1 2	<b>TITLE:</b> Trophic ecology of the deep-sea cephalopod assemblage near Bear Seamount in the Northwest Atlantic Ocean
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28	ABSTRACT
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30	Cephalopods comprise a vital component of marine food-webs worldwide, yet
31	their trophic roles remain largely unresolved. This study used stable carbon and nitrogen
32	isotopes to describe the trophic structure, ontogeny, and isotopic niche overlap of
33	cephalopod groups from pelagic and near-bottom habitats around Bear Seamount in the
34	Northwest Atlantic Ocean. Beaks from 225 specimens (13 families; 27 species),
35	primarily from juvenile and sub-adult life stages, were collected during a deep-sea
36	biodiversity cruise conducted in 2012. Differences in mean $\delta^{15}N$ and $\delta^{13}C$ values were
37	detected among some families, and across species within the families Ommastrephidae,

1 Histioteuthidae, Mastigoteuthidae, and the superfamily Argonautoidea. Trophic positions 2 ranged from 2.7-4.5 across assemblage members, with top positions held by *Illex* 3 illecebrosus, Histioteuthis reversa, Octopoteuthis sicula, Taonius payo, and Haliphron 4 atlanticus. Cephalopod families exhibiting the broadest and most diverse isotopic niches 5 widths overall included Ommastrephidae, Cranchiidae, and Octopoteuthidae. Families 6 with the narrowest isotopic niches included Onychoteuthidae, and the monospecific 7 Joubiniteuthidae, and Vampyroteuthidae. Trophic position increased significantly with 8 body size (mantle length) across all individuals sampled, and ontogenetic shifts in  $\delta^{15}$ N 9 values were detected in seven species. The continuous gradient and broad range of 10 isotope values across families, species, and body sizes suggest an unstructured 11 assemblage comprised of generalist and specialist foragers distributed throughout a 12 vertical depth range of pelagic (depleted  $\delta^{13}$ C values) to near-bottom bathy/benthopelagic (enriched  $\delta^{13}$ C values) habitats. Results provide some of the first quantitative trophic 13 metrics for many poorly studied species and advance our understanding of the diversity 14 15 of cephalopod ecological roles in marine ecosystems. 16 17 **KEY WORDS:** Cephalopods, deep-sea, mesopelagic, bathy/benthopelagic, seamount, 18 stable-isotope analysis, community structure, trophic position, ontogenetic shifts

#### 1. INTRODUCTION

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2 Cephalopods comprise a vital component of marine food-webs worldwide. They are generally known as primary forage for predators of ecological and conservation 3 4 importance including teleosts, elasmobranchs, marine mammals, and seabirds (Smale 5 1996, Dawe & Brodziak 1998, Staudinger & Juanes 2010; Staudinger et al. 2013, Teffer 6 et al. 2015; Xavier et al. 2018). Cephalopods are also important consumers of secondary 7 producers (e.g., zooplankton), fishes, other cephalopods, and gelatinous animals (e.g., 8 medusa, siphonophores, ctenophores) (Hunsicker & Essington 2006, 2008, Martínez-9 Baena et al. 2016, Rosas-Luis et al. 2016, Choy et al., 2017, Hoving & Haddock 2017). 10 Because of their generalist foraging habits, fast growth rates and high energetic demands, 11 cephalopods serve as a critical intermediate link and conduit between lower and upper 12 trophic levels in marine food-webs. Nonetheless, the specific functional roles of many 13 species as well as the trophic structure of cephalopod assemblages, especially in the deep-14 sea, remain largely unknown (Cherel et al. 2009a, b, Coll et al. 2013). Mesopelagic and 15 bathy/benthopelagic species occupying deep-sea environments off the continental slope 16 and in the open ocean live at depths that are not well sampled with any regularity. Some 17 species avoid survey gear through strong swimming capabilities, while more gelatinous 18 species are prone to damage during sampling and therefore difficult to collect. Much of 19 what we do know about the trophic roles of offshore and deep-sea cephalopods has been 20 determined from digested remains found in the stomachs of their predators, including marine mammals, seabirds, and fishes (Clarke 1996, Croxall & Prince 1996, Klages 21 22 1996, Smale 1996, Clarke 2006, Cherel et al. 2007). Using predators as biological 23 samplers has been a crucial method to obtain information on rare or elusive species, but

1 to date, has been limited to understanding cephalopod's trophic role as prey (Cherel & 2 Hobson, 2005, Logan & Lutcavage 2013, Staudinger et al. 2013, Young et al. 2010). 3 Because cephalopods take small bites out of their prey and have high digestion 4 rates, using traditional stomach content analysis to determine what they are eating is 5 subject to inherent biases (e.g., towards prey where hard parts were consumed), and may 6 not fully capture their complete diets (Martínez-Baena et al. 2016, Rosas-Luis et al. 7 2016). In comparison, molecular techniques (e.g., DNA barcoding) and biochemical 8 tracers such as fatty acids and stable isotopes have led to recent advances in resolving 9 cephalopod feeding habits and trophic roles (Cherel & Hobson 2005, Cherel et al. 2009a, 10 b, Guerra et al. 2010, Navarro et al. 2013, Parry 2006, Ruiz-Cooley et al. 2004). Stable isotopes of carbon ( $\delta^{13}$ C) and nitrogen ( $\delta^{15}$ N) are useful for inferring foraging ecology 11 12 and trophic relationships, with consumer tissues becoming more enriched in  $\delta^{15}N$  and corresponding to increasing trophic level as the lighter isotope  $\delta^{14}N$  is excreted (Post 13 2002, Fry 2006).  $\delta^{13}$ C values provide information about sources of primary production at 14 15 the base of different food-webs in which animals are feeding throughout their life history (Cherel & Hobson 2005). In marine environments, relatively negative  $\delta^{13}$ C values 16 indicate offshore or pelagic habitats, while relatively positive  $\delta^{13}$ C values indicate inshore 17 18 or near bottom (demersal and benthic) environments (Graham et al. 2010, Ozcarowitz et 19 al. 2016). Various tissue types reflect different isotopic time-frames ranging from weeks 20 to months based on organ-specific fractionation rates and turnover times (Logan et al. 21 2008). In cephalopods and other soft bodied animals, measuring isotope values from hard 22 tissues such as beaks, statoliths, and eye lenses offer unique opportunities to elucidate 23 trophic roles and ontogenetic shifts in comparison with soft tissues (e.g., mantle muscle).

