > 0) {
  names(area.nespp4.bioland.spp)[names(area.nespp4.bioland.spp)==year[j]] <- 'AREA.NESPP4.N'
  temp25 <- merge(temp24,area.nespp4.bioland.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
 } else {
  temp25 <- temp24
  temp25$AREA.NESPP4.N <- 0
 }
 if(nrow(port.negear.area.bioland.spp) > 0) {
  names(port.negear.area.bioland.spp)[names(port.negear.area.bioland.spp)==year[j]] <-
'PORT.NEGEAR.AREA.N'
  temp26 <- merge(temp25,port.negear.area.bioland.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
 } else {
  temp26 <- temp25
  temp26$PORT.NEGEAR.AREA.N <- 0
 }
 if(nrow(port.negear.nespp4.bioland.spp) > 0) {
  names(port.negear.nespp4.bioland.spp)[names(port.negear.nespp4.bioland.spp)==year[j]] <-
'PORT.NEGEAR.NESPP4.N'
  temp27 <- merge(temp26,port.negear.nespp4.bioland.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
 } else {
  temp27 <- temp26
  temp27$PORT.NEGEAR.NESPP4.N <- 0
 }
 if(nrow(port.area.nespp4.bioland.spp) > 0) {
  names(port.area.nespp4.bioland.spp)[names(port.area.nespp4.bioland.spp)==year[j]] <-
'PORT.AREA.NESPP4.N'
  temp28 <- merge(temp27,port.area.nespp4.bioland.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
 } else {
  temp28 <- temp27
  temp28$PORT.AREA.NESPP4.N <- 0
 }
 if(nrow(negear.area.nespp4.bioland.spp) > 0) {
```

```
  names(negear.area.nespp4.bioland.spp)[names(negear.area.nespp4.bioland.spp)==year[j]] <-
'NEGEAR.AREA.NESPP4.N'
  temp29 <- merge(temp28,negear.area.nespp4.bioland.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
 } else {
  temp29 <- temp28
  temp29$NEGEAR.AREA.NESPP4.N <- 0
 }
 if(nrow(port.negear.area.nespp4.bioland.spp) > 0) {
  names(port.negear.area.nespp4.bioland.spp)[names(port.negear.area.nespp4.bioland.spp)==year[j]] <-
'PORT.NEGEAR.AREA.NESPP4.N'
  temp30 <- merge(temp29,port.negear.area.nespp4.bioland.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
 } else {
  temp30 <- temp29
  temp30$PORT.NEGEAR.AREA.NESPP4.N <- 0
 }
 #Replace NAs with 0s to calculate proportions
 temp30[is.na(temp30)] <- 0

 #Calculate proportions of length samples matched
 bioland.p <- temp30
 bioland.p$MATCH.P <- bioland.p$MATCH.N/bioland.p$TOTAL.N
 bioland.p$NOMATCH.P <- bioland.p$NOMATCH.N/bioland.p$TOTAL.N
 bioland.p$PORT.P <- bioland.p$PORT.N/bioland.p$TOTAL.N
 bioland.p$NEGEAR.P <- bioland.p$NEGEAR.N/bioland.p$TOTAL.N
 bioland.p$AREA.P <- bioland.p$AREA.N/bioland.p$TOTAL.N
 bioland.p$NESPP4.P <- bioland.p$NESPP4.N/bioland.p$TOTAL.N
 bioland.p$PORT.NEGEAR.P <- bioland.p$PORT.NEGEAR.N/bioland.p$TOTAL.N
 bioland.p$PORT.AREA.P <- bioland.p$PORT.AREA.N/bioland.p$TOTAL.N
 bioland.p$PORT.NESPP4.P <- bioland.p$PORT.NESPP4.N/bioland.p$TOTAL.N
 bioland.p$NEGEAR.AREA.P <- bioland.p$NEGEAR.AREA.N/bioland.p$TOTAL.N
 bioland.p$NEGEAR.NESPP4.P <- bioland.p$NEGEAR.NESPP4.N/bioland.p$TOTAL.N
 bioland.p$AREA.NESPP4.P <- bioland.p$AREA.NESPP4.N/bioland.p$TOTAL.N
 bioland.p$PORT.NEGEAR.AREA.P <- bioland.p$PORT.NEGEAR.AREA.N/bioland.p$TOTAL.N
 bioland.p$PORT.NEGEAR.NESPP4.P <- bioland.p$PORT.NEGEAR.NESPP4.N/bioland.p$TOTAL.N
 bioland.p$PORT.AREA.NESPP4.P <- bioland.p$PORT.AREA.NESPP4.N/bioland.p$TOTAL.N
 bioland.p$NEGEAR.AREA.NESPP4.P <- bioland.p$NEGEAR.AREA.NESPP4.N/bioland.p$TOTAL.N
 bioland.p$PORT.NEGEAR.AREA.NESPP4.P <-
bioland.p$PORT.NEGEAR.AREA.NESPP4.N/bioland.p$TOTAL.N
 bioland.p$TOTAL.P <-
rowSums(bioland.p[,c('MATCH.P','NOMATCH.P','PORT.P','NEGEAR.P','AREA.P','NESPP4.P','PORT.NEGEAR
.P','PORT.AREA.P','PORT.NESPP4.P','NEGEAR.AREA.P','NEGEAR.NESPP4.P','AREA.NESPP4.P','PORT.NEGEA
R.AREA.P','PORT.NEGEAR.NESPP4.P','PORT.AREA.NESPP4.P','NEGEAR.AREA.NESPP4.P','PORT.NEGEAR.AR
EA.NESPP4.P')])

 #Proportions of age samples matched for output
 bioland.out <-
bioland.p[,c('SPPNM','SPPNM8','TRIP.N','TOTAL.N','MATCH.P','NOMATCH.P','PORT.P','NEGEAR.P','AREA.
P','NESPP4.P','PORT.NEGEAR.P','PORT.AREA.P','PORT.NESPP4.P','NEGEAR.AREA.P','NEGEAR.NESPP4.P','A
```

```
REA.NESPP4.P','PORT.NEGEAR.AREA.P','PORT.NEGEAR.NESPP4.P','PORT.AREA.NESPP4.P','NEGEAR.AREA.
NESPP4.P','PORT.NEGEAR.AREA.NESPP4.P','TOTAL.P')]

 #Calculate total proportion of ages samples that partially match length samples
 bioland.sum <-
cbind(bioland.out[,c('SPPNM','SPPNM8','TRIP.N','TOTAL.N','MATCH.P','NOMATCH.P')],rowSums(bioland.
out[,c('PORT.P','NEGEAR.P','AREA.P','NESPP4.P','PORT.NEGEAR.P','PORT.AREA.P','PORT.NESPP4.P','NEGE
AR.AREA.P','NEGEAR.NESPP4.P','AREA.NESPP4.P','PORT.NEGEAR.AREA.P','PORT.NEGEAR.NESPP4.P','POR
T.AREA.NESPP4.P','NEGEAR.AREA.NESPP4.P','PORT.NEGEAR.AREA.NESPP4.P')]))
 names(bioland.sum)[7] <- 'PARTMATCH.P'
 bioland.sum$TOTAL.P <- rowSums(bioland.sum[,c('MATCH.P','NOMATCH.P','PARTMATCH.P')])
 names(bioland.sum)[which(names(bioland.sum) %in% c('TRIP.N'))] <- paste(year[j],'.TRIP.N',sep = "")
 names(bioland.sum)[which(names(bioland.sum) %in% c('TOTAL.N'))] <- paste(year[j],'.TOTAL.N',sep =
"")
 names(bioland.sum)[which(names(bioland.sum) %in% c('MATCH.P'))] <- paste(year[j],'.MATCH.P',sep =
"")
 names(bioland.sum)[which(names(bioland.sum) %in% c('NOMATCH.P'))] <-
paste(year[j],'.NOMATCH.P',sep = "")
 names(bioland.sum)[which(names(bioland.sum) %in% c('PARTMATCH.P'))] <-
paste(year[j],'.PARTMATCH.P',sep = "")

#Write output to CSV files
 write.csv(biosamp.out, file = paste(direct,"age_length_match_prop_",year[j],".csv",sep=""))
 write.csv(bioland.out, file = paste(direct,"length_land_match_prop_",year[j],".csv",sep=""))

#Append all of the check values
 check <-
cbind(year[j],cflen.samp.check,cflen.num.check,cfage.samp.check,cfage.num.check,biosamp.length.che
ck,biosamp.age.check,bioland.check)

 for(i in 3:ncol(temp30)){
  names(temp30)[i] <- paste(year[j],'.',names(temp30)[i],sep = "")
 }
 for(i in 3:ncol(temp13)){
  names(temp13)[i] <- paste(year[j],'.',names(temp13)[i],sep = "")
 }

#Append output values across years
 if(j == 1) {
  check.all <- check
  bioland.all <- bioland.sum[,c('SPPNM','SPPNM8',paste(year[j],'.TRIP.N',sep =
""),paste(year[j],'.TOTAL.N',sep = ""),paste(year[j],'.MATCH.P',sep = ""),paste(year[j],'.NOMATCH.P',sep =
""),paste(year[j],'.PARTMATCH.P',sep = ""))]
  biosamp.all <- biosamp.sum[,c('SPPNM','SPPNM8',paste(year[j],'.TOTAL.N',sep =
""),paste(year[j],'.MATCH.P',sep = ""),paste(year[j],'.NOMATCH.P',sep =
""),paste(year[j],'.PARTMATCH.P',sep = ""))]
  partial.all <- merge(temp30,part.trip.spp,by = c('SPPNM','SPPNM8'),all = TRUE)
  biosamp.part.all <- temp13
```

```
  bioland.all.check <- bioland.sum[,c('SPPNM','TOTAL.P')]
  names(bioland.all.check)[which(names(bioland.all.check) %in% c('TOTAL.P'))] <-
paste(year[j],'.TOTAL.P',sep = "")
  biosamp.all.check <- biosamp.sum[,c('SPPNM','TOTAL.P')]
  names(biosamp.all.check)[which(names(biosamp.all.check) %in% c('TOTAL.P'))] <-
paste(year[j],'.TOTAL.P',sep = "")
 } else {
  check.all <- rbind(check.all,check)
  bioland.all <- merge(bioland.all,bioland.sum[,c('SPPNM','SPPNM8',paste(year[j],'.TRIP.N',sep =
""),paste(year[j],'.TOTAL.N',sep = ""),paste(year[j],'.MATCH.P',sep = ""),paste(year[j],'.NOMATCH.P',sep =
""),paste(year[j],'.PARTMATCH.P',sep = ""))],by = c('SPPNM','SPPNM8'),all = TRUE)
  biosamp.all <- merge(biosamp.all,biosamp.sum[,c('SPPNM','SPPNM8',paste(year[j],'.TOTAL.N',sep =
""),paste(year[j],'.MATCH.P',sep = ""),paste(year[j],'.NOMATCH.P',sep =
""),paste(year[j],'.PARTMATCH.P',sep = ""))],by = c('SPPNM','SPPNM8'),all = TRUE)
  partial.all <- merge(partial.all,merge(temp30,part.trip.spp,by = c('SPPNM','SPPNM8'),all = TRUE),by =
c('SPPNM','SPPNM8'),all = TRUE)
  biosamp.part.all <- merge(biosamp.part.all,temp13,by = c('SPPNM','SPPNM8'),all = TRUE)
  bioland.all.check <- merge(bioland.all.check,bioland.sum[,c('SPPNM','TOTAL.P')],by = c('SPPNM'),all =
TRUE)
  names(bioland.all.check)[which(names(bioland.all.check) %in% c('TOTAL.P'))] <-
paste(year[j],'.TOTAL.P',sep = "")
  biosamp.all.check <- merge(biosamp.all.check,biosamp.sum[,c('SPPNM','TOTAL.P')],by = c('SPPNM'),all
= TRUE)
  names(biosamp.all.check)[which(names(biosamp.all.check) %in% c('TOTAL.P'))] <-
paste(year[j],'.TOTAL.P',sep = "")
 }
}  #End of year loop

 #Write output to CSV files
 write.csv(check.all, file =
paste(direct,"length_land_match_check_",year[1],"_",year[n.yr],".csv",sep=""))
 write.csv(bioland.all, file =
paste(direct,"length_land_prop_summary_",year[1],"_",year[n.yr],".csv",sep=""))
 write.csv(biosamp.all, file =
paste(direct,"age_length_prop_summary_",year[1],"_",year[n.yr],".csv",sep=""))
 write.csv(bioland.all.check, file =
paste(direct,"length_land_prop_check_",year[1],"_",year[n.yr],".csv",sep=""))
 write.csv(biosamp.all.check, file =
paste(direct,"age_length_prop_check_",year[1],"_",year[n.yr],".csv",sep=""))

 #Replace NAs with 0s
 bioland.all[is.na(bioland.all)] <- 0
 biosamp.all[is.na(biosamp.all)] <- 0
 partial.all[is.na(partial.all)] <- 0
 biosamp.part.all[is.na(biosamp.part.all)] <- 0
 for(j in 1:n.yr){ #Second loop over years
 if(j == 1){
  #Sum length-landings match sample numbers across years
```

```
  bioland.all$TOTAL.MATCH.N <- bioland.all[,c(paste(year[j],'.MATCH.P',sep =
""))]*bioland.all[,c(paste(year[j],'.TOTAL.N',sep = ""))]
  bioland.all$TOTAL.NOMATCH.N <- bioland.all[,c(paste(year[j],'.NOMATCH.P',sep =
""))]*bioland.all[,c(paste(year[j],'.TOTAL.N',sep = ""))]
  bioland.all$TOTAL.PARTMATCH.N <- bioland.all[,c(paste(year[j],'.PARTMATCH.P',sep =
""))]*bioland.all[,c(paste(year[j],'.TOTAL.N',sep = ""))]
  bioland.all$TOTAL.TRIP.N <- bioland.all[,c(paste(year[j],'.TRIP.N',sep = ""))]
  bioland.all$TOTAL.TOTAL.N <- bioland.all[,c(paste(year[j],'.TOTAL.N',sep = ""))]

 #Sum age-length match sample numbers across years
  biosamp.all$TOTAL.MATCH.N <- biosamp.all[,c(paste(year[j],'.MATCH.P',sep =
""))]*biosamp.all[,c(paste(year[j],'.TOTAL.N',sep = ""))]
  biosamp.all$TOTAL.NOMATCH.N <- biosamp.all[,c(paste(year[j],'.NOMATCH.P',sep =
""))]*biosamp.all[,c(paste(year[j],'.TOTAL.N',sep = ""))]
  biosamp.all$TOTAL.PARTMATCH.N <- biosamp.all[,c(paste(year[j],'.PARTMATCH.P',sep =
""))]*biosamp.all[,c(paste(year[j],'.TOTAL.N',sep = ""))]
  biosamp.all$TOTAL.TOTAL.N <- biosamp.all[,c(paste(year[j],'.TOTAL.N',sep = ""))]