1 Hard tissues, beaks in particular, may be derived from specimens collected during new and historical studies that represent both direct collections (e.g., from biodiversity 2 3 cruises) or indirectly acquired from investigations of their predators (Staudinger et al. 4 2014, Seco et al. 2016). 5 Studies utilizing stable isotopes to investigate the trophic ecology of cephalopods both in terms of their foraging habits and their roles as prey are increasing in number and 6 7 scope (Coll et al. 2013, Navarro et al. 2013), with notable advances from studies of the 8 Southern (e.g., Cherel & Hobson 2005, Guerreiro et al. 2015, Rosas-Luis et al. 2016), 9 Pacific (e.g., Madigan et al. 2012, Choy et al. 2015), Arctic (Golikov et al. 2018), and 10 Northeast Atlantic Oceans (e.g., Cherel & Hobson 2007, Cherel et al. 2009b, Merten et 11 al. 2017). While some evidence exists for a structured cephalopod trophic assembly in 12 polar regions (e.g. e.g., Cherel & Hobson 2005, Guerreiro et al., 2015, Golikov et al. 13 2018), midwater cephalopods appear to form unstructured assemblages comprised of 14 generalist foragers (e.g. Cherel et al. 2009b, Madigan et al. 2012, Choy et al. 2015, 15 Rosas-Luis et al. 2016, Merten et al. 2017). However, fewer studies exist for cephalopods in the Northwest Atlantic Ocean. A recent study by Shea et al. (2017) reported that 77 16 17 cephalopod species occur in pelagic and benthic waters surrounding Bear Seamount. This 18 extinct undersea volcano located south of Georges Bank is one of over 30 seamounts that 19 comprise the New England Seamount chain and is central to the newly designated New 20 England Canyons and Seamounts Marine National Monument. Pelagic and bathyal 21 habitats above and surrounding Bear Seamount are influenced by the Gulf Stream and the 22 deep Western Boundary undercurrents, bringing a mixture of warm and cold water 23 masses, respectively, and stimulating upwelling and mixing (Moore et al. 2003). The

influence of such diverse oceanographic processes, along with complex topography and heterogeneous habitats, fosters high biodiversity (Clarke et al. 2012) and makes this an 2 ideal system to explore a broad range of cephalopod taxa. Here we use stable isotopes of 4 carbon and nitrogen to quantify trophic aspects of assemblage structure and ontogeny, as 5 well as individual trophic roles of an array of cephalopod species and families. The diversity of the Bear Seamount assemblage has been shown to be representative of the broader Northwest Atlantic (Vecchione & Pohle 2002, Vecchione et al. 2010, Shea et al. 2017), therefore this study offers novel insights into regional deep-sea ecosystem

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#### 2. MATERIALS & METHODS

#### 2.1. Sample collection

structure and function.

A deep-sea biodiversity survey of Bear Seamount, between 39° 45' to 40° 00' N and 066° 55' to 067° 40' W in the Northwest Atlantic Ocean (Figure 1), was conducted between August 30<sup>th</sup> - September 7<sup>th</sup>, 2012 by the National Marine Fisheries Service aboard the NOAA ship *Pisces*. Twenty-seven midwater and two bottom tows were conducted. Midwater sampling used a Superior double-warp trawl rigged with deepwater floats and White Nets midwater doors (Appendix 1). These open tows averaged 51 minutes at target depths and net monitoring indicated sampled depths ranging from 602 -1,921m. Additionally, two bottom trawls using a 4-Seam double-warp trawl rigged with deep-water floats and rock-hopper sweep with Perfect Doors were conducted for approximately 90 minutes across the flat top of the seamount at maximum depths of 1,297 m. Fishes, cephalopods, other invertebrates, and vegetation were removed from the

1 net mesh using forceps to ensure the majority of individuals remained intact and in good 2 condition. All specimens were sorted by major taxonomic group, counted, and measured 3 to the nearest millimeter (mm). 4 In total, 1,150 mesopelagic and bathy/benthopelagic cephalopods representing 5 approximately 62 species (confirmation at the species level was not possible for 15 6 specimens) were collected. Intact cephalopods were identified to the highest taxonomic 7 resolution possible and measured for mantle length (ML). The buccal masses of 216 8 squids and octopods representing 26 species in 13 families were removed, frozen and 9 transported to the National Museum of Natural History in Washington, D.C. where they 10 were later prepared and processed for stable isotope analyses. 11 Nine specimens of Argonauta sp. were also included in our analyses so their 12 trophic ecology could be assessed relative to other co-occurring cephalopod species. 13 Specimens of Argonauta sp. were recovered from the stomachs of white marlin 14 (Tetrapturus albidus) and roundscale spearfish (T. georgii) caught in nearby waters of the 15 continental slope just to the south and west of Bear Seamount. Beaks that exhibited little 16 to no signs of erosion from digestion or were from partially intact individuals (i.e., tissue 17 and external egg-cases were partially present) were used in an effort to evaluate 18 specimens that were consumed recently and had the highest likelihood of being from 19 nearby waters. 20 Lower and upper beaks from all cephalopods were extracted from the buccal 21 masses, cleaned of remaining tissue, photographed for reference, and lower rostral length 22 (LRL) or lower hood length (LHL) was measured. Maturity stage was classified as either 23 juvenile, sub-adult, or adult based on the level of darkening and transparency present in

the lateral walls and wings (Cherel et al. 2009a). Juveniles were designated when the
lateral walls and wings of the beak were almost completely transparent; subadults when
the lateral walls and/or wings of the beak were darkening but edges showed some
transparency; adults were defined when beaks were completely darkened with no visible
transparent portions. The majority of beaks were classified as juveniles or sub-adults, and
only three individuals (*Chiroteuthis mega*, *Vampyroteuthis infernalis*, and *Bolitaena* 

#### 2.2. Stable isotope analysis (SIA)

pygmaea) were designated as adults.

The formation and chemical composition of cephalopod beak tissue varies with growth and development. Beaks darken with growth and the level of transparency or darkness serves as an indicator of maturity (Cherel et al. 2009a). Younger beaks contain a higher proportion of chitin, while the darkened portions of the beak are made up of a mixture of chitin and proteinaceous material (Cherel et al. 2009a). Relatively high carbon content in transparent portions of beak tissue often requires increased dilution for the mass spectrometer to produce adequate peaks for isotopic analysis. To determine the minimum amount of tissue needed to obtain isotopic results as well as to establish the degree of bias imposed by portions of the beak containing high chitin, a series of pilot samples was evaluated from the smallest sizes, and earliest maturity stages of five species: *Leachia atlantica*, *Pyroteuthis margaritifera*, *Ornithoteuthis antillarum*, *Octopoteuthis sicula*, and *Magnoteuthis magna*. High C:N ratios (> 4.0) were measured in transparent portions of beaks indicating chitin bias. For all subsequent analyses lower beaks were processed by the systematic removal of transparent portions. This effectively

- 1 eliminated chitin bias from the remaining samples, with 96% of individuals having C:N
- 2 ratios  $\leq$  4.0 (species mean C:N range: 3.30 3.71). Values reported in this study therefore
- 3 represent the integrated life history of each individual through approximately the sub-
- 4 adult life phase.
- 5 All beak samples were rinsed with deionized water, placed into a drying oven at
- 6 65°C for 24-48 hours, and homogenized using a mortar and pestle. Aliquots of
- 7 homogenized beaks (<1.0 mg) were measured into tin cups and analyzed for  $\delta^{15}$ N,  $\delta^{13}$ C,
- 8 wt %N, wt %C, and C:N ratios. Samples were loaded into a Costech Zero-Blank
- 9 autosampler and combusted in a Costech 4010 Elemental Analyzer coupled to a Thermo
- 10 Delta V Advantage continuous flow mass spectrometer at the Smithsonian Museum
- 11 Conservation Institute. Isotope values were corrected to international reference materials
- using a 2-point linear correction on calibrated house standards: acetanilide and urea-
- 13 UIN3 (Schimmelmann et al. 2009). Weight percent and C:N ratios were calculated based
- on known abundances in a homogenous acetanilide standard.
- 15 Stable isotope abundances are expressed in  $\delta$  notation in per mille units (‰),
- 16 according to the equation:

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$$\delta X = \left[ \left( \frac{R_{Sample}}{R_{standard}} \right) - 1 \right] \times 1000$$
 [Eqn 1]

- where X is  $^{13}$ C or  $^{15}$ N and  $R_{Sample}$  is the corresponding ratio  $^{13}$ C: $^{12}$ C or  $^{15}$ N: $^{14}$ N. The
- 19 R<sub>standard</sub> values were based on the Vienna PeeDee Belemnite (VPDB) for <sup>13</sup>C and
- atmospheric N<sub>2</sub> for <sup>15</sup>N. Reproducibility based on replicate analyses of standards was
- <0.2% (1 $\sigma$ ) for  $\delta^{15}$ N and  $\delta^{13}$ C; all data presented here have an associated error of  $\pm 0.2\%$
- 22 (1 $\sigma$ ). Error associated with wt %N and wt %C is  $\pm 0.5\%$  (1 $\sigma$ ).

Because beak tissues are depleted in  $\delta^{15}N$  compared to soft tissues, raw values were adjusted by adding 3.5% following Cherel et al. (2009a, b). This correction factor was also applied so that cephalopod trophic positions could be related to results reported in regional studies of co-occurring competitors and predators (e.g., pelagic fishes and marine mammals).