#Sum length-landings partial match sample numbers across years
  partial.all$PART.N <- partial.all[,c(paste(year[j],'.PART.N',sep = ""))]
  partial.all$PORT.N <- partial.all[,c(paste(year[j],'.PORT.N',sep = ""))]
  partial.all$NEGEAR.N <- partial.all[,c(paste(year[j],'.NEGEAR.N',sep = ""))]
  partial.all$AREA.N <- partial.all[,c(paste(year[j],'.AREA.N',sep = ""))]
  partial.all$NESPP4.N <- partial.all[,c(paste(year[j],'.NESPP4.N',sep = ""))]
  partial.all$PORT.NEGEAR.N <- partial.all[,c(paste(year[j],'.PORT.NEGEAR.N',sep = ""))]
  partial.all$PORT.AREA.N <- partial.all[,c(paste(year[j],'.PORT.AREA.N',sep = ""))]
  partial.all$PORT.NESPP4.N <- partial.all[,c(paste(year[j],'.PORT.NESPP4.N',sep = ""))]
  partial.all$NEGEAR.AREA.N <- partial.all[,c(paste(year[j],'.NEGEAR.AREA.N',sep = ""))]
  partial.all$NEGEAR.NESPP4.N <- partial.all[,c(paste(year[j],'.NEGEAR.NESPP4.N',sep = ""))]
  partial.all$AREA.NESPP4.N <- partial.all[,c(paste(year[j],'.AREA.NESPP4.N',sep = ""))]
  partial.all$PORT.NEGEAR.AREA.N <- partial.all[,c(paste(year[j],'.PORT.NEGEAR.AREA.N',sep = ""))]
  partial.all$PORT.NEGEAR.NESPP4.N <- partial.all[,c(paste(year[j],'.PORT.NEGEAR.NESPP4.N',sep = ""))]
  partial.all$PORT.AREA.NESPP4.N <- partial.all[,c(paste(year[j],'.PORT.AREA.NESPP4.N',sep = ""))]
  partial.all$NEGEAR.AREA.NESPP4.N <- partial.all[,c(paste(year[j],'.NEGEAR.AREA.NESPP4.N',sep = ""))]
  partial.all$PORT.NEGEAR.AREA.NESPP4.N <-
partial.all[,c(paste(year[j],'.PORT.NEGEAR.AREA.NESPP4.N',sep = ""))]

#Sum age-length partial match sample numbers across years
  biosamp.part.all$PORT.N <- biosamp.part.all[,c(paste(year[j],'.PORT.N',sep = ""))]
  biosamp.part.all$NEGEAR.N <- biosamp.part.all[,c(paste(year[j],'.NEGEAR.N',sep = ""))]
  biosamp.part.all$AREA.N <- biosamp.part.all[,c(paste(year[j],'.AREA.N',sep = ""))]
  biosamp.part.all$NESPP4.N <- biosamp.part.all[,c(paste(year[j],'.NESPP4.N',sep = ""))]
  biosamp.part.all$PORT.NEGEAR.N <- biosamp.part.all[,c(paste(year[j],'.PORT.NEGEAR.N',sep = ""))]
  biosamp.part.all$PORT.AREA.N <- biosamp.part.all[,c(paste(year[j],'.PORT.AREA.N',sep = ""))]
  biosamp.part.all$PORT.NESPP4.N <- biosamp.part.all[,c(paste(year[j],'.PORT.NESPP4.N',sep = ""))]
  biosamp.part.all$NEGEAR.AREA.N <- biosamp.part.all[,c(paste(year[j],'.NEGEAR.AREA.N',sep = ""))]
  biosamp.part.all$NEGEAR.NESPP4.N <- biosamp.part.all[,c(paste(year[j],'.NEGEAR.NESPP4.N',sep = ""))]
  biosamp.part.all$AREA.NESPP4.N <- biosamp.part.all[,c(paste(year[j],'.AREA.NESPP4.N',sep = ""))]
```

```
  biosamp.part.all$PORT.NEGEAR.AREA.N <-
biosamp.part.all[,c(paste(year[j],'.PORT.NEGEAR.AREA.N',sep = ""))]
  biosamp.part.all$PORT.NEGEAR.NESPP4.N <-
biosamp.part.all[,c(paste(year[j],'.PORT.NEGEAR.NESPP4.N',sep = ""))]
  biosamp.part.all$PORT.AREA.NESPP4.N <- biosamp.part.all[,c(paste(year[j],'.PORT.AREA.NESPP4.N',sep
= ""))]
  biosamp.part.all$NEGEAR.AREA.NESPP4.N <-
biosamp.part.all[,c(paste(year[j],'.NEGEAR.AREA.NESPP4.N',sep = ""))]
  biosamp.part.all$PORT.NEGEAR.AREA.NESPP4.N <-
biosamp.part.all[,c(paste(year[j],'.PORT.NEGEAR.AREA.NESPP4.N',sep = ""))]
  } else {
 #Sum length-landings match sample numbers across years
  bioland.all$TOTAL.MATCH.N <- bioland.all[,c(paste(year[j],'.MATCH.P',sep =
""))]*bioland.all[,c(paste(year[j],'.TOTAL.N',sep = ""))] + bioland.all$TOTAL.MATCH.N
  bioland.all$TOTAL.NOMATCH.N <- bioland.all[,c(paste(year[j],'.NOMATCH.P',sep =
""))]*bioland.all[,c(paste(year[j],'.TOTAL.N',sep = ""))] + bioland.all$TOTAL.NOMATCH.N
  bioland.all$TOTAL.PARTMATCH.N <- bioland.all[,c(paste(year[j],'.PARTMATCH.P',sep =
""))]*bioland.all[,c(paste(year[j],'.TOTAL.N',sep = ""))] + bioland.all$TOTAL.PARTMATCH.N
  bioland.all$TOTAL.TRIP.N <- bioland.all[,c(paste(year[j],'.TRIP.N',sep = ""))] + bioland.all$TOTAL.TRIP.N
  bioland.all$TOTAL.TOTAL.N <- bioland.all[,c(paste(year[j],'.TOTAL.N',sep = ""))] +
bioland.all$TOTAL.TOTAL.N
 #Sum age-length match sample numbers across years
  biosamp.all$TOTAL.MATCH.N <- biosamp.all[,c(paste(year[j],'.MATCH.P',sep =
""))]*biosamp.all[,c(paste(year[j],'.TOTAL.N',sep = ""))] + biosamp.all$TOTAL.MATCH.N
  biosamp.all$TOTAL.NOMATCH.N <- biosamp.all[,c(paste(year[j],'.NOMATCH.P',sep =
""))]*biosamp.all[,c(paste(year[j],'.TOTAL.N',sep = ""))] + biosamp.all$TOTAL.NOMATCH.N
  biosamp.all$TOTAL.PARTMATCH.N <- biosamp.all[,c(paste(year[j],'.PARTMATCH.P',sep =
""))]*biosamp.all[,c(paste(year[j],'.TOTAL.N',sep = ""))] + biosamp.all$TOTAL.PARTMATCH.N
  biosamp.all$TOTAL.TOTAL.N <- biosamp.all[,c(paste(year[j],'.TOTAL.N',sep = ""))] +
biosamp.all$TOTAL.TOTAL.N
 #Sum length-landings partial match sample numbers across years
  partial.all$PART.N <- partial.all[,c(paste(year[j],'.PART.N',sep = ""))] + partial.all$PART.N
  partial.all$PORT.N <- partial.all[,c(paste(year[j],'.PORT.N',sep = ""))] + partial.all$PORT.N
  partial.all$NEGEAR.N <- partial.all[,c(paste(year[j],'.NEGEAR.N',sep = ""))] + partial.all$NEGEAR.N
  partial.all$AREA.N <- partial.all[,c(paste(year[j],'.AREA.N',sep = ""))] + partial.all$AREA.N
  partial.all$NESPP4.N <- partial.all[,c(paste(year[j],'.NESPP4.N',sep = ""))] + partial.all$NESPP4.N
  partial.all$PORT.NEGEAR.N <- partial.all[,c(paste(year[j],'.PORT.NEGEAR.N',sep = ""))] +
partial.all$PORT.NEGEAR.N
  partial.all$PORT.AREA.N <- partial.all[,c(paste(year[j],'.PORT.AREA.N',sep = ""))] +
partial.all$PORT.AREA.N
  partial.all$PORT.NESPP4.N <- partial.all[,c(paste(year[j],'.PORT.NESPP4.N',sep = ""))] +
partial.all$PORT.NESPP4.N
  partial.all$NEGEAR.AREA.N <- partial.all[,c(paste(year[j],'.NEGEAR.AREA.N',sep = ""))] +
partial.all$NEGEAR.AREA.N
  partial.all$NEGEAR.NESPP4.N <- partial.all[,c(paste(year[j],'.NEGEAR.NESPP4.N',sep = ""))] +
partial.all$NEGEAR.NESPP4.N
  partial.all$AREA.NESPP4.N <- partial.all[,c(paste(year[j],'.AREA.NESPP4.N',sep = ""))] +
partial.all$AREA.NESPP4.N
```

```
  partial.all$PORT.NEGEAR.AREA.N <- partial.all[,c(paste(year[j],'.PORT.NEGEAR.AREA.N',sep = ""))] +
partial.all$PORT.NEGEAR.AREA.N
  partial.all$PORT.NEGEAR.NESPP4.N <- partial.all[,c(paste(year[j],'.PORT.NEGEAR.NESPP4.N',sep = ""))] +
partial.all$PORT.NEGEAR.NESPP4.N
  partial.all$PORT.AREA.NESPP4.N <- partial.all[,c(paste(year[j],'.PORT.AREA.NESPP4.N',sep = ""))] +
partial.all$PORT.AREA.NESPP4.N
  partial.all$NEGEAR.AREA.NESPP4.N <- partial.all[,c(paste(year[j],'.NEGEAR.AREA.NESPP4.N',sep = ""))] +
partial.all$NEGEAR.AREA.NESPP4.N
  partial.all$PORT.NEGEAR.AREA.NESPP4.N <-
partial.all[,c(paste(year[j],'.PORT.NEGEAR.AREA.NESPP4.N',sep = ""))] +
partial.all$PORT.NEGEAR.AREA.NESPP4.N
#Sum age-length partial match sample numbers across years
  biosamp.part.all$PORT.N <- biosamp.part.all[,c(paste(year[j],'.PORT.N',sep = ""))] +
biosamp.part.all$PORT.N
  biosamp.part.all$NEGEAR.N <- biosamp.part.all[,c(paste(year[j],'.NEGEAR.N',sep = ""))] +
biosamp.part.all$NEGEAR.N
  biosamp.part.all$AREA.N <- biosamp.part.all[,c(paste(year[j],'.AREA.N',sep = ""))] +
biosamp.part.all$AREA.N
  biosamp.part.all$NESPP4.N <- biosamp.part.all[,c(paste(year[j],'.NESPP4.N',sep = ""))] +
biosamp.part.all$NESPP4.N
  biosamp.part.all$PORT.NEGEAR.N <- biosamp.part.all[,c(paste(year[j],'.PORT.NEGEAR.N',sep = ""))] +
biosamp.part.all$PORT.NEGEAR.N
  biosamp.part.all$PORT.AREA.N <- biosamp.part.all[,c(paste(year[j],'.PORT.AREA.N',sep = ""))] +
biosamp.part.all$PORT.AREA.N
  biosamp.part.all$PORT.NESPP4.N <- biosamp.part.all[,c(paste(year[j],'.PORT.NESPP4.N',sep = ""))] +
biosamp.part.all$PORT.NESPP4.N
  biosamp.part.all$NEGEAR.AREA.N <- biosamp.part.all[,c(paste(year[j],'.NEGEAR.AREA.N',sep = ""))] +
biosamp.part.all$NEGEAR.AREA.N
  biosamp.part.all$NEGEAR.NESPP4.N <- biosamp.part.all[,c(paste(year[j],'.NEGEAR.NESPP4.N',sep = ""))]
+ biosamp.part.all$NEGEAR.NESPP4.N
  biosamp.part.all$AREA.NESPP4.N <- biosamp.part.all[,c(paste(year[j],'.AREA.NESPP4.N',sep = ""))] +
biosamp.part.all$AREA.NESPP4.N
  biosamp.part.all$PORT.NEGEAR.AREA.N <-
biosamp.part.all[,c(paste(year[j],'.PORT.NEGEAR.AREA.N',sep = ""))] +
biosamp.part.all$PORT.NEGEAR.AREA.N
  biosamp.part.all$PORT.NEGEAR.NESPP4.N <-
biosamp.part.all[,c(paste(year[j],'.PORT.NEGEAR.NESPP4.N',sep = ""))] +
biosamp.part.all$PORT.NEGEAR.NESPP4.N
  biosamp.part.all$PORT.AREA.NESPP4.N <- biosamp.part.all[,c(paste(year[j],'.PORT.AREA.NESPP4.N',sep
= ""))] + biosamp.part.all$PORT.AREA.NESPP4.N
  biosamp.part.all$NEGEAR.AREA.NESPP4.N <-
biosamp.part.all[,c(paste(year[j],'.NEGEAR.AREA.NESPP4.N',sep = ""))] +
biosamp.part.all$NEGEAR.AREA.NESPP4.N
  biosamp.part.all$PORT.NEGEAR.AREA.NESPP4.N <-
biosamp.part.all[,c(paste(year[j],'.PORT.NEGEAR.AREA.NESPP4.N',sep = ""))] +
biosamp.part.all$PORT.NEGEAR.AREA.NESPP4.N
  }
 }  #End of second year loop
```

```
#Calculate total (across all years) length-landings matching proportions
 bioland.all.n <-
bioland.all[,c('SPPNM','SPPNM8','TOTAL.TRIP.N','TOTAL.TOTAL.N','TOTAL.MATCH.N','TOTAL.NOMATCH.
N','TOTAL.PARTMATCH.N')]
 bioland.all.n$TOTAL.MATCH.P <- bioland.all.n$TOTAL.MATCH.N/bioland.all.n$TOTAL.TOTAL.N
 bioland.all.n$TOTAL.NOMATCH.P <- bioland.all.n$TOTAL.NOMATCH.N/bioland.all.n$TOTAL.TOTAL.N
 bioland.all.n$TOTAL.PARTMATCH.P <-
bioland.all.n$TOTAL.PARTMATCH.N/bioland.all.n$TOTAL.TOTAL.N

#Calculate total (across all years) age-length matching proportions
 biosamp.all.n <-
biosamp.all[,c('SPPNM','SPPNM8','TOTAL.TOTAL.N','TOTAL.MATCH.N','TOTAL.NOMATCH.N','TOTAL.PAR
TMATCH.N')]
 biosamp.all.n$TOTAL.MATCH.P <- biosamp.all.n$TOTAL.MATCH.N/biosamp.all.n$TOTAL.TOTAL.N
 biosamp.all.n$TOTAL.NOMATCH.P <- biosamp.all.n$TOTAL.NOMATCH.N/biosamp.all.n$TOTAL.TOTAL.N
 biosamp.all.n$TOTAL.PARTMATCH.P <-
biosamp.all.n$TOTAL.PARTMATCH.N/biosamp.all.n$TOTAL.TOTAL.N

#Calculate total (across all years) length-landings partial match proportions
 partial.all.p <-
partial.all[,c('SPPNM','SPPNM8','PART.N','PORT.N','NEGEAR.N','AREA.N','NESPP4.N','PORT.NEGEAR.N','P
ORT.AREA.N','PORT.NESPP4.N','NEGEAR.AREA.N','NEGEAR.NESPP4.N','AREA.NESPP4.N','PORT.NEGEAR.A
REA.N','PORT.NEGEAR.NESPP4.N','PORT.AREA.NESPP4.N','NEGEAR.AREA.NESPP4.N','PORT.NEGEAR.ARE
A.NESPP4.N')]
 partial.all.p$TOTAL.N <-
rowSums(partial.all.p[,c('PORT.N','NEGEAR.N','AREA.N','NESPP4.N','PORT.NEGEAR.N','PORT.AREA.N','PO
RT.NESPP4.N','NEGEAR.AREA.N','NEGEAR.NESPP4.N','AREA.NESPP4.N','PORT.NEGEAR.AREA.N','PORT.NE
GEAR.NESPP4.N','PORT.AREA.NESPP4.N','NEGEAR.AREA.NESPP4.N','PORT.NEGEAR.AREA.NESPP4.N')])
 partial.all.p$PORT.P <- partial.all.p$PORT.N/partial.all.p$TOTAL.N
 partial.all.p$NEGEAR.P <- partial.all.p$NEGEAR.N/partial.all.p$TOTAL.N
 partial.all.p$AREA.P <- partial.all.p$AREA.N/partial.all.p$TOTAL.N
 partial.all.p$NESPP4.P <- partial.all.p$NESPP4.N/partial.all.p$TOTAL.N
 partial.all.p$PORT.NEGEAR.P <- partial.all.p$PORT.NEGEAR.N/partial.all.p$TOTAL.N
 partial.all.p$PORT.AREA.P <- partial.all.p$PORT.AREA.N/partial.all.p$TOTAL.N
 partial.all.p$PORT.NESPP4.P <- partial.all.p$PORT.NESPP4.N/partial.all.p$TOTAL.N
 partial.all.p$NEGEAR.AREA.P <- partial.all.p$NEGEAR.AREA.N/partial.all.p$TOTAL.N
 partial.all.p$NEGEAR.NESPP4.P <- partial.all.p$NEGEAR.NESPP4.N/partial.all.p$TOTAL.N
 partial.all.p$AREA.NESPP4.P <- partial.all.p$AREA.NESPP4.N/partial.all.p$TOTAL.N
 partial.all.p$PORT.NEGEAR.AREA.P <- partial.all.p$PORT.NEGEAR.AREA.N/partial.all.p$TOTAL.N
 partial.all.p$PORT.NEGEAR.NESPP4.P <- partial.all.p$PORT.NEGEAR.NESPP4.N/partial.all.p$TOTAL.N
 partial.all.p$PORT.AREA.NESPP4.P <- partial.all.p$PORT.AREA.NESPP4.N/partial.all.p$TOTAL.N
 partial.all.p$NEGEAR.AREA.NESPP4.P <- partial.all.p$NEGEAR.AREA.NESPP4.N/partial.all.p$TOTAL.N
 partial.all.p$PORT.NEGEAR.AREA.NESPP4.P <-
partial.all.p$PORT.NEGEAR.AREA.NESPP4.N/partial.all.p$TOTAL.N
 partial.all.p$TOTAL.P <-
rowSums(partial.all.p[,c('PORT.P','NEGEAR.P','AREA.P','NESPP4.P','PORT.NEGEAR.P','PORT.AREA.P','PORT
```

```
.NESPP4.P','NEGEAR.AREA.P','NEGEAR.NESPP4.P','AREA.NESPP4.P','PORT.NEGEAR.AREA.P','PORT.NEGEA
R.NESPP4.P','PORT.AREA.NESPP4.P','NEGEAR.AREA.NESPP4.P','PORT.NEGEAR.AREA.NESPP4.P')])

 #Filter out species with no partial matches
 partial.all.filter <- partial.all.p[!is.na(partial.all.p$TOTAL.P),]
 #Sort partial matches for output
 partial.all.sort <- partial.all.filter[order(partial.all.filter$SPPNM8,decreasing=T),]

 #Calculate total (across all years) age-length partial match proportions
 biosamp.part.all.p <-
biosamp.part.all[,c('SPPNM','SPPNM8','PORT.N','NEGEAR.N','AREA.N','NESPP4.N','PORT.NEGEAR.N','POR
T.AREA.N','PORT.NESPP4.N','NEGEAR.AREA.N','NEGEAR.NESPP4.N','AREA.NESPP4.N','PORT.NEGEAR.ARE
A.N','PORT.NEGEAR.NESPP4.N','PORT.AREA.NESPP4.N','NEGEAR.AREA.NESPP4.N','PORT.NEGEAR.AREA.
NESPP4.N')]
 biosamp.part.all.p$TOTAL.N <-
rowSums(biosamp.part.all.p[,c('PORT.N','NEGEAR.N','AREA.N','NESPP4.N','PORT.NEGEAR.N','PORT.AREA.
N','PORT.NESPP4.N','NEGEAR.AREA.N','NEGEAR.NESPP4.N','AREA.NESPP4.N','PORT.NEGEAR.AREA.N','PO
RT.NEGEAR.NESPP4.N','PORT.AREA.NESPP4.N','NEGEAR.AREA.NESPP4.N','PORT.NEGEAR.AREA.NESPP4.
N')])
 biosamp.part.all.p$PORT.P <- biosamp.part.all.p$PORT.N/biosamp.part.all.p$TOTAL.N
 biosamp.part.all.p$NEGEAR.P <- biosamp.part.all.p$NEGEAR.N/biosamp.part.all.p$TOTAL.N
 biosamp.part.all.p$AREA.P <- biosamp.part.all.p$AREA.N/biosamp.part.all.p$TOTAL.N
 biosamp.part.all.p$NESPP4.P <- biosamp.part.all.p$NESPP4.N/biosamp.part.all.p$TOTAL.N
 biosamp.part.all.p$PORT.NEGEAR.P <- biosamp.part.all.p$PORT.NEGEAR.N/biosamp.part.all.p$TOTAL.N
 biosamp.part.all.p$PORT.AREA.P <- biosamp.part.all.p$PORT.AREA.N/biosamp.part.all.p$TOTAL.N
 biosamp.part.all.p$PORT.NESPP4.P <- biosamp.part.all.p$PORT.NESPP4.N/biosamp.part.all.p$TOTAL.N
 biosamp.part.all.p$NEGEAR.AREA.P <- biosamp.part.all.p$NEGEAR.AREA.N/biosamp.part.all.p$TOTAL.N
 biosamp.part.all.p$NEGEAR.NESPP4.P <-
biosamp.part.all.p$NEGEAR.NESPP4.N/biosamp.part.all.p$TOTAL.N
 biosamp.part.all.p$AREA.NESPP4.P <- biosamp.part.all.p$AREA.NESPP4.N/biosamp.part.all.p$TOTAL.N
 biosamp.part.all.p$PORT.NEGEAR.AREA.P <-
biosamp.part.all.p$PORT.NEGEAR.AREA.N/biosamp.part.all.p$TOTAL.N
 biosamp.part.all.p$PORT.NEGEAR.NESPP4.P <-
biosamp.part.all.p$PORT.NEGEAR.NESPP4.N/biosamp.part.all.p$TOTAL.N
 biosamp.part.all.p$PORT.AREA.NESPP4.P <-
biosamp.part.all.p$PORT.AREA.NESPP4.N/biosamp.part.all.p$TOTAL.N
 biosamp.part.all.p$NEGEAR.AREA.NESPP4.P <-
biosamp.part.all.p$NEGEAR.AREA.NESPP4.N/biosamp.part.all.p$TOTAL.N
 biosamp.part.all.p$PORT.NEGEAR.AREA.NESPP4.P <-
biosamp.part.all.p$PORT.NEGEAR.AREA.NESPP4.N/biosamp.part.all.p$TOTAL.N
 biosamp.part.all.p$TOTAL.P <-
rowSums(biosamp.part.all.p[,c('PORT.P','NEGEAR.P','AREA.P','NESPP4.P','PORT.NEGEAR.P','PORT.AREA.P
','PORT.NESPP4.P','NEGEAR.AREA.P','NEGEAR.NESPP4.P','AREA.NESPP4.P','PORT.NEGEAR.AREA.P','PORT.
NEGEAR.NESPP4.P','PORT.AREA.NESPP4.P','NEGEAR.AREA.NESPP4.P','PORT.NEGEAR.AREA.NESPP4.P')])

 #Filter out species with no partial matches
 biosamp.part.all.filter <- biosamp.part.all.p[!is.na(biosamp.part.all.p$TOTAL.P),]
 #Sort partial matches for output
```

```
 biosamp.part.all.sort <- biosamp.part.all.filter[order(biosamp.part.all.filter$SPPNM8,decreasing=T),]

 #Write output to CSV files
 write.csv(biosamp.all.n, file =
paste(direct,"age_length_annual_summary_",year[1],"_",year[n.yr],".csv",sep=""))
 write.csv(bioland.all.n, file =
paste(direct,"length_land_annual_summary_",year[1],"_",year[n.yr],".csv",sep=""))
 write.csv(partial.all.sort, file =
paste(direct,"length_land_partial_summary_",year[1],"_",year[n.yr],".csv",sep=""))
 write.csv(biosamp.part.all.sort, file =
paste(direct,"age_length_partial_summary_",year[1],"_",year[n.yr],".csv",sep=""))

####################
 ###  Make Plots  ###
 ####################

#Stacked barplot of age-length matches
 biosamp.all.sort <- biosamp.all.n[order(biosamp.all.n$SPPNM8,decreasing=T),]
 counts.biosamp <-
rbind(biosamp.all.sort$TOTAL.MATCH.P,biosamp.all.sort$TOTAL.NOMATCH.P,biosamp.all.sort$TOTAL.P
ARTMATCH.P)
 png(paste(direct,'figure_1.png',sep=''),width=700,height=700)
 par(oma=c(1,1.7,1,2.5))

barplot(height=counts.biosamp,horiz=T,col=c('red','yellow','blue'),names.arg=biosamp.all.sort$SPPNM8,
las=2,axes=F,xlab='PROPORTION',cex.names=1)
 box(lty='solid')
 axis(side=1)

axis(side=4,at=seq(0.75,18.75,length.out=length(biosamp.all.sort$TOTAL.TOTAL.N)),labels=biosamp.all.s
ort$TOTAL.TOTAL.N,las=2,tick=F,cex.axis=1)
 mtext(text='NUMBER OF SAMPLES',side=4,line=3.3)
 par(fig=c(0,1,0,1),oma=c(0,0,3,0),mar=c(0,0,0,0),new=T)
 plot(0,0,type='n',bty='n',xaxt='n',yaxt='n')

legend('top',legend=c('MATCH','ORPHAN','PARTIAL'),fill=c('red','yellow','blue'),horiz=T,xpd=F,bty='n',cex
=1)
 dev.off()

#Stacked barplot of biosample-landings matches
 bioland.all.sort <- bioland.all.n[order(bioland.all.n$SPPNM8,decreasing=T),]
 counts.p <-
rbind(bioland.all.sort$TOTAL.MATCH.P,bioland.all.sort$TOTAL.NOMATCH.P,bioland.all.sort$TOTAL.PART
MATCH.P)
 png(paste(direct,'figure_2.png',sep=''),width=700,height=700)
 par(oma=c(1,1.7,1,2.5))
```

```
barplot(height=counts.p,horiz=T,col=c('red','yellow','blue'),names.arg=bioland.all.sort$SPPNM8,las=2,ax
es=F,xlab='PROPORTION',cex.names=1)
 box(lty='solid')
 axis(side=1)

axis(side=4,at=seq(0.75,35.5,length.out=length(bioland.all.sort$TOTAL.TOTAL.N)),labels=bioland.all.sort
$TOTAL.TOTAL.N,las=2,tick=F,cex.axis=1)
 mtext(text='NUMBER OF SAMPLES',side=4,line=3.3)
 par(fig=c(0,1,0,1),oma=c(0,0,3,0),mar=c(0,0,0,0),new=T)
 plot(0,0,type='n',bty='n',xaxt='n',yaxt='n')

legend('top',legend=c('MATCH','ORPHAN','PARTIAL'),fill=c('red','yellow','blue'),horiz=T,xpd=F,bty='n',cex
=1)
 dev.off()

#Stacked barplot of biosample-landings partial matches
 counts.partial <-
rbind(partial.all.sort$PORT.P,partial.all.sort$NEGEAR.P,partial.all.sort$AREA.P,partial.all.sort$NESPP4.P,
partial.all.sort$PORT.NEGEAR.P,partial.all.sort$PORT.AREA.P,partial.all.sort$PORT.NESPP4.P,partial.all.s
ort$NEGEAR.AREA.P,partial.all.sort$NEGEAR.NESPP4.P,partial.all.sort$AREA.NESPP4.P,partial.all.sort$P
ORT.NEGEAR.AREA.P,partial.all.sort$PORT.NEGEAR.NESPP4.P,partial.all.sort$PORT.AREA.NESPP4.P,parti
al.all.sort$NEGEAR.AREA.NESPP4.P,partial.all.sort$PORT.NEGEAR.AREA.NESPP4.P)
 partial.filter <- counts.partial[rowSums(counts.partial,na.rm = T)>0,]
 partial.names <-
c('PORT','NEGEAR','AREA','NESPP4','PORT.NEGEAR','PORT.AREA','PORT.NESPP4','NEGEAR.AREA','NEGEA
R.NESPP4','AREA.NESPP4','PORT.NEGEAR.AREA','PORT.NEGEAR.NESPP4','PORT.AREA.NESPP4','NEGEAR.
AREA.NESPP4','PORT.NEGEAR.AREA.NESPP4')
 names.filter <- partial.names[rowSums(counts.partial,na.rm = T)>0]

 png(paste(direct,'figure_3.png',sep=''),width=700,height=700)

 layout(rbind(1,2),heights=c(7,1))
 par(oma=c(0,2,0,3),mar=c(0,4,6.5,2))

barplot(height=partial.filter,horiz=T,names.arg=partial.all.sort$SPPNM8,las=2,axes=F,xlab='Proportion',c
ex.names=1,col=rainbow(nrow(partial.filter)))
 box(lty='solid')
 axis(side=1)

axis(side=4,at=seq(0.75,32.0,length.out=length(partial.all.sort$TOTAL.N)),labels=partial.all.sort$TOTAL.N
,las=2,tick=F,cex.axis=1)
 mtext(text='NUMBER OF SAMPLES',side=4,line=3.3)
 mtext(text='PROPORTION',side=1,line=3)
 par(fig=c(0,1,0,1),oma=c(0,0,0,0),mar=c(0,0,0.5,0),new=T)
 plot(0,0,type='n',bty='n',xaxt='n',yaxt='n')
```