## 2.3. Community structure and ontogenetic shifts

Differences in  $\delta^{13}$ C and  $\delta^{15}$ N values among and within major cephalopod families were tested using either a one-way ANOVA or Kruskal-Wallis non-parametric analysis depending on whether assumptions of normality were met by each group of data. Pairwise multiple comparisons were made by applying the Tukey–Kramer or the Dunn's method for parametric and non-parametric tests, respectively. Linear regression was used to evaluate how trophic level (estimated from  $\delta^{15}$ N values) and foraging habitat ( $\delta^{13}$ C) changed with increasing body size (ML) across the Bear Seamount cephalopod assemblage for all specimens with paired length and isotopic data, as well as for subsets of species with adequate sample sizes.

Trophic position was estimated for each species using  $\delta^{15}N$  values of beak tissues following the equation:

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$$TP = \lambda + \frac{\delta^{15} N_{Secondary\ consumer} - \delta^{15} N_{Base}}{\Delta n}$$
 [Eqn 2]

Stomatopod larvae, a common omnivorous zooplankton (Kline 2002) collected in the vicinity of Bear Seamount (N= 3), were chosen as a lower-trophic-level-organism representing *Base* for species distributed throughout midwater habitats and assigned a  $\lambda$  (TP) value of 2.5. A second baseline organism, *Munida valida*, was chosen to represent

- 1 near bottom, benthopelagic habitats. This species was found to have a  $\lambda$  (TP) value of 2.7
- 2 in submarine canyons of a nearby deep-sea community (Demopoulos et al. 2017). For all
- 3 calculations,  $\Delta n$  was assumed to be 3.4% on average and was the best trophic enrichment
- 4 factor (TEF) available for deep-sea marine food-web studies (Fry 1988, Post 2002).

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## 2.4. Isotopic niche width and overlap

Bayesian ellipses were used to calculate and evaluate differences in isotopic niche width among cephalopod families (Stable Isotope Bayesian Ellipses in R; Jackson et al. 2011). Using this approach, isotopic niche width is measured as the standard ellipse areas (SEA) in  $\delta^{13}$ C and  $\delta^{15}$ N space and is equivalent to standard deviations (SD) in univariate analyses. Standard ellipses were corrected for small sample sizes (SEA<sub>C</sub>) to compare the degree of isotopic niche overlap among major cephalopod families, where SEA<sub>C</sub> contains approximately 40% of the isotopic data and represents the mean core area of each group's isotopic niche. Overall niche diversity was calculated as the total area (TA) of the convex hull, which encompasses all data points for each species (Layman et al. 2007, Jackson et al. 2011). Measures of niche diversity should be interpreted with some caution due to small and unequal sample sizes. Trophic similarity was assessed by calculating overlap between all pairwise combinations of family groups using size-corrected ellipses and then diving the area (‰²) of overlap by the combined areas (‰²) of each pair of ellipses (Jackson et al. 2011). Two families, Bolitaenidae and Pyroteuthidae, were excluded from these analyses because they did not have adequate paired  $\delta^{13}$ C and  $\delta^{15}$ N values. All metrics were calculated using R (R Development Core Team, 2016) vs. 3.5.3 and the statistical package SIAR (Parnell et al. 2010).

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## 3. RESULTS

## 3.1. Structure of the cephalopod assemblage at Bear Seamount

4 Overall, corrected values in cephalopod beaks ranged from +4.8 to +14.2% for  $\delta^{15}$ N, and -21.16 to -16.82% for  $\delta^{13}$ C (Table 1; Figure 2). Significant differences in mean 5 6  $\delta^{15}N$  (H = 120.48, df = 12, p < 0.001) and  $\delta^{13}C$  (H = 99.91, df = 12, p < 0.001) values 7 were detected among all families (Table 2). Pairwise multiple comparisons (Dunn's) test 8 showed the 13 families included in this analysis generally grouped into one of three tiers of  $\delta^{15}$ N and  $\delta^{13}$ C values (Table 2). Species with the most enriched  $\delta^{15}$ N and  $\delta^{13}$ C values 9 10 included representatives from the families Mastigoteuthidae, Joubiniteuthidae, and 11 Vampyroteuthidae, while squids from the families Onychoteuthidae, Ommastrephidae, and Enoploteuthidae exhibited the most depleted  $\delta^{15}N$  and  $\delta^{13}C$  values. The remaining 12 13 families generally were intermediate to these high (enriched) and low (depleted) tiers 14 (Table 2; Figure 3A). 15 Trophic position increased with mantle length (N = 172) at a moderate but significant rate across all individuals sampled ( $R^2 = 0.19$ , F = 39.5, p < 0.001) and 16 17 showed a stronger trend (Figure 4A) than was found among species-specific values of trophic position and mantle length ( $R^2 = 0.13$ , F = 3.6, p = 0.07). High variability in 18 19 trophic level was evident across all families and species (Figure 5). Only a few 20 individuals from the families Mastigoteuthidae (N=1), Cranchiidae (N=9) and 21 Ommastrephidae (N=4) were sampled at the sizes  $\geq 200$  mm ML. Estimated trophic 22 levels for these largest individuals in some cases were similar to values found in much 23 smaller individuals from the same species.