```
legend('top',legend=names.filter,fill=rainbow(nrow(partial.filter)),horiz=F,xpd=T,bty='n',cex=1,ncol=3,x.intersp=1)
 dev.off()

 #Stacked barplot of age-length partial matches
 counts.biosamp.part <- rbind(biosamp.part.all.sort$PORT.P,biosamp.part.all.sort$NEGEAR.P,biosamp.part.all.sort$AREA.P,biosamp.part.all.sort$NESPP4.P,biosamp.part.all.sort$PORT.NEGEAR.P,biosamp.part.all.sort$PORT.AREA.P,biosamp.part.all.sort$PORT.NESPP4.P,biosamp.part.all.sort$NEGEAR.AREA.P,biosamp.part.all.sort$NEGEAR.NESPP4.P,biosamp.part.all.sort$AREA.NESPP4.P,biosamp.part.all.sort$PORT.NEGEAR.AREA.P,biosamp.part.all.sort$PORT.NEGEAR.NESPP4.P,biosamp.part.all.sort$PORT.AREA.NESPP4.P,biosamp.part.all.sort$NEGEAR.AREA.NESPP4.P,biosamp.part.all.sort$PORT.NEGEAR.AREA.NESPP4.P)
 biosamp.part.filter <- counts.biosamp.part[rowSums(counts.biosamp.part,na.rm = T)>0,]
 biosamp.part.names <- c('PORT','NEGEAR','AREA','NESPP4','PORT.NEGEAR','PORT.AREA','PORT.NESPP4','NEGEAR.AREA','NEGEAR.NESPP4','AREA.NESPP4','PORT.NEGEAR.AREA','PORT.NEGEAR.NESPP4','PORT.AREA.NESPP4','NEGEAR.AREA.NESPP4','PORT.NEGEAR.AREA.NESPP4')
 names.filter <- biosamp.part.names[rowSums(counts.biosamp.part,na.rm = T)>0]

 png(paste(direct,'figure_4.png',sep=''),width=700,height=700)

 layout(rbind(1,2),heights=c(7,1))
 par(oma=c(0,2,0,3),mar=c(0,4,6.5,2))

barplot(height=biosamp.part.filter,horiz=T,names.arg=biosamp.part.all.sort$SPPNM8,las=2,axes=F,xlab='Proportion',cex.names=1,col=c('red','orange','yellow','blue','purple'))
 box(lty='solid')
 axis(side=1)

axis(side=4,at=seq(0.75,14.0,length.out=length(biosamp.part.all.sort$TOTAL.N)),labels=biosamp.part.all.sort$TOTAL.N,las=2,tick=F,cex.axis=1)
 mtext(text='NUMBER OF SAMPLES',side=4,line=3.3)
 mtext(text='PROPORTION',side=1,line=3)
 par(fig=c(0,1,0,1),oma=c(0,0,0,0),mar=c(0,0,0.5,0),new=T)
 plot(0,0,type='n',bty='n',xaxt='n',yaxt='n')