1	A significant and positive relationship was observed between $\delta^{13}$ C values (N =
2	193) and mantle length ( $R^2 = 0.10$ , $F = 20.7$ , $p < 0.001$ ), with larger individuals becoming
3	more enriched in $\delta^{13}C$ and suggestive of deeper foraging habitats with growth (Figure
4	4B). Two outlier samples, both from the family Cranchiidae (Taonius pavo and
5	Megalocranchia sp.), exhibited relatively depleted carbon signals compared to other
6	samples. The C:N ratios of these two samples were not exceptionally high (< 3.8)
7	therefore it is unclear whether the isotopic signals from these individuals reflect true
8	habitat use (more pelagic), or chitin-biased samples. Since these are the first reported
9	isotope values of these species from the Northwest Atlantic, we chose not to exclude
10	them from our results.
11	Top trophic positions within the overall assemblage $(4.0 - 4.5)$ were held by <i>Illex</i>
12	illecebrosus, Histioteuthis reversa, Octopoteuthis sicula, T. pavo, and H. atlanticus
13	(Table 1). Intermediate trophic positions (3.5 - 4.0) included several bathy /
14	benthopelagic species M. agassizii, M. magna, J. portieri, and Megalocranchia sp., the
15	histioteuthids H. corona, H. meleagroteuthis and S. arcturi, as well as Pyroteuthis
16	margaritifera, and the pelagic octopod, Argonauta sp. The lowest trophic positions (2.7 –
17	3.4) included small ommastrephids, specifically juvenile <i>Ommastrephes bartramii</i> ,
18	Sthenoteuthis pteropus, and Ornithoteuthis antillarum, as well as Onychoteuthis banksii,
19	Bolitaena pygmaea, and Abraliopsis morisii (Table 1; Figure 2A).
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21	3.2. Isotopic niche width and overlap
22	Isotopic niche breadth (SEAc) and overall niche diversity (TA) ranged from 0.31-
23	4.86 and 0.24 – 14.18, respectively, across 11 cephalopod families. Isotopic niche breadth

1 and diversity metrics were not found to be significantly related to the number of species 2 within each family unit (p-values > 0.08). Mean family values of isotopic niche breadth  $(R^2 = 0.43, F = 6.65, p = 0.03)$  and diversity  $(R^2 = 0.52, F = 9.58, p = 0.02)$  were found to 3 4 be positively related to mean mantle length. Cephalopod families exhibiting the 5 narrowest isotopic niche breadth and niche diversity included Joubiniteuthidae, 6 Onychoteuthidae, and Vampyroteuthidae (Figure 3B). Conversely, the families 7 Ommastrephidae, Cranchiidae, and Octopoteuthidae showed the broadest isotopic niches 8 overall (Table 2; Appendix 2). Overlap in SEAc values occurred to some extent for all 9 but 5 family pair-wise combinations, and approximately a third of all groups shared 10 relatively high isotopic niche space (overlap values ranged 20-39%) with another family 11 (Table 3). Families with the largest isotopic niches (Ommastrephidae, Octopoteuthidae, 12 Cranchiidae, Chiroteuthidae) showed high overlap with each other (20-35%). The three 13 bathy/benthopelagic families, Joubiniteuthidae, Mastigoteuthidae, and 14 Vampyroteuthidae, occupied similar niche space, with overlap values ranging from 18-15 39%. Octopoteuthidae shared isotopic niche space with Mastigoteuthidae (25%), 16 Vampyroteuthidae (19%) and to a lesser extent Joubiniteuthidae (7%). Joubiniteuthidae 17 had the smallest and most unique (least amount of overlap: 0-22%) isotopic niche of all 18 families evaluated. Ommastrephidae encompassed the isotopic niches of Argonautoidea, 19 Onychoteuthidae and Enoploteuthidae (100%), and Cranchiidae completely overlapped 20 the isotopic niche space of Histioteuthidae, Argonautoidea, Vampyroteuthidae, and 21 Joubiniteuthidae (Table 3; Figure 3B).

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#### 3.3. Within-family differences and species-specific ontogenetic shifts

Significant differences in  $\delta^{15}$ N and  $\delta^{13}$ C values were found among species within 1 2 the families Ommastrephidae (N<sub>species</sub>= 4), Histoteuthidae (N<sub>species</sub>= 5), Mastigoteuthidae 3 (N<sub>species</sub>= 3), and the superfamily Argonautoidea (N<sub>species</sub>= 2) (Table 4; Figure 6). 4 Although data were available for multiple species within the families Chiroteuthidae and 5 Cranchiidae (3 species in each family), significant differences were not found (p-values > 6 0.05). Within their respective family groups, *Illex illecebrosus* (Ommastrephidae), 7 Histioteuthis reversa (Histioteuthidae), Mastigoteuthis agassizii (Mastigoteuthidae), and Haliphron atlanticus (superfamily Argonautoidea) exhibited the highest  $\delta^{15}$ N values and 8 9 inferred trophic positions; Histioteuthis reversa and Haliphron atlanticus also exhibited 10 significantly enriched carbon values compared to close relatives, potentially indicating 11 different sources of primary productivity and thus habitat use within their respective 12 groups (Table 4; Figure 6). Positive and significant ontogenetic shifts in  $\delta^{15}N$  values with increasing body 13 size were detected within the species, Abraliopsis morisii (N = 12;  $R^2$  = 0.52, F = 11.82, 14 p = 0.006), O. sicula (N = 13;  $R^2 = 0.82$ , F = 54.04, p < 0.0001), T. pavo (N = 21;  $R^2 = 0.0001$ ) 15 16 0.37, p = 0.0034), and multiple species from the family Ommastrephidae: *I. illecebrosus*  $(N = 4, R^2 = 0.96, p = 0.022)$ , Ornithoteuthis antillarum  $(N = 7, R^2 = 0.71, p = 0.02)$ , 17 Ommastrephes bartramii (N = 6,  $R^2$  = 0.73, p = 0.03), and Sthenoteuthis pteropus (N = 18 11,  $R^2 = 0.60$ , p = 0.005) (Figure 7). The only species from the family Histioteuthidae to 19 show a significant ontogenetic shift was *Histioteuthis corona* (N = 4,  $R^2 = 0.99$ , p =20 0.004), and  $\delta^{15}$ N values declined with size; however, results were based on a relatively 21 22 small sample size (N=4) over a narrow range of mantle lengths and may not represent a true trend. Shifts in  $\delta^{15}$ N values as a function of body size were tested but not found to be 23