legend('top',legend=names.filter,fill=c('red','orange','yellow','blue','purple'),horiz=F,xpd=T,bty='n',cex=1,ncol=3,x.intersp=1)
 dev.off()
```

APPENDIX B

Table B-1. Proportion of commercial length samples that could be matched to commercial trips (Match) by species for 2006. No. of Trips is the number of commercial trips from which length samples were collected. No. of Samples is the number of length samples collected. Orphan is the proportion of orphan length samples that remained orphans after using the reduced variable sets to match. PORT, NEGEAR, AREA, and NESPP4 are the proportion of partially matched length samples where the value of that variable differed between the length samples and commercial trips. Multiple variable names (e.g., PORT.NEGEAR) are the proportion of partially matched age samples where the values of those variables differed between the length samples and commercial trips.

Species	No. of Trips	No. of Samples	Match	Orphan	PORT	NEGEAR	AREA	NESPP4	PORT. NEGEAR	PORT. AREA	PORT. NESPP4	NEGEAR. AREA	NEGEAR. NESPP4	AREA. NESPP4	PORT. NEGEAR. AREA	PORT. NEGEAR. NESPP4	PORT. AREA. NESPP4	NEGEAR. AREA. NESPP4	PORT. NEGEAR. AREA. NESPP4
ANGLERFISH *Lophius americanus*	163	187	0.6096	0.1604	0.0588	0.0160	0.0909	0.0535	0.0000	0.0053	0.0000	0.0053	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
BLUEFISH *Pomatomus saltatrix*	50	60	0.1833	0.5167	0.0167	0.1167	0.0167	0.0500	0.0000	0.0000	0.0000	0.0000	0.0333	0.0000	0.0333	0.0000	0.0000	0.0167	0.0167
BUTTERFISH *Peprilus triacanthus*	46	50	0.2800	0.5600	0.0000	0.0200	0.0000	0.0800	0.0000	0.0200	0.0200	0.0000	0.0200	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
COD, ATLANTIC *Gadus morhua*	404	512	0.6992	0.1621	0.0391	0.0176	0.0332	0.0059	0.0000	0.0039	0.0000	0.0371	0.0000	0.0000	0.0020	0.0000	0.0000	0.0000	0.0000
CUSK *Brosme brosme*	46	47	0.6170	0.1489	0.0000	0.0213	0.0000	0.1277	0.0213	0.0000	0.0000	0.0426	0.0000	0.0213	0.0000	0.0000	0.0000	0.0000	0.0000
DOGFISH, SPINY *Squalus acanthias*	60	60	0.4833	0.2167	0.0000	0.0833	0.0500	0.1333	0.0000	0.0000	0.0167	0.0000	0.0167	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, AM. PLAICE *Hippoglossoides platessoides*	60	70	0.7286	0.0571	0.0429	0.0429	0.1000	0.0000	0.0000	0.0143	0.0000	0.0143	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, SAND-DAB *Scophthalmus aquosus*	19	19	0.2632	0.4211	0.0000	0.0000	0.0526	0.1579	0.0000	0.0000	0.0000	0.0526	0.0000	0.0526	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, SUMMER *Paralichthys dentatus*	161	223	0.6009	0.2018	0.0045	0.0224	0.0269	0.0987	0.0000	0.0000	0.0224	0.0135	0.0000	0.0045	0.0000	0.0000	0.0045	0.0000	0.0000
FLOUNDER, WINTER *Pseudopleuronectes americanus*	174	206	0.5583	0.1796	0.0485	0.0097	0.0777	0.0485	0.0194	0.0049	0.0049	0.0340	0.0000	0.0049	0.0097	0.0000	0.0000	0.0000	0.0000
FLOUNDER, WITCH *Glyptocephalus cynoglossus*	126	148	0.7365	0.1149	0.0135	0.0203	0.0743	0.0000	0.0000	0.0000	0.0000	0.0405	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, YELLOWTAIL *Limanda ferruginea*	138	188	0.5585	0.1702	0.0160	0.0266	0.1223	0.0213	0.0053	0.0053	0.0000	0.0532	0.0000	0.0000	0.0213	0.0000	0.0000	0.0000	0.0000
HADDOCK *Melanogrammus aeglefinus*	170	230	0.7391	0.1043	0.0217	0.0261	0.0435	0.0130	0.0043	0.0000	0.0000	0.0435	0.0000	0.0043	0.0000	0.0000	0.0000	0.0000	0.0000

Table B-1, continued. Proportion of commercial length samples that could be matched to commercial trips (Match) by species for 2006. No. of Trips is the number of commercial trips from which length samples were collected. No. of Samples is the number of length samples collected. Orphan is the proportion of orphan length samples that remained orphans after using the reduced variable sets to match. PORT, NEGEAR, AREA, and NESPP4 are the proportion of partially matched length samples where the value of that variable differed between the length samples and commercial trips. Multiple variable names (e.g., PORT.NEGEAR) are the proportion of partially matched age samples where the values of those variables differed between the length samples and commercial trips.

Species	No. of Trips	No. of Samples	Match	Orphan	PORT	NEGEAR	AREA	NESPP4	PORT. NEGEAR	PORT. AREA	PORT. NESPP4	NEGEAR. AREA	NEGEAR. NESPP4	AREA. NESPP4	PORT. NEGEAR. AREA	PORT. NEGEAR. NESPP4	PORT. AREA. NESPP4	NEGEAR. AREA. NESPP4	PORT. NEGEAR. AREA. NESPP4
HAGFISH *Myxine glutinosa*	20	20	0.4000	0.6000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, OFFSHORE *Merluccius albidus*	1	1	0.0000	1.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, RED *Urophycis chuss*	28	29	0.4138	0.5862	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, SILVER *Merluccius bilinearis*	122	163	0.2331	0.5583	0.0000	0.0000	0.0123	0.1718	0.0000	0.0000	0.0061	0.0061	0.0000	0.0123	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, WHITE *Urophycis tenuis*	77	93	0.7419	0.0430	0.0000	0.0323	0.1075	0.0323	0.0000	0.0108	0.0000	0.0215	0.0000	0.0108	0.0000	0.0000	0.0000	0.0000	0.0000
HALIBUT, ATLANTIC *Hippoglossus hippoglossus*	91	91	0.0769	0.1429	0.0110	0.0000	0.0110	0.6264	0.0000	0.0000	0.0440	0.0110	0.0220	0.0549	0.0000	0.0000	0.0000	0.0000	0.0000
HERRING, ATLANTIC *Clupea harengus*	4	5	0.0000	1.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MACKEREL, ATLANTIC *Scomber scombrus*	45	54	0.1481	0.3148	0.0000	0.1481	0.0185	0.0741	0.0000	0.0000	0.0000	0.0741	0.1481	0.0185	0.0185	0.0185	0.0000	0.0185	0.0000
POLLOCK *Pollachius virens*	82	98	0.7245	0.1429	0.0408	0.0000	0.0306	0.0306	0.0102	0.0000	0.0000	0.0102	0.0000	0.0102	0.0000	0.0000	0.0000	0.0000	0.0000
POUT, OCEAN *Zoarces americanus*	4	4	0.0000	1.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
REDFISH *Sebastes fasciatus*	15	15	0.4667	0.3333	0.0000	0.0000	0.1333	0.0000	0.0667	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SCUP *Stenotomus chrysops*	114	154	0.3701	0.3701	0.0649	0.0195	0.0195	0.0974	0.0000	0.0065	0.0195	0.0000	0.0000	0.0065	0.0130	0.0065	0.0000	0.0000	0.0065
SEA BASS, BLACK *Centropristis striata*	72	98	0.3367	0.4388	0.0408	0.0000	0.0102	0.0918	0.0000	0.0000	0.0000	0.0204	0.0000	0.0102	0.0102	0.0000	0.0000	0.0102	0.0306
TILEFISH, GOLDEN *Lopholatilus chamaeleonticeps*	44	83	0.3373	0.5181	0.0482	0.0000	0.0120	0.0482	0.0000	0.0000	0.0241	0.0000	0.0000	0.0120	0.0000	0.0000	0.0000	0.0000	0.0000
WOLFFISH, ATLANTIC *Anarhichas lupus*	151	151	0.7881	0.0596	0.0331	0.0066	0.0927	0.0000	0.0000	0.0000	0.0000	0.0199	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

Table B-2. Proportion of commercial length samples that could be matched to commercial trips (Match) by species for 2007. No. of Trips is the number of commercial trips from which length samples were collected. No. of Samples is the number of length samples collected. Orphan is the proportion of orphan length samples that remained orphans after using the reduced variable sets to match. PORT, NEGEAR, AREA, and NESPP4 are the proportion of partially matched length samples where the value of that variable differed between the length samples and commercial trips. Multiple variable names (e.g., PORT.NEGEAR) are the proportion of partially matched age samples where the values of those variables differed between the length samples and commercial trips.

Species	No. of Trips	No. of Samples	Match	Orphan	PORT	NEGEAR	AREA	NESPP4	PORT. NEGEAR	PORT. AREA	PORT. NESPP4	NEGEAR. AREA	NEGEAR. NESPP4	AREA. NESPP4	PORT. NEGEAR. AREA	PORT. NEGEAR. NESPP4	PORT. AREA. NESPP4	NEGEAR. AREA. NESPP4	PORT. NEGEAR. AREA. NESPP4
ANGLERFISH *Lophius americanus*	109	126	0.6111	0.2143	0.0397	0.0238	0.0635	0.0317	0.0000	0.0079	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0079	0.0000
BLUEFISH *Pomatomus saltatrix*	71	83	0.1446	0.6988	0.0120	0.0241	0.0000	0.0723	0.0000	0.0000	0.0241	0.0241	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
BUTTERFISH *Peprilus triacanthus*	61	63	0.3968	0.4444	0.0000	0.0000	0.0000	0.1270	0.0000	0.0000	0.0159	0.0000	0.0000	0.0159	0.0000	0.0000	0.0000	0.0000	0.0000
COD, ATLANTIC *Gadus morhua*	455	560	0.6982	0.1500	0.0339	0.0304	0.0589	0.0036	0.0054	0.0071	0.0018	0.0036	0.0000	0.0000	0.0071	0.0000	0.0000	0.0000	0.0000
CUSK *Brosme brosme*	58	58	0.6379	0.1897	0.0000	0.0690	0.0172	0.0862	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
DOGFISH, SPINY *Squalus acanthias*	35	40	0.5250	0.3500	0.0000	0.1000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0250	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, AM. PLAICE *Hippoglossoides platessoides*	62	75	0.7600	0.0400	0.0133	0.0267	0.1467	0.0133	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, SAND-DAB *Scophthalmus aquosus*	42	42	0.6905	0.1190	0.0000	0.0000	0.1190	0.0714	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, SUMMER *Paralichthys dentatus*	252	349	0.5358	0.3410	0.0057	0.0315	0.0372	0.0344	0.0000	0.0000	0.0029	0.0000	0.0000	0.0029	0.0000	0.0000	0.0086	0.0000	0.0000
FLOUNDER, WINTER *Pseudopleuronectes americanus*	156	191	0.6335	0.1885	0.0209	0.0000	0.0838	0.0471	0.0000	0.0052	0.0052	0.0105	0.0000	0.0000	0.0052	0.0000	0.0000	0.0000	0.0000
FLOUNDER, WITCH *Glyptocephalus cynoglossus*	141	166	0.7952	0.1024	0.0361	0.0060	0.0602	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, YELLOWTAIL *Limanda ferruginea*	166	228	0.6623	0.1140	0.0263	0.0000	0.0921	0.0877	0.0000	0.0000	0.0000	0.0000	0.0000	0.0044	0.0132	0.0000	0.0000	0.0000	0.0000
HADDOCK *Melanogrammus aeglefinus*	195	251	0.6375	0.1633	0.0398	0.0359	0.1116	0.0080	0.0040	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

Table B-2, continued. Proportion of commercial length samples that could be matched to commercial trips (Match) by species for 2007. No. of Trips is the number of commercial trips from which length samples were collected. No. of Samples is the number of length samples collected. Orphan is the proportion of orphan length samples that remained orphans after using the reduced variable sets to match. PORT, NEGEAR, AREA, and NESPP4 are the proportion of partially matched length samples where the value of that variable differed between the length samples and commercial trips. Multiple variable names (e.g., PORT.NEGEAR) are the proportion of partially matched age samples where the values of those variables differed between the length samples and commercial trips.

Species	No. of Trips	No. of Samples	Match	Orphan	PORT	NEGEAR	AREA	NESPP4	PORT. NEGEAR	PORT. AREA	PORT. NESPP4	NEGEAR. AREA	NEGEAR. NESPP4	AREA. NESPP4	PORT. NEGEAR. AREA	PORT. NEGEAR. NESPP4	PORT. AREA. NESPP4	NEGEAR. AREA. NESPP4	PORT. NEGEAR. AREA. NESPP4
HAGFISH *Myxine glutinosa*	19	19	0.5789	0.4211	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, RED *Urophycis chuss*	53	54	0.5185	0.4630	0.0185	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, SILVER *Merluccius bilinearis*	142	195	0.2718	0.4769	0.0000	0.0000	0.0103	0.2205	0.0000	0.0000	0.0103	0.0000	0.0000	0.0103	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, WHITE *Urophycis tenuis*	83	99	0.6566	0.1515	0.0202	0.0404	0.0202	0.0808	0.0303	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HALIBUT, ATLANTIC *Hippoglossus hippoglossus*	78	78	0.1538	0.3462	0.0000	0.0000	0.0000	0.4615	0.0000	0.0000	0.0000	0.0000	0.0128	0.0256	0.0000	0.0000	0.0000	0.0000	0.0000
HERRING, ATLANTIC *Clupea harengus*	5	5	0.0000	1.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MACKEREL, ATLANTIC *Scomber scombrus*	62	95	0.0632	0.3579	0.0000	0.1579	0.0105	0.0526	0.0000	0.0000	0.0105	0.1684	0.0737	0.0316	0.0000	0.0000	0.0105	0.0632	0.0000
POLLOCK *Pollachius virens*	92	112	0.6339	0.1607	0.0089	0.0446	0.0446	0.0536	0.0357	0.0000	0.0000	0.0000	0.0000	0.0179	0.0000	0.0000	0.0000	0.0000	0.0000
POUT, OCEAN *Zoarces americanus*	3	3	0.3333	0.6667	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
REDFISH *Sebastes fasciatus*	16	16	0.6875	0.1875	0.0625	0.0625	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SCUP *Stenotomus chrysops*	137	203	0.2562	0.6158	0.0049	0.0000	0.0197	0.0788	0.0000	0.0000	0.0049	0.0000	0.0000	0.0197	0.0000	0.0000	0.0000	0.0000	0.0000
SEA BASS, BLACK *Centropristis striata*	84	126	0.3333	0.5873	0.0159	0.0238	0.0159	0.0238	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SHAD, AMERICAN *Alosa sapidissima*	3	3	0.0000	0.6667	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.3333
TILEFISH, GOLDEN *Lopholatilus chamaeleonticeps*	50	98	0.3367	0.5408	0.0408	0.0000	0.0000	0.0714	0.0000	0.0000	0.0102	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
WOLFFISH, ATLANTIC *Anarhichas lupus*	145	145	0.6690	0.1310	0.0552	0.0414	0.0828	0.0000	0.0000	0.0069	0.0000	0.0069	0.0000	0.0000	0.0069	0.0000	0.0000	0.0000	0.0000

Table B-3. Proportion of commercial length samples that could be matched to commercial trips (Match) by species for 2008. No. of Trips is the number of commercial trips from which length samples were collected. No. of Samples is the number of length samples collected. Orphan is the proportion of orphan length samples that remained orphans after using the reduced variable sets to match. PORT, NEGEAR, AREA, and NESPP4 are the proportion of partially matched length samples where the value of that variable differed between the length samples and commercial trips. Multiple variable names (e.g., PORT.NEGEAR) are the proportion of partially matched age samples where the values of those variables differed between the length samples and commercial trips.

Species	No. of Trips	No. of Samples	Match	Orphan	PORT	NEGEAR	AREA	NESPP4	PORT. NEGEAR	PORT. AREA	PORT. NESPP4	NEGEAR. AREA	NEGEAR. NESPP4	AREA. NESPP4	PORT. NEGEAR. AREA	PORT. NEGEAR. NESPP4	PORT. AREA. NESPP4	NEGEAR. AREA. NESPP4	PORT. NEGEAR. AREA. NESPP4
ANGLERFISH *Lophius americanus*	95	114	0.4386	0.4649	0.0526	0.0000	0.0175	0.0263	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
BLUEFISH *Pomatomus saltatrix*	121	135	0.2519	0.4148	0.0000	0.0222	0.0222	0.2593	0.0000	0.0000	0.0148	0.0000	0.0000	0.0148	0.0000	0.0000	0.0000	0.0000	0.0000
BUTTERFISH *Peprilus triacanthus*	40	42	0.1905	0.6667	0.0000	0.0000	0.0000	0.1190	0.0000	0.0000	0.0000	0.0000	0.0238	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
COD, ATLANTIC *Gadus morhua*	455	564	0.4947	0.4060	0.0355	0.0266	0.0195	0.0053	0.0018	0.0035	0.0000	0.0018	0.0000	0.0018	0.0035	0.0000	0.0000	0.0000	0.0000
CUSK *Brosme brosme*	44	45	0.2000	0.5333	0.0000	0.0444	0.0000	0.1333	0.0000	0.0000	0.0000	0.0000	0.0667	0.0222	0.0000	0.0000	0.0000	0.0000	0.0000
DOGFISH, SPINY *Squalus acanthias*	45	45	0.5333	0.2667	0.0444	0.0444	0.0667	0.0000	0.0000	0.0000	0.0000	0.0222	0.0000	0.0000	0.0222	0.0000	0.0000	0.0000	0.0000
FLOUNDER, AM. PLAICE *Hippoglossoides platessoides*	78	99	0.3535	0.6162	0.0000	0.0000	0.0202	0.0101	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, SANDDAB *Scophthalmus aquosus*	33	33	0.3333	0.5758	0.0000	0.0000	0.0000	0.0606	0.0000	0.0000	0.0000	0.0303	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, SUMMER *Paralichthys dentatus*	190	249	0.4498	0.4659	0.0080	0.0281	0.0120	0.0241	0.0000	0.0000	0.0040	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0080	0.0000