- 1 significant in H. reversa, H. bonnellii, H. meleagroteuthis, Stigmatoteuthis arcturi,
- 2 Onychoteuthis banksii, C. mega, C. spoeli, Megalocranchia sp., M. agassizii, M. magna,
- 3 B. pygmaea Haliphron atlanticus, and Vampyroteuthis infernalis.

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#### 4. DISCUSSION

Stable isotope data from Bear Seamount quantify the trophic roles of approximately one third of all deep-sea cephalopod species reported in temperate waters of the Northwest Atlantic Ocean (Shea et al. 2017) and provide the first description of the overall trophic structure of this guild. Specimens analyzed in this study primarily represent the integrated life history of juvenile and sub-adult life stages. Mean trophic positions spanned 1.8 levels across the 27 species and 13 families of cephalopods, ranging from 2.7 in *Histioteuthis bonnellii* to 4.5 in *Illex illecebrosus*. Individuals from multiple families and across a wide range of body sizes (30 - 350 mm ML) were often found to occupy similar trophic positions. The continuous gradient, relatively high overlap, and broad range of isotopic values across families, species, and body sizes suggests an unstructured assemblage comprised of generalist and specialist foragers distributed throughout a vertical depth range of midwater pelagic habitats (Miller et al. 2010, Madigan et al. 2012, Soares et al. 2014). These findings are similar to other cephalopod food-webs documented in the Pacific and Northeast Atlantic but provide more nuanced trophic descriptions than have been reported previously (e.g. Cherel et al. 2009b, Madigan et al. 2012, Choy et al. 2015, Rosas-Luis et al. 2016, Merten et al. 2017).

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## 4.1. Isotopic niche overlap and breadth

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Trophic similarity was high among approximately a third of all family members, though distinct trophic niches emerged on either end of the spectrum of nitrogen and carbon values. We expected groups known to undergo diel vertical migration to have wider isotopic niches and a broader range of carbon values representing multiple vertical habitat baselines, compared to non-migrators. This assumption held for a few families including Ommastrephidae, Cranchiidae and Chiroteuthidae, which exhibited the broadest isotopic niche areas, and have varying vertical distribution patterns. However, Octopoteuthiidae had a broad overall isotopic niche, though they are found throughout the water column with no diel vertical migration pattern (Roper & Young 1975, Judkins et al. In preparation). Broad niches and high isotopic variability were observed at the family and species level in both very small (Bolitaena pygmaea), and very large-sized species (T. pavo and Megalocranchia sp.). These patterns either reflect ontogenetic shifts in foraging behavior or variation in isotopic baselines resulting from different habitat use in the early portions of their lives. Ontogenetic shifts were demonstrated in O. sicula and T. pavo; however, trends were insignificant for other species within the Cranchiidae and Chiroteuthidae families perhaps due to low samples sizes. Additional factors influencing niche breadth include opportunistic foraging on a range of nektonic prey as well as small sinking and suspended particles (Demopoulos et al. 2017, Gloeckler et al. 2018). Cannibalism is common in many species (Ibanez & Keyl 2010, Choy et al. 2017), and there have been observations of squids feeding on prey of equal size or larger than themselves, which

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could also expand their trophic niche even at small body sizes (Rodhouse & Nigmatullin 2 1996). 3 Cephalopod families exhibiting the narrowest isotopic niche widths and overall 4 diversity metrics at Bear Seamount included Joubiniteuthidae, Vampyroteuthidae, and 5 Onychoteuthidae. Within these groups, the more gelatinous *V. infernalis* does not rise 6 above 600 m throughout its lifetime, and the more muscular squids, Joubiniteuthis 7 portieri and small specimens of Onychoteuthis banksii are distributed throughout the 8 water column with no vertical migration pattern (Judkins & Vecchione, in preparation). 9 While these species showed similar niche dimensions, the trophic niche of O. banksii was 10 positioned much lower in the food-web compared to the more bathy/benthopelagic species and showed more variation in  $\delta^{15}$ N values. In the Gulf of Mexico the diet of O. 11 12 banksii includes copepods, euphausiids, and fishes (Passarella & Hopkins 1991). Little to 13 nothing is known about the diet of *J. portieiri*, while *V. infernalis* has been characterized 14 as having a passive feeding mode on detritus (Hoving & Robson 2012). We hypothesize 15 that the relatively narrow niche dimensions and for these families are explained by a lack 16 of diel vertical migration and occupation of distinct water masses through their integrated 17 life history, which represents the period leading up to the juvenile and/or sub-adult phase. 18 These isotopic patterns suggest they are specialists relative to other families at similar life 19 stages in the Bear Seamount assemblage. 20 In the Monterey Submarine Canyon of the northeastern Pacific Ocean, V. 21 infernalis is a non-migratory resident of low oxygen (0.4ml/l) pelagic waters (Hoving & 22 Robison 2012). To the best of our knowledge stable isotope analyses have not been 23 published on specimens from this area; however, in the eastern Atlantic, V. infernalis was