FLOUNDER, WINTER *Pseudopleuronectes americanus*	146	191	0.3717	0.5131	0.0052	0.0000	0.0262	0.0419	0.0000	0.0000	0.0209	0.0105	0.0000	0.0052	0.0000	0.0000	0.0000	0.0000	0.0052
FLOUNDER, WITCH *Glyptocephalus cynoglossus*	126	154	0.4935	0.4416	0.0000	0.0000	0.0455	0.0065	0.0000	0.0000	0.0065	0.0000	0.0000	0.0000	0.0065	0.0000	0.0000	0.0000	0.0000
FLOUNDER, YELLOWTAIL *Limanda ferruginea*	151	212	0.2689	0.5896	0.0094	0.0047	0.0236	0.0849	0.0000	0.0000	0.0047	0.0047	0.0000	0.0094	0.0000	0.0000	0.0000	0.0000	0.0000
HADDOCK *Melanogrammus aeglefinus*	173	226	0.4513	0.4735	0.0177	0.0177	0.0310	0.0088	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

Table B-3, continued. Proportion of commercial length samples that could be matched to commercial trips (Match) by species for 2008. No. of Trips is the number of commercial trips from which length samples were collected. No. of Samples is the number of length samples collected. Orphan is the proportion of orphan length samples that remained orphans after using the reduced variable sets to match. PORT, NEGEAR, AREA, and NESPP4 are the proportion of partially matched length samples where the value of that variable differed between the length samples and commercial trips. Multiple variable names (e.g., PORT.NEGEAR) are the proportion of partially matched age samples where the values of those variables differed between the length samples and commercial trips.

Species	No. of Trips	No. of Samples	Match	Orphan	PORT	NEGEAR	AREA	NESPP4	PORT. NEGEAR	PORT. AREA	PORT. NESPP4	NEGEAR. AREA	NEGEAR. NESPP4	AREA. NESPP4	PORT. NEGEAR. AREA	PORT. NEGEAR. NESPP4	PORT. AREA. NESPP4	NEGEAR. AREA. NESPP4	PORT. NEGEAR. AREA. NESPP4
HAGFISH *Myxine glutinosa*	17	18	0.5000	0.3333	0.0000	0.0000	0.0556	0.0000	0.0000	0.0000	0.0000	0.1111	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, RED *Urophycis chuss*	50	50	0.5800	0.3800	0.0000	0.0200	0.0000	0.0000	0.0000	0.0000	0.0000	0.0200	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, SILVER *Merluccius bilinearis*	127	155	0.2968	0.4129	0.0129	0.0000	0.0129	0.2387	0.0000	0.0000	0.0000	0.0065	0.0000	0.0065	0.0000	0.0000	0.0000	0.0129	0.0000
HAKE, WHITE *Urophycis tenuis*	70	93	0.3226	0.6237	0.0000	0.0000	0.0000	0.0430	0.0000	0.0000	0.0000	0.0000	0.0000	0.0108	0.0000	0.0000	0.0000	0.0000	0.0000
HALIBUT, ATLANTIC *Hippoglossus hippoglossus*	78	78	0.1667	0.6923	0.0128	0.0000	0.0000	0.1026	0.0000	0.0000	0.0256	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HERRING, ATLANTIC *Clupea harengus*	4	4	0.0000	1.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MACKEREL, ATLANTIC *Scomber scombrus*	72	118	0.0847	0.2119	0.0085	0.4661	0.0085	0.0932	0.0000	0.0000	0.0000	0.0339	0.0339	0.0000	0.0000	0.0000	0.0000	0.0593	0.0000
POLLOCK *Pollachius virens*	75	88	0.4773	0.4205	0.0341	0.0341	0.0114	0.0114	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0114	0.0000
POUT, OCEAN *Zoarces americanus*	5	5	0.0000	1.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
REDFISH *Sebastes fasciatus*	17	17	0.5294	0.2941	0.0000	0.0000	0.0588	0.1176	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SCUP *Stenotomus chrysops*	114	155	0.3742	0.5419	0.0129	0.0129	0.0194	0.0258	0.0000	0.0000	0.0000	0.0065	0.0000	0.0065	0.0000	0.0000	0.0000	0.0000	0.0000
SEA BASS, BLACK *Centropristis striata*	90	115	0.3739	0.4435	0.0522	0.0174	0.0174	0.0435	0.0000	0.0000	0.0000	0.0522	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
TILEFISH, GOLDEN *Lopholatilus chamaeleonticeps*	49	89	0.2584	0.6404	0.0449	0.0000	0.0000	0.0337	0.0000	0.0112	0.0000	0.0112	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
WOLFFISH, ATLANTIC *Anarhichas lupus*	67	67	0.4328	0.5075	0.0299	0.0149	0.0000	0.0000	0.0000	0.0149	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

Table B-4. Proportion of commercial length samples that could be matched to commercial trips (Match) by species for 2009. No. of Trips is the number of commercial trips from which length samples were collected. No. of Samples is the number of length samples collected. Orphan is the proportion of orphan length samples that remained orphans after using the reduced variable sets to match. PORT, NEGEAR, AREA, and NESPP4 are the proportion of partially matched length samples where the value of that variable differed between the length samples and commercial trips. Multiple variable names (e.g., PORT.NEGEAR) are the proportion of partially matched age samples where the values of those variables differed between the length samples and commercial trips.

Species	No. of Trips	No. of Samples	Match	Orphan	PORT	NEGEAR	AREA	NESPP4	PORT. NEGEAR	PORT. AREA	PORT. NESPP4	NEGEAR. AREA	NEGEAR. NESPP4	AREA. NESPP4	PORT. NEGEAR. AREA	PORT. NEGEAR. NESPP4	PORT. AREA. NESPP4	NEGEAR. AREA. NESPP4	PORT. NEGEAR. AREA. NESPP4
ANGLERFISH *Lophius americanus*	89	109	0.3761	0.4954	0.0459	0.0183	0.0000	0.0275	0.0000	0.0000	0.0092	0.0183	0.0000	0.0000	0.0000	0.0000	0.0000	0.0092	0.0000
BLUEFISH *Pomatomus saltatrix*	87	101	0.2871	0.3366	0.0000	0.0891	0.0099	0.2772	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
BUTTERFISH *Peprilus triacanthus*	25	25	0.2800	0.3600	0.0000	0.0000	0.0000	0.3600	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
COD, ATLANTIC *Gadus morhua*	595	717	0.5286	0.3236	0.0795	0.0460	0.0098	0.0014	0.0042	0.0028	0.0028	0.0000	0.0014	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CUSK *Brosme brosme*	156	160	0.2375	0.5438	0.0750	0.0500	0.0125	0.0813	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
DOGFISH, SPINY *Squalus acanthias*	62	62	0.7581	0.1290	0.0323	0.0323	0.0000	0.0000	0.0161	0.0161	0.0000	0.0161	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, AM. PLAICE *Hippoglossoides platessoides*	85	107	0.2523	0.6729	0.0467	0.0000	0.0280	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, SANDDAB *Scophthalmus aquosus*	26	26	0.2308	0.3846	0.0000	0.0000	0.0000	0.3462	0.0000	0.0000	0.0385	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, SUMMER *Paralichthys dentatus*	188	251	0.5737	0.2869	0.0000	0.0518	0.0319	0.0518	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0040	0.0000	0.0000
FLOUNDER, WINTER *Pseudopleuronectes americanus*	141	177	0.2429	0.6158	0.0056	0.0056	0.0056	0.0678	0.0169	0.0000	0.0113	0.0056	0.0000	0.0000	0.0226	0.0000	0.0000	0.0000	0.0000
FLOUNDER, WITCH *Glyptocephalus cynoglossus*	103	130	0.3769	0.5769	0.0308	0.0000	0.0077	0.0000	0.0000	0.0000	0.0000	0.0000	0.0077	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, YELLOWTAIL *Limanda ferruginea*	138	200	0.2200	0.7250	0.0000	0.0050	0.0150	0.0300	0.0050	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HADDOCK *Melanogrammus aeglefinus*	164	219	0.3333	0.5890	0.0320	0.0000	0.0183	0.0091	0.0046	0.0046	0.0000	0.0091	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

Table B-4, continued. Proportion of commercial length samples that could be matched to commercial trips (Match) by species for 2009. No. of Trips is the number of commercial trips from which length samples were collected. No. of Samples is the number of length samples collected. Orphan is the proportion of orphan length samples that remained orphans after using the reduced variable sets to match. PORT, NEGEAR, AREA, and NESPP4 are the proportion of partially matched length samples where the value of that variable differed between the length samples and commercial trips. Multiple variable names (e.g., PORT.NEGEAR) are the proportion of partially matched age samples where the values of those variables differed between the length samples and commercial trips.

Species	No. of Trips	No. of Samples	Match	Orphan	PORT	NEGEAR	AREA	NESPP4	PORT. NEGEAR	PORT. AREA	PORT. NESPP4	NEGEAR. AREA	NEGEAR. NESPP4	AREA. NESPP4	PORT. NEGEAR. AREA	PORT. NEGEAR. NESPP4	PORT. AREA. NESPP4	NEGEAR. AREA. NESPP4	PORT. NEGEAR. AREA. NESPP4
HAGFISH *Myxine glutinosa*	16	16	0.6875	0.1875	0.0000	0.1250	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, RED *Urophycis chuss*	27	27	0.4815	0.5185	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, SILVER *Merluccius bilinearis*	102	130	0.3615	0.3538	0.0000	0.0000	0.0000	0.2692	0.0000	0.0000	0.0154	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, WHITE *Urophycis tenuis*	66	86	0.3023	0.6163	0.0349	0.0116	0.0233	0.0000	0.0000	0.0000	0.0000	0.0116	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HALIBUT, ATLANTIC *Hippoglossus hippoglossus*	46	46	0.2609	0.2826	0.0000	0.0000	0.0217	0.3478	0.0000	0.0000	0.0217	0.0000	0.0217	0.0435	0.0000	0.0000	0.0000	0.0000	0.0000
HERRING, ATLANTIC *Clupea harengus*	3	3	0.0000	1.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MACKEREL, ATLANTIC *Scomber scombrus*	46	50	0.2000	0.1400	0.0000	0.0800	0.0000	0.3400	0.0000	0.0000	0.0200	0.0600	0.0600	0.0200	0.0000	0.0000	0.0000	0.0800	0.0000
POLLOCK *Pollachius virens*	90	103	0.3786	0.4466	0.0874	0.0291	0.0388	0.0097	0.0000	0.0000	0.0000	0.0000	0.0000	0.0097	0.0000	0.0000	0.0000	0.0000	0.0000
POUT, OCEAN *Zoarces americanus*	3	3	0.0000	1.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
REDFISH *Sebastes fasciatus*	18	20	0.5500	0.4000	0.0000	0.0000	0.0500	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SCUP *Stenotomus chrysops*	89	112	0.4375	0.4196	0.0446	0.0000	0.0089	0.0714	0.0000	0.0000	0.0179	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SEA BASS, BLACK *Centropristis striata*	60	85	0.3529	0.4588	0.0118	0.0588	0.0706	0.0118	0.0000	0.0000	0.0000	0.0000	0.0000	0.0235	0.0118	0.0000	0.0000	0.0000	0.0000
TILEFISH, GOLDEN *Lopholatilus chamaeleonticeps*	48	85	0.2588	0.7412	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
WOLFFISH, ATLANTIC *Anarhichas lupus*	79	80	0.4125	0.4125	0.1125	0.0375	0.0000	0.0000	0.0125	0.0000	0.0000	0.0125	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

Table B-5 Proportion of commercial length samples that could be matched to commercial trips (Match) by species for 2010. No. of Trips is the number of commercial trips from which length samples were collected. No. of Samples is the number of length samples collected. Orphan is the proportion of orphan length samples that remained orphans after using the reduced variable sets to match. PORT, NEGEAR, AREA, and NESPP4 are the proportion of partially matched length samples where the value of that variable differed between the length samples and commercial trips. Multiple variable names (e.g., PORT.NEGEAR) are the proportion of partially matched age samples where the values of those variables differed between the length samples and commercial trips.

Species	No. of Trips	No. of Samples	Match	Orphan	PORT	NEGEAR	AREA	NESPP4	PORT. NEGEAR	PORT. AREA	PORT. NESPP4	NEGEAR. AREA	NEGEAR. NESPP4	AREA. NESPP4	PORT. NEGEAR. AREA	PORT. NEGEAR. NESPP4	PORT. AREA. NESPP4	NEGEAR. AREA. NESPP4	PORT. NEGEAR. AREA. NESPP4
ANGLERFISH *Lophius americanus*	83	98	0.5102	0.3367	0.0306	0.0306	0.0000	0.0714	0.0000	0.0000	0.0000	0.0000	0.0204	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
BLUEFISH *Pomatomus saltatrix*	80	91	0.4505	0.3626	0.0000	0.0440	0.0000	0.1319	0.0000	0.0000	0.0000	0.0000	0.0000	0.0110	0.0000	0.0000	0.0000	0.0000	0.0000
BUTTERFISH *Peprilus triacanthus*	32	32	0.3125	0.4375	0.0000	0.0000	0.0625	0.1875	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
COD, ATLANTIC *Gadus morhua*	467	626	0.5224	0.4073	0.0383	0.0256	0.0000	0.0016	0.0000	0.0000	0.0000	0.0048	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CUSK *Brosme brosme*	68	68	0.3676	0.4412	0.0294	0.0882	0.0294	0.0147	0.0000	0.0000	0.0000	0.0000	0.0147	0.0000	0.0000	0.0000	0.0000	0.0147	0.0000
DOGFISH, SPINY *Squalus acanthias*	68	68	0.7059	0.1618	0.0735	0.0294	0.0294	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, AM. PLAICE *Hippoglossoides platessoides*	76	103	0.2621	0.6505	0.0194	0.0388	0.0000	0.0097	0.0000	0.0000	0.0097	0.0097	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, SANDDAB *Scophthalmus aquosus*	21	21	0.3333	0.2381	0.0000	0.0000	0.0000	0.3810	0.0000	0.0476	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, SUMMER *Paralichthys dentatus*	132	184	0.5652	0.3098	0.0000	0.0326	0.0109	0.0652	0.0000	0.0000	0.0000	0.0109	0.0000	0.0054	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, WINTER *Pseudopleuronectes americanus*	168	215	0.1860	0.6279	0.0093	0.0279	0.0047	0.0744	0.0000	0.0047	0.0279	0.0140	0.0140	0.0000	0.0000	0.0047	0.0047	0.0000	0.0000
FLOUNDER, WITCH *Glyptocephalus cynoglossus*	120	148	0.3243	0.6284	0.0203	0.0068	0.0000	0.0135	0.0000	0.0000	0.0068	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, YELLOWTAIL *Limanda ferruginea*	144	212	0.1887	0.7311	0.0000	0.0189	0.0094	0.0377	0.0094	0.0000	0.0000	0.0000	0.0000	0.0000	0.0047	0.0000	0.0000	0.0000	0.0000
HADDOCK *Melanogrammus aeglefinus*	199	291	0.2921	0.6357	0.0000	0.0481	0.0000	0.0000	0.0000	0.0000	0.0000	0.0241	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

Table B-5, continued. Proportion of commercial length samples that could be matched to commercial trips (Match) by species for 2010. No. of Trips is the number of commercial trips from which length samples were collected. No. of Samples is the number of length samples collected. Orphan is the proportion of orphan length samples that remained orphans after using the reduced variable sets to match. PORT, NEGEAR, AREA, and NESPP4 are the proportion of partially matched length samples where the value of that variable differed between the length samples and commercial trips. Multiple variable names (e.g., PORT.NEGEAR) are the proportion of partially matched age samples where the values of those variables differed between the length samples and commercial trips.

Species	No. of Trips	No. of Samples	Match	Orphan	PORT	NEGEAR	AREA	NESPP4	PORT. NEGEAR	PORT. AREA	PORT. NESPP4	NEGEAR. AREA	NEGEAR. NESPP4	AREA. NESPP4	PORT. NEGEAR. AREA	PORT. NEGEAR. NESPP4	PORT. AREA. NESPP4	NEGEAR. AREA. NESPP4	PORT. NEGEAR. AREA. NESPP4
HAGFISH *Myxine glutinosa*	20	20	0.5500	0.1500	0.0000	0.2000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, OFFSHORE *Merluccius albidus*	2	4	0.0000	1.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, RED *Urophycis chuss*	29	30	0.4667	0.4667	0.0000	0.0000	0.0333	0.0000	0.0000	0.0333	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, SILVER *Merluccius bilinearis*	105	144	0.3264	0.5000	0.0000	0.0000	0.0000	0.1667	0.0000	0.0000	0.0000	0.0000	0.0000	0.0069	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, WHITE *Urophycis tenuis*	75	120	0.4333	0.4667	0.0250	0.0583	0.0083	0.0083	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HALIBUT, ATLANTIC *Hippoglossus hippoglossus*	45	45	0.0444	0.4667	0.0000	0.0444	0.0000	0.3778	0.0000	0.0000	0.0222	0.0000	0.0444	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HERRING, ATLANTIC *Clupea harengus*	2	2	1.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MACKEREL, ATLANTIC *Scomber scombrus*	26	30	0.0333	0.4667	0.0000	0.0667	0.0000	0.2000	0.0000	0.0000	0.0000	0.0333	0.1333	0.0333	0.0000	0.0000	0.0000	0.0333	0.0000