1 found to have some of the most depleted isotopic values of all cephalopods observed 2 (Cherel et al. 2009b). This is in stark contrast to the relatively enriched  $\delta^{15}$ N values and intermediate trophic position estimated for *V. infernalis* at Bear Seamount. Emerging 3 4 research has shown *V. infernalis* consume other cephalopods when given the opportunity 5 (Siebel, unpublished data) and it may not be a strict detritovore as previously thought 6 (Hoving & Robison 2012). Our findings suggest significant regional ecological 7 differences may exist for *V. infernalis* possibly due to the lack of a physiologically 8 important oxygen-minimum zone in the Northwest Atlantic and different baseline 9 conditions inherent in various ocean basins. A multi-ocean basin comparative approach 10 using a combination of gut content analysis, metabarcoding of stomach contents, and 11 compound specific stable isotopes would be useful to resolve potential ecological 12 differences in *V. infernalis* across its global range (McMahon et al. 2016). 13 Some of the smallest squids (17-85 mm) evaluated in this study included the 14 muscular vertically migrating enoploteuthid, pyroteuthid, and ommastrephid squids 15 Abraliopsis morisii, Pyroteuthis margaritifera, and Ornithoteuthis antillarum. It was 16 somewhat surprising that these species occupied lower or equivalent trophic positions to 17 that of gelatinous species (e.g., B. pygmaea, Leachia atlantica), which are generally 18 assumed to be more passive foragers (Gloeckler et al. 2018). Muscular body types and 19 swimming abilities lead to the assumption that these squids should be capable of hunting 20 and capturing mobile mid-trophic level prey such as fishes and other cephalopods even at 21 small body sizes. Enoploteuthids, such as A. morisii and P. margaritifera remain 22 relatively small throughout their lives (Maximum ML = 45 mm) (Jereb & Roper 2010) 23 feeding primarily on copepods, euphausiids, other small invertebrates, and to a lesser

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extent small fishes and cephalopods (Passarella & Hopkins 1991). Isotopic niche areas show an ontogenetic shift for A. morisii, but insufficient nitrogen data was recovered from beak samples in P. margaritifera to make any inferences. For the early to mid-life stages represented in our evaluations, these squids appear to be primarily tracking and consuming lower trophic level prey (e.g., zooplankton) as they migrate vertically in the water column. It is possible that these species could be utilizing habitats with different isotopic baselines that confounded estimations of trophic positions. Few studies have described the isotopic structure of deep-sea habitats of the Northwest Atlantic; therefore high uncertainty exists for fine scale habitat use and trophic relationships. Ommastrephid squids occupied the broadest of all isotopic niches and had high trophic redundancy with several other midwater families. They are active predators, foraging throughout the water column as they migrate on a diurnal basis, consuming a mixture of crustaceans, fishes such as myctophids, and other cephalopods (Boyle & Rodhouse 2005). Relative amounts of prev consumed varies by ommastrephid species, region, and season, with juveniles generally consuming more crustaceans than older life phases (Lipiński & Linkowski 1988, Dawe et al. 1997, Dawe & Brodziack 1998, Watanabe et al. 2004, Parry 2006). Interestingly, the two large squids I. illecebrosus and O. bartramii occupied vastly different trophic positions. In the Southwest Atlantic, O. bartramii have been shown to be cannibalistic as well as consuming histioteuthids, enoploteuthids, and argonauts (Lipiński & Linkowski 1988). The diet of *I. illecebrosus* is primarily known from specimens captured in shelf waters but also indicates high levels of cannibalism, predation on inshore fishes and the longfin inshore squid, *Doryteuthis* pealeii (Maurer and Bowman 1985, Cargnelli et al. 1999), the latter likely not being

1 representative of the diet of the population living in deep water environments of Bear 2 Seamount. Ommastrephes bartramii, S. pteropus, and O. antillarum attain body sizes much larger than were evaluated here (Jereb & Roper 2010). Conversely, large (> 200 3 4 mm ML) I. illecebrosus were some of the few adult specimens evaluated at Bear 5 Seamount and reveal new details on the offshore component of the population which is 6 quite poorly known (Dawe et al. 1997, Dawe & Brodziack 1998, Cargnelli et al. 1999). 7 Based on results in other ocean basins (Takai et al. 2000, Golikov et al. 2018), 8 additional sampling of larger, mature individuals across many Bear Seamount species is 9 expected to reveal more pronounced ontogenetic shifts, higher trophic levels, and 10 expanded isotopic niche breadths than were measured here. Additional studies that 11 analyze multiple beak structures (e.g., rostrum, wing, lateral walls) would be useful to 12 reconstruct distinct portions of the trophic history and resolve remaining uncertainties 13 (Cherel & Hobson 2005, Cherel et al. 2009a, Guerra et al. 2010, Parry 2006, Queirós et 14 al. 2018).

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#### 4.2. Conflicting patterns in body size and isotopic enrichment

Mantle length was a good overall predictor of trophic level across the cephalopod community at Bear Seamount, but there was substantial variation in the range of body sizes representing high and low trophic positions at the individual and species level. For example, some of the species that grow large (e.g., *Ommastrephes bartramii*) on average occupied some of the lowest trophic positions. Individual body size is usually a better indicator of trophic position within a community, more so even than species (Jennings & Reynolds 2007) and this pattern held true for cephalopods at Bear Seamount. However,

in deep-sea habitats a range of factors can confound the relationship between body size

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2 and trophic position, when patterns are interpreted using  $\delta^{15}N$  values. In the Northwest Atlantic and other ocean basins, it is well known that  $\delta^{15}N$ 3 4 values become enriched with depth due to bacterial remineralization of Particulate 5 Organic Matter (POM) and the upwelling of nutrient-rich bottom waters from slope 6 environments (Mintenbeck et al. 2007, McMahon et al. 2013, Ozcarowitz et al. 2016, 7 Demopoulos et al. 2017, Richards et al. 2018). Relatively enriched  $\delta^{15}$ N values were 8 characteristic of bathy / benthopelagic species from the families Chiroteuthidae, 9 Mastigoteuthidae, Vampyroteuthidae, and Joubiniteuthidae caught at Bear Seamount. 10 Individuals were not particularly large, are weakly muscular to gelatinous, and do not 11 possess morphological characteristics consistent with that of active searching predators 12 (Hoving & Robson 2012). When estimating trophic position, we accounted for the 13 influence of nitrogen enrichment with depth by using a deep-sea benthic species as a 14 baseline (Demopoulos et al. 2017), which would otherwise have resulted in elevated 15 trophic positions for these species where it may not have been ecologically warranted. It 16 is certainly possible that other species within the assemblage at Bear Seamount could also 17 be influenced by deep or multiple isotopic baselines occurring across the depth zones 18 sampled (up to ~1900 m); however, we did not have sufficient information to assign 19 many cephalopod species with confidence to more narrowly defined depth zones and 20 corresponding isotopic baseline. Nonetheless, there is emerging evidence that organisms 21 distributed throughout epipelagic, mesopelagic and some bathypelagic habitats are 22 supported by surface production that is either consumed and transported to depth by 23 vertically migrating prey or fast-sinking particles (Richards et al. 2018). Additional

constraints included assumptions of a constant trophic enrichment factor (TEF) in our 1 2 calculations of trophic position and a fixed chitin correction factor to account for beak to tissue conversions, which may not be appropriate for all species; however, specific 3 4 fractionation rates are not readily available for deep-sea species (Post 2002, Demopoulos 5 et al. 2017). Our results were based on bulk stable isotope analysis, which is not able to 6 fully differentiate among sources of production from the surface and POM suspended at 7 deeper depths. Future work using compound specific stable isotopes would help clarify 8 fine scale trophic and spatial differences within this and other deep-sea food-webs 9 (Demopoulos et al. 2017, Richards et al. 2018). 10 11 4.3. Trends in cephalopod biodiversity and abundance relative to trophic roles 12 Cephalopods documented at Bear Seamount during 2012 represent a year of 13 relatively high biodiversity and abundance compared to the long-term series conducted between 2000-2014 (Shea et al. 2017). Six of the 27 species collected during 2012 and 14 15 evaluated in the present study, Mastigoteuthis agassizii, Magnoteuthis magna, 16 *Vampyroteuthis infernalis, Illex illecebrosus, Histioteuthis reversa*, and *Taonius pavo*, 17 were persistent (found during all eight cruises) and numerically dominant (comprising 18 75% of all specimens caught) over the 14 year sampling period at Bear Seamount. These 19 species are common prey to medium and large cetaceans such as sperm whales (*Physeter* 20 macrocephalus), long-finned pilot whales (Globicephala melas), pygmy (Kogia 21 breviceps) and dwarf (K. sima) sperm whales in the Atlantic Ocean (Clarke et al. 1993, 22 Gannon et al. 1997, Spitz et al. 2011, Staudinger et al. 2014), as well as large pelagic fishes and sharks (Staudinger et al. 2013). These species appear to be present in high 23

numbers during a substantial portion of the annual cycle, possibly year-round, and are an essential part of the regional food-web both as mid-water consumers and as food to apex predators of high conservation and management concern. It is also noteworthy that specimens of *Haliphron atlanticus* collected in 2012 were among the largest ever collected at Bear Seamount. The anomalous diversity, abundance, and body sizes of cephalopods observed during this year, could be the result of unique oceanographic conditions characterized by the warmest year in the Northwest Atlantic Ocean since the 1980s and a notably strong NAO Index (Mills et al. 2013, Oczkowski et al. 2016). Water and chlorophyll samples collected on the continental shelf also showed regional primary productivity rates were elevated and higher than average  $\delta^{13}$ C values were present during 2012 (Oczkowski et al. 2016). These anomalous conditions likely affected isotopic signatures in cephalopod tissues and future studies in the region will be useful to compare results across average and extreme years to determine how cephalopod biodiversity and trophic roles may vary accordingly.

#### 4.4. An evolving understanding of cephalopod trophic ecology

Differences in isotopic baselines make direct comparisons with other regions problematic; however, some insights can be gained on how cephalopod trophic roles may vary or be similar between regions based on relative positions and overall isotopic ranges within their respective food-webs. High overlap among families, high intra-family variability, and increasing trophic position with growth were consistent findings for cephalopods at Bear Seamount and specimens obtained from large pelagic fish diets in nearby habitats of the central North Atlantic (Logan & Lutcavage 2013). Trophic

1 diversity was similar at Bear Seamount and in the Bay of Biscay in the Northeast 2 Atlantic, where 19 cephalopod species spanned a narrower range of isotope values, 3 covering 1.5 trophic levels (Cherel et al. 2009b). In