POLLOCK *Pollachius virens*	109	138	0.3623	0.5000	0.1014	0.0072	0.0290	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SCUP *Stenotomus chrysops*	80	105	0.4952	0.3810	0.0000	0.0000	0.0381	0.0762	0.0000	0.0000	0.0000	0.0000	0.0000	0.0095	0.0000	0.0000	0.0000	0.0000	0.0000
SEA BASS, BLACK *Centropristis striata*	42	57	0.6842	0.1404	0.0175	0.0702	0.0000	0.0702	0.0000	0.0000	0.0175	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
TILEFISH, GOLDEN *Lopholatilus chamaeleonticeps*	58	143	0.3287	0.6154	0.0000	0.0000	0.0070	0.0490	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
WOLFFISH, ATLANTIC *Anarhichas lupus*	22	22	0.6818	0.2273	0.0000	0.0909	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

Table B-6. Proportion of commercial length samples that could be matched to commercial trips (Match) by species for 2011. No. of Trips is the number of commercial trips from which length samples were collected. No. of Samples is the number of length samples collected. Orphan is the proportion of orphan length samples that remained orphans after using the reduced variable sets to match. PORT, NEGEAR, AREA, and NESPP4 are the proportion of partially matched length samples where the value of that variable differed between the length samples and commercial trips. Multiple variable names (e.g., PORT.NEGEAR) are the proportion of partially matched age samples where the values of those variables differed between the length samples and commercial trips.

Species	No. of Trips	No. of Samples	Match	Orphan	PORT	NEGEAR	AREA	NESPP4	PORT. NEGEAR	PORT. AREA	PORT. NESPP4	NEGEAR. AREA	NEGEAR. NESPP4	AREA. NESPP4	PORT. NEGEAR. AREA	PORT. NEGEAR. NESPP4	PORT. AREA. NESPP4	NEGEAR. AREA. NESPP4	PORT. NEGEAR. AREA. NESPP4
ANGLERFISH *Lophius americanus*	73	83	0.7229	0.0964	0.1084	0.0120	0.0482	0.0000	0.0000	0.0000	0.0120	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
BLUEFISH *Pomatomus saltatrix*	92	112	0.3750	0.1161	0.0000	0.0357	0.0000	0.4643	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0089	0.0000	0.0000	0.0000
BUTTERFISH *Peprilus triacanthus*	23	24	0.4167	0.0417	0.0000	0.0000	0.0000	0.4583	0.0000	0.0000	0.0417	0.0000	0.0000	0.0417	0.0000	0.0000	0.0000	0.0000	0.0000
COD, ATLANTIC *Gadus morhua*	365	532	0.6842	0.0959	0.1278	0.0564	0.0226	0.0038	0.0000	0.0000	0.0000	0.0094	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CUSK *Brosme brosme*	89	89	0.5618	0.1124	0.1011	0.0787	0.0225	0.0899	0.0000	0.0000	0.0112	0.0112	0.0112	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
DOGFISH, SPINY *Squalus acanthias*	62	62	0.8387	0.0484	0.0484	0.0484	0.0161	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, AM. PLAICE *Hippoglossoides platessoides*	65	95	0.5895	0.1579	0.0947	0.0421	0.0211	0.0737	0.0000	0.0000	0.0000	0.0211	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, SANDDAB *Scophthalmus aquosus*	6	6	0.0000	0.6667	0.0000	0.0000	0.0000	0.3333	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, SUMMER *Paralichthys dentatus*	125	175	0.6514	0.2286	0.0114	0.0400	0.0229	0.0400	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0057	0.0000
FLOUNDER, WINTER *Pseudopleuronectes americanus*	110	176	0.5739	0.2045	0.0114	0.0852	0.0284	0.0625	0.0000	0.0000	0.0000	0.0284	0.0000	0.0000	0.0000	0.0000	0.0000	0.0057	0.0000
FLOUNDER, WITCH *Glyptocephalus cynoglossus*	138	173	0.5838	0.1503	0.1561	0.0173	0.0347	0.0000	0.0058	0.0058	0.0173	0.0231	0.0000	0.0000	0.0000	0.0000	0.0058	0.0000	0.0000
FLOUNDER, YELLOWTAIL *Limanda ferruginea*	141	220	0.6545	0.1409	0.0045	0.0727	0.0455	0.0636	0.0000	0.0000	0.0000	0.0182	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HADDOCK *Melanogrammus aeglefinus*	159	259	0.6486	0.1544	0.0077	0.1120	0.0270	0.0000	0.0000	0.0000	0.0000	0.0502	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

Table B-6, continued. Proportion of commercial length samples that could be matched to commercial trips (Match) by species for 2011. No. of Trips is the number of commercial trips from which length samples were collected. No. of Samples is the number of length samples collected. Orphan is the proportion of orphan length samples that remained orphans after using the reduced variable sets to match. PORT, NEGEAR, AREA, and NESPP4 are the proportion of partially matched length samples where the value of that variable differed between the length samples and commercial trips. Multiple variable names (e.g., PORT.NEGEAR) are the proportion of partially matched age samples where the values of those variables differed between the length samples and commercial trips.

Species	No. of Trips	No. of Samples	Match	Orphan	PORT	NEGEAR	AREA	NESPP4	PORT. NEGEAR	PORT. AREA	PORT. NESPP4	NEGEAR. AREA	NEGEAR. NESPP4	AREA. NESPP4	PORT. NEGEAR. AREA	PORT. NEGEAR. NESPP4	PORT. AREA. NESPP4	NEGEAR. AREA. NESPP4	PORT. NEGEAR. AREA. NESPP4
HAGFISH *Myxine glutinosa*	21	21	0.6667	0.1905	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.1429	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, OFFSHORE *Merluccius albidus*	10	14	0.0000	1.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, RED *Urophycis chuss*	35	37	0.8919	0.1081	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, SILVER *Merluccius bilinearis*	104	141	0.5816	0.0567	0.0426	0.0071	0.0213	0.2837	0.0000	0.0000	0.0000	0.0000	0.0071	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, WHITE *Urophycis tenuis*	86	133	0.6241	0.2180	0.0376	0.0226	0.0451	0.0526	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HALIBUT, ATLANTIC *Hippoglossus hippoglossus*	50	50	0.3400	0.0800	0.0200	0.0400	0.0600	0.3800	0.0000	0.0000	0.0400	0.0000	0.0000	0.0000	0.0000	0.0400	0.0000	0.0000	0.0000
HERRING, ATLANTIC *Clupea harengus*	4	4	1.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MACKEREL, ATLANTIC *Scomber scombrus*	25	28	0.4286	0.0714	0.0000	0.1071	0.0000	0.3214	0.0000	0.0000	0.0000	0.0000	0.0714	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
POLLOCK *Pollachius virens*	105	119	0.6555	0.0840	0.1345	0.0504	0.0084	0.0252	0.0000	0.0168	0.0000	0.0168	0.0084	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
REDFISH *Sebastes fasciatus*	16	16	0.8125	0.0625	0.0000	0.0000	0.0625	0.0000	0.0000	0.0000	0.0000	0.0625	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SCUP *Stenotomus chrysops*	70	99	0.8384	0.0808	0.0000	0.0000	0.0101	0.0707	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SEA BASS, BLACK *Centropristis striata*	70	94	0.6489	0.2447	0.0106	0.0213	0.0000	0.0532	0.0000	0.0000	0.0000	0.0213	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
TILEFISH, GOLDEN *Lopholatilus chamaeleonticeps*	61	137	0.6496	0.1825	0.0365	0.0000	0.0000	0.1095	0.0000	0.0000	0.0219	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

Table B-7. Proportion of commercial length samples that could be matched to commercial trips (Match) by species for 2012. No. of Trips is the number of commercial trips from which length samples were collected. No. of Samples is the number of length samples collected. Orphan is the proportion of orphan length samples that remained orphans after using the reduced variable sets to match. PORT, NEGEAR, AREA, and NESPP4 are the proportion of partially matched length samples where the value of that variable differed between the length samples and commercial trips. Multiple variable names (e.g., PORT.NEGEAR) are the proportion of partially matched age samples where the values of those variables differed between the length samples and commercial trips.

Species	No. of Trips	No. of Samples	Match	Orphan	PORT	NEGEAR	AREA	NESPP4	PORT. NEGEAR	PORT. AREA	PORT. NESPP4	NEGEAR. AREA	NEGEAR. NESPP4	AREA. NESPP4	PORT. NEGEAR. AREA	PORT. NEGEAR. NESPP4	PORT. AREA. NESPP4	NEGEAR. AREA. NESPP4	PORT. NEGEAR. AREA. NESPP4
ANGLERFISH *Lophius americanus*	77	92	0.6848	0.1522	0.0761	0.0326	0.0326	0.0217	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
BLUEFISH *Pomatomus saltatrix*	116	132	0.5758	0.1591	0.0152	0.0758	0.0152	0.0985	0.0000	0.0076	0.0076	0.0379	0.0000	0.0076	0.0000	0.0000	0.0000	0.0000	0.0000
BUTTERFISH *Peprilus triacanthus*	22	22	0.4545	0.0455	0.0000	0.0000	0.0000	0.5000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
COD, ATLANTIC *Gadus morhua*	338	498	0.7149	0.0582	0.1827	0.0060	0.0241	0.0040	0.0020	0.0000	0.0020	0.0060	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CUSK *Brosme brosme*	84	85	0.7294	0.1059	0.0471	0.0118	0.0000	0.0588	0.0000	0.0000	0.0000	0.0000	0.0471	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
DOGFISH, SPINY *Squalus acanthias*	51	51	0.7647	0.0196	0.1176	0.0980	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, AM. PLAICE *Hippoglossoides platessoides*	72	109	0.7431	0.0826	0.1193	0.0183	0.0000	0.0275	0.0000	0.0000	0.0000	0.0092	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, SANDDAB *Scophthalmus aquosus*	1	1	0.0000	1.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, SUMMER *Paralichthys dentatus*	110	151	0.7351	0.1523	0.0066	0.0132	0.0000	0.0728	0.0000	0.0000	0.0000	0.0000	0.0199	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, WINTER *Pseudopleuronectes americanus*	107	149	0.7450	0.0940	0.0134	0.0067	0.1007	0.0336	0.0000	0.0000	0.0000	0.0067	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, WITCH *Glyptocephalus cynoglossus*	122	158	0.7405	0.0886	0.0506	0.0253	0.0506	0.0063	0.0000	0.0000	0.0253	0.0127	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, YELLOWTAIL *Limanda ferruginea*	126	188	0.7819	0.0638	0.0319	0.0213	0.0266	0.0532	0.0000	0.0000	0.0106	0.0053	0.0000	0.0000	0.0000	0.0000	0.0000	0.0053	0.0000
HADDOCK *Melanogrammus aeglefinus*	140	226	0.8142	0.0442	0.0133	0.0398	0.0708	0.0000	0.0000	0.0000	0.0000	0.0177	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

Table B-7, continued. Proportion of commercial length samples that could be matched to commercial trips (Match) by species for 2012. No. of Trips is the number of commercial trips from which length samples were collected. No. of Samples is the number of length samples collected. Orphan is the proportion of orphan length samples that remained orphans after using the reduced variable sets to match. PORT, NEGEAR, AREA, and NESPP4 are the proportion of partially matched length samples where the value of that variable differed between the length samples and commercial trips. Multiple variable names (e.g., PORT.NEGEAR) are the proportion of partially matched age samples where the values of those variables differed between the length samples and commercial trips.

Species	No. of Trips	No. of Samples	Match	Orphan	PORT	NEGEAR	AREA	NESPP4	PORT. NEGEAR	PORT. AREA	PORT. NESPP4	NEGEAR. AREA	NEGEAR. NESPP4	AREA. NESPP4	PORT. NEGEAR. AREA	PORT. NEGEAR. NESPP4	PORT. AREA. NESPP4	NEGEAR. AREA. NESPP4	PORT. NEGEAR. AREA. NESPP4
HAGFISH *Myxine glutinosa*	18	18	0.3333	0.6667	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, OFFSHORE *Merluccius albidus*	8	9	0.0000	1.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, RED *Urophycis chuss*	32	32	0.8438	0.1250	0.0000	0.0000	0.0313	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, SILVER *Merluccius bilinearis*	130	174	0.6494	0.0805	0.0345	0.0115	0.0115	0.1954	0.0000	0.0000	0.0000	0.0000	0.0000	0.0115	0.0000	0.0000	0.0057	0.0000	0.0000
HAKE, WHITE *Urophycis tenuis*	75	97	0.7423	0.1134	0.0515	0.0412	0.0000	0.0515	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HALIBUT, ATLANTIC *Hippoglossus hippoglossus*	53	53	0.2453	0.0755	0.0189	0.0000	0.0189	0.5660	0.0000	0.0000	0.0566	0.0000	0.0189	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MACKEREL, ATLANTIC *Scomber scombrus*	20	27	0.0370	0.3333	0.0370	0.2222	0.0000	0.2593	0.0000	0.0000	0.0370	0.0000	0.0741	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
POLLOCK *Pollachius virens*	113	139	0.6547	0.0935	0.1223	0.0216	0.0288	0.0719	0.0000	0.0000	0.0000	0.0072	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
REDFISH *Sebastes fasciatus*	15	15	0.6000	0.2000	0.0000	0.0667	0.1333	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SCUP *Stenotomus chrysops*	85	103	0.6602	0.1650	0.0291	0.0000	0.0097	0.0971	0.0000	0.0097	0.0000	0.0291	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SEA BASS, BLACK *Centropristis striata*	100	139	0.5468	0.1727	0.0863	0.0791	0.0216	0.0647	0.0000	0.0000	0.0000	0.0072	0.0216	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
TILEFISH, GOLDEN *Lopholatilus chamaeleonticeps*	44	90	0.7556	0.1889	0.0000	0.0000	0.0000	0.0556	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

Table B-8. Proportion of commercial length samples that could be matched to commercial trips (Match) by species for 2013. No. of Trips is the number of commercial trips from which length samples were collected. No. of Samples is the number of length samples collected. Orphan is the proportion of orphan length samples that remained orphans after using the reduced variable sets to match. PORT, NEGEAR, AREA, and NESPP4 are the proportion of partially matched length samples where the value of that variable differed between the length samples and commercial trips. Multiple variable names (e.g., PORT.NEGEAR) are the proportion of partially matched age samples where the values of those variables differed between the length samples and commercial trips.

Species	No. of Trips	No. of Samples	Match	Orphan	PORT	NEGEAR	AREA	NESPP4	PORT. NEGEAR	PORT. AREA	PORT. NESPP4	NEGEAR. AREA	NEGEAR. NESPP4	AREA. NESPP4	PORT. NEGEAR. AREA	PORT. NEGEAR. NESPP4	PORT. AREA. NESPP4	NEGEAR. AREA. NESPP4	PORT. NEGEAR. AREA. NESPP4
ANGLERFISH *Lophius americanus*	85	96	0.6250	0.1979	0.0625	0.0208	0.0625	0.0313	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
BLUEFISH *Pomatomus saltatrix*	64	73	0.5890	0.0822	0.0548	0.1370	0.0137	0.0959	0.0000	0.0000	0.0000	0.0000	0.0000	0.0137	0.0000	0.0000	0.0000	0.0137	0.0000
BUTTERFISH *Peprilus triacanthus*	32	33	0.3636	0.2424	0.0000	0.0000	0.0000	0.3939	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
COD, ATLANTIC *Gadus morhua*	377	550	0.7018	0.1455	0.0818	0.0291	0.0182	0.0036	0.0000	0.0073	0.0091	0.0036	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CUSK *Brosme brosme*	115	115	0.7913	0.1391	0.0261	0.0174	0.0261	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
DOGFISH, SPINY *Squalus acanthias*	63	63	0.7619	0.0952	0.0476	0.0317	0.0000	0.0476	0.0000	0.0000	0.0000	0.0159	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, AM. PLAICE *Hippoglossoides platessoides*	64	96	0.7292	0.1146	0.0729	0.0313	0.0208	0.0313	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, SUMMER *Paralichthys dentatus*	156	221	0.6833	0.1765	0.0226	0.0090	0.0181	0.0814	0.0000	0.0000	0.0045	0.0045	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, WINTER *Pseudopleuronectes americanus*	86	132	0.7424	0.1212	0.0152	0.0152	0.0379	0.0303	0.0000	0.0000	0.0152	0.0227	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, WITCH *Glyptocephalus cynoglossus*	142	175	0.7371	0.1029	0.0457	0.0457	0.0457	0.0000	0.0000	0.0057	0.0057	0.0000	0.0000	0.0057	0.0000	0.0000	0.0057	0.0000	0.0000
FLOUNDER, YELLOWTAIL *Limanda ferruginea*	97	147	0.5850	0.2517	0.0816	0.0136	0.0000	0.0340	0.0000	0.0000	0.0204	0.0136	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HADDOCK *Melanogrammus aeglefinus*	169	273	0.7729	0.1172	0.0000	0.0330	0.0256	0.0403	0.0000	0.0000	0.0000	0.0000	0.0037	0.0073	0.0000	0.0000	0.0000	0.0000	0.0000

Table B-8, continued. Proportion of commercial length samples that could be matched to commercial trips (Match) by species for 2013. No. of Trips is the number of commercial trips from which length samples were collected. No. of Samples is the number of length samples collected. Orphan is the proportion of orphan length samples that remained orphans after using the reduced variable sets to match. PORT, NEGEAR, AREA, and NESPP4 are the proportion of partially matched length samples where the value of that variable differed between the length samples and commercial trips. Multiple variable names (e.g., PORT.NEGEAR) are the proportion of partially matched age samples where the values of those variables differed between the length samples and commercial trips.

Species	No. of Trips	No. of Samples	Match	Orphan	PORT	NEGEAR	AREA	NESPP4	PORT. NEGEAR	PORT. AREA	PORT. NESPP4	NEGEAR. AREA	NEGEAR. NESPP4	AREA. NESPP4	PORT. NEGEAR. AREA	PORT. NEGEAR. NESPP4	PORT. AREA. NESPP4	NEGEAR. AREA. NESPP4	PORT. NEGEAR. AREA. NESPP4
HAGFISH *Myxine glutinosa*	24	24	0.3333	0.6667	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, OFFSHORE *Merluccius albidus*	8	8	0.0000	1.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, RED *Urophycis chuss*	30	31	0.8065	0.1613	0.0000	0.0323	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, SILVER *Merluccius bilinearis*	147	191	0.5759	0.1675	0.0471	0.0262	0.0000	0.1623	0.0000	0.0052	0.0000	0.0052	0.0000	0.0105	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, WHITE *Urophycis tenuis*	109	141	0.4823	0.3475	0.0426	0.0142	0.0071	0.1064	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HALIBUT, ATLANTIC *Hippoglossus hippoglossus*	123	123	0.1382	0.1138	0.0000	0.0000	0.0081	0.6179	0.0000	0.0000	0.0244	0.0000	0.0407	0.0407	0.0000	0.0000	0.0000	0.0163	0.0000
MACKEREL, ATLANTIC *Scomber scombrus*	33	34	0.4118	0.2941	0.0294	0.0882	0.0000	0.0882	0.0000	0.0294	0.0294	0.0000	0.0294	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
POLLOCK *Pollachius virens*	124	153	0.7320	0.1176	0.0654	0.0196	0.0196	0.0261	0.0000	0.0065	0.0000	0.0065	0.0065	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
REDFISH *Sebastes fasciatus*	22	22	0.7727	0.0909	0.0000	0.0000	0.0000	0.1364	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SCUP *Stenotomus chrysops*	90	136	0.6912	0.2279	0.0000	0.0000	0.0074	0.0662	0.0000	0.0000	0.0000	0.0000	0.0000	0.0074	0.0000	0.0000	0.0000	0.0000	0.0000
SEA BASS, BLACK *Centropristis striata*	78	102	0.3235	0.4216	0.0980	0.0000	0.0196	0.0980	0.0098	0.0000	0.0098	0.0000	0.0196	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
TILEFISH, GOLDEN *Lopholatilus chamaeleonticeps*	63	115	0.6348	0.2348	0.0174	0.0609	0.0000	0.0522	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

Table B-9. Proportion of commercial length samples that could be matched to commercial trips (Match) by species for 2014. No. of Trips is the number of commercial trips from which length samples were collected. No. of Samples is the number of length samples collected. Orphan is the proportion of orphan length samples that remained orphans after using the reduced variable sets to match. PORT, NEGEAR, AREA, and NESPP4 are the proportion of partially matched length samples where the value of that variable differed between the length samples and commercial trips. Multiple variable names (e.g., PORT.NEGEAR) are the proportion of partially matched age samples where the values of those variables differed between the length samples and commercial trips.

Species	No. of Trips	No. of Samples	Match	Orphan	PORT	NEGEAR	AREA	NESPP4	PORT. NEGEAR	PORT. AREA	PORT. NESPP4	NEGEAR. AREA	NEGEAR. NESPP4	AREA. NESPP4	PORT. NEGEAR. AREA	PORT. NEGEAR. NESPP4	PORT. AREA. NESPP4	NEGEAR. AREA. NESPP4	PORT. NEGEAR. AREA. NESPP4
ANGLERFISH *Lophius americanus*	71	80	0.7625	0.1125	0.0125	0.0750	0.0375	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
BLUEFISH *Pomatomus saltatrix*	36	38	0.4737	0.1842	0.0000	0.1842	0.0000	0.1579	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
BUTTERFISH *Peprilus triacanthus*	33	33	0.3333	0.1818	0.0000	0.0303	0.0000	0.4545	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
COD, ATLANTIC *Gadus morhua*	277	396	0.8232	0.0783	0.0328	0.0379	0.0051	0.0152	0.0000	0.0000	0.0051	0.0025	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CUSK *Brosme brosme*	89	89	0.8090	0.1011	0.0225	0.0562	0.0000	0.0000	0.0000	0.0000	0.0000	0.0112	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
DOGFISH, SPINY *Squalus acanthias*	53	53	0.7547	0.0755	0.0377	0.0755	0.0000	0.0377	0.0189	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, AM. PLAICE *Hippoglossoides platessoides*	51	71	0.6620	0.1127	0.0282	0.1408	0.0563	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, SUMMER *Paralichthys dentatus*	125	175	0.6743	0.2114	0.0114	0.0000	0.0114	0.0743	0.0000	0.0000	0.0057	0.0057	0.0000	0.0000	0.0000	0.0000	0.0000	0.0057	0.0000
FLOUNDER, WINTER *Pseudopleuronectes americanus*	61	96	0.6563	0.0833	0.0104	0.0521	0.0417	0.0729	0.0000	0.0000	0.0208	0.0313	0.0104	0.0104	0.0000	0.0000	0.0000	0.0104	0.0000
FLOUNDER, WITCH *Glyptocephalus cynoglossus*	109	143	0.8182	0.0559	0.0490	0.0280	0.0420	0.0070	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, YELLOWTAIL *Limanda ferruginea*	68	93	0.6129	0.2473	0.0215	0.0215	0.0108	0.0645	0.0000	0.0000	0.0000	0.0215	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HADDOCK *Melanogrammus aeglefinus*	139	240	0.7875	0.0375	0.0042	0.0583	0.0083	0.0542	0.0000	0.0000	0.0000	0.0333	0.0167	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

Table B-9,continued. Proportion of commercial length samples that could be matched to commercial trips (Match) by species for 2014. No. of Trips is the number of commercial trips from which length samples were collected. No. of Samples is the number of length samples collected. Orphan is the proportion of orphan length samples that remained orphans after using the reduced variable sets to match. PORT, NEGEAR, AREA, and NESPP4 are the proportion of partially matched length samples where the value of that variable differed between the length samples and commercial trips. Multiple variable names (e.g., PORT.NEGEAR) are the proportion of partially matched age samples where the values of those variables differed between the length samples and commercial trips.

Species	No. of Trips	No. of Samples	Match	Orphan	PORT	NEGEAR	AREA	NESPP4	PORT. NEGEAR	PORT. AREA	PORT. NESPP4	NEGEAR. AREA	NEGEAR. NESPP4	AREA. NESPP4	PORT. NEGEAR. AREA	PORT. NEGEAR. NESPP4	PORT. AREA. NESPP4	NEGEAR. AREA. NESPP4	PORT. NEGEAR. AREA. NESPP4
HAGFISH *Myxine glutinosa*	23	23	0.2174	0.6522	0.0000	0.0435	0.0435	0.0000	0.0000	0.0000	0.0000	0.0435	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, OFFSHORE *Merluccius albidus*	7	8	0.0000	1.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, RED *Urophycis chuss*	34	34	0.7941	0.1471	0.0294	0.0000	0.0294	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, SILVER *Merluccius bilinearis*	112	148	0.6216	0.1622	0.0135	0.0000	0.0135	0.1689	0.0000	0.0000	0.0000	0.0135	0.0000	0.0000	0.0000	0.0000	0.0000	0.0068	0.0000
HAKE, WHITE *Urophycis tenuis*	133	170	0.3412	0.4294	0.0059	0.0176	0.0059	0.1824	0.0000	0.0000	0.0000	0.0176	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HALIBUT, ATLANTIC *Hippoglossus hippoglossus*	141	141	0.2695	0.0638	0.0000	0.0426	0.0142	0.5674	0.0000	0.0000	0.0000	0.0071	0.0284	0.0071	0.0000	0.0000	0.0000	0.0000	0.0000
MACKEREL, ATLANTIC *Scomber scombrus*	37	37	0.5405	0.2432	0.0000	0.0000	0.0541	0.1351	0.0000	0.0000	0.0000	0.0000	0.0270	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
POLLOCK *Pollachius virens*	118	148	0.7838	0.0270	0.0608	0.0338	0.0203	0.0405	0.0000	0.0000	0.0000	0.0068	0.0203	0.0000	0.0000	0.0000	0.0000	0.0068	0.0000
REDFISH *Sebastes fasciatus*	27	27	0.7037	0.1111	0.0000	0.1111	0.0000	0.0741	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SCUP *Stenotomus chrysops*	98	141	0.7447	0.1064	0.0000	0.0000	0.0426	0.0922	0.0000	0.0071	0.0000	0.0000	0.0000	0.0071	0.0000	0.0000	0.0000	0.0000	0.0000
SEA BASS, BLACK *Centropristis striata*	74	96	0.4375	0.1458	0.0000	0.0417	0.1667	0.1771	0.0000	0.0208	0.0000	0.0000	0.0000	0.0104	0.0000	0.0000	0.0000	0.0000	0.0000
TILEFISH, GOLDEN *Lopholatilus chamaeleonticeps*	52	113	0.6814	0.2212	0.0354	0.0000	0.0000	0.0619	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

Table B-10. Proportion of commercial length samples that could be matched to commercial trips (Match) by species for 2015. No. of Trips is the number of commercial trips from which length samples were collected. No. of Samples is the number of length samples collected. Orphan is the proportion of orphan length samples that remained orphans after using the reduced variable sets to match. PORT, NEGEAR, AREA, and NESPP4 are the proportion of partially matched length samples where the value of that variable differed between the length samples and commercial trips. Multiple variable names (e.g., PORT.NEGEAR) are the proportion of partially matched age samples where the values of those variables differed between the length samples and commercial trips.

Species	No. of Trips	No. of Samples	Match	Orphan	PORT	NEGEAR	AREA	NESPP4	PORT. NEGEAR	PORT. AREA	PORT. NESPP4	NEGEAR. AREA	NEGEAR. NESPP4	AREA. NESPP4	PORT. NEGEAR. AREA	PORT. NEGEAR. NESPP4	PORT. AREA. NESPP4	NEGEAR. AREA. NESPP4	PORT. NEGEAR. AREA. NESPP4
ANGLERFISH *Lophius americanus*	57	59	0.6102	0.1356	0.0678	0.1186	0.0169	0.0169	0.0000	0.0000	0.0000	0.0169	0.0000	0.0169	0.0000	0.0000	0.0000	0.0000	0.0000
BLUEFISH *Pomatomus saltatrix*	48	50	0.6600	0.0800	0.0000	0.1400	0.0000	0.1000	0.0000	0.0000	0.0200	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
BUTTERFISH *Peprilus triacanthus*	27	30	0.4667	0.1333	0.0000	0.0000	0.1000	0.2667	0.0000	0.0000	0.0000	0.0000	0.0333	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
COD, ATLANTIC *Gadus morhua*	287	421	0.7482	0.0950	0.0451	0.0475	0.0404	0.0024	0.0000	0.0000	0.0000	0.0214	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
CUSK *Brosme brosme*	105	105	0.7048	0.1048	0.0095	0.0857	0.0381	0.0000	0.0000	0.0000	0.0000	0.0571	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
DOGFISH, SPINY *Squalus acanthias*	43	43	0.7442	0.0465	0.0930	0.0698	0.0233	0.0000	0.0000	0.0000	0.0000	0.0233	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, AM. PLAICE *Hippoglossoides platessoides*	75	100	0.7400	0.1100	0.0000	0.0900	0.0200	0.0100	0.0000	0.0000	0.0100	0.0200	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, SAND-DAB *Scophthalmus aquosus*	3	3	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, SUMMER *Paralichthys dentatus*	157	202	0.8168	0.0792	0.0000	0.0297	0.0396	0.0149	0.0000	0.0000	0.0099	0.0099	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, WINTER *Pseudopleuronectes americanus*	81	109	0.4220	0.1468	0.0459	0.1193	0.0275	0.1376	0.0092	0.0000	0.0000	0.0183	0.0367	0.0092	0.0000	0.0000	0.0000	0.0275	0.0000
FLOUNDER, WITCH *Glyptocephalus cynoglossus*	124	144	0.7222	0.1528	0.0139	0.0556	0.0208	0.0139	0.0000	0.0000	0.0000	0.0208	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
FLOUNDER, YELLOWTAIL *Limanda ferruginea*	93	116	0.7241	0.1466	0.0690	0.0000	0.0000	0.0517	0.0000	0.0000	0.0000	0.0086	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HADDOCK *Melanogrammus aeglefinus*	155	233	0.6180	0.1202	0.0129	0.0858	0.0172	0.0901	0.0000	0.0000	0.0000	0.0343	0.0172	0.0043	0.0000	0.0000	0.0000	0.0000	0.0000

Table B-10, continued. Proportion of commercial length samples that could be matched to commercial trips (Match) by species for 2015. No. of Trips is the number of commercial trips from which length samples were collected. No. of Samples is the number of length samples collected. Orphan is the proportion of orphan length samples that remained orphans after using the reduced variable sets to match. PORT, NEGEAR, AREA, and NESPP4 are the proportion of partially matched length samples where the value of that variable differed between the length samples and commercial trips. Multiple variable names (e.g., PORT.NEGEAR) are the proportion of partially matched age samples where the values of those variables differed between the length samples and commercial trips.

Species	No. of Trips	No. of Samples	Match	Orphan	PORT	NEGEAR	AREA	NESPP4	PORT. NEGEAR	PORT. AREA	PORT. NESPP4	NEGEAR. AREA	NEGEAR. NESPP4	AREA. NESPP4	PORT. NEGEAR. AREA	PORT. NEGEAR. NESPP4	PORT. AREA. NESPP4	NEGEAR. AREA. NESPP4	PORT. NEGEAR. AREA. NESPP4
HAGFISH *Myxine glutinosa*	14	14	0.5000	0.2143	0.0000	0.2857	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, OFFSHORE *Merluccius albidus*	4	4	0.0000	1.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, RED *Urophycis chuss*	30	30	0.8000	0.2000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, SILVER *Merluccius bilinearis*	154	178	0.7360	0.0955	0.0000	0.0112	0.0112	0.1348	0.0000	0.0000	0.0000	0.0000	0.0112	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
HAKE, WHITE *Urophycis tenuis*	129	179	0.4246	0.1173	0.0112	0.0000	0.0112	0.4190	0.0000	0.0000	0.0000	0.0000	0.0000	0.0168	0.0000	0.0000	0.0000	0.0000	0.0000
HALIBUT, ATLANTIC *Hippoglossus hippoglossus*	168	168	0.2143	0.1548	0.0060	0.0655	0.0417	0.4286	0.0000	0.0000	0.0357	0.0179	0.0119	0.0179	0.0000	0.0000	0.0000	0.0060	0.0000
MACKEREL, ATLANTIC *Scomber scombrus*	49	57	0.2982	0.3158	0.0175	0.0702	0.0000	0.1579	0.0175	0.0000	0.0000	0.0526	0.0175	0.0000	0.0000	0.0175	0.0000	0.0351	0.0000
POLLOCK *Pollachius virens*	155	177	0.6554	0.0904	0.0226	0.0282	0.0113	0.1073	0.0000	0.0000	0.0056	0.0169	0.0508	0.0056	0.0000	0.0000	0.0000	0.0056	0.0000
REDFISH *Sebastes fasciatus*	22	22	0.7727	0.0455	0.0455	0.0000	0.0000	0.0455	0.0000	0.0000	0.0000	0.0455	0.0000	0.0000	0.0000	0.0000	0.0000	0.0455	0.0000
SCUP *Stenotomus chrysops*	117	154	0.7468	0.1558	0.0065	0.0195	0.0195	0.0390	0.0000	0.0000	0.0000	0.0000	0.0065	0.0065	0.0000	0.0000	0.0000	0.0000	0.0000
SEA BASS, BLACK *Centropristis striata*	52	66	0.7121	0.0606	0.0000	0.0303	0.1364	0.0000	0.0000	0.0455	0.0000	0.0000	0.0000	0.0000	0.0000	0.0152	0.0000	0.0000	0.0000
TILEFISH, BLUELINE *Caulolatilus microps*	8	11	0.5455	0.0909	0.0000	0.0000	0.0000	0.3636	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
TILEFISH, GOLDEN *Lopholatilus chamaeleonticeps*	51	103	0.7573	0.0194	0.1748	0.0000	0.0000	0.0194	0.0000	0.0291	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

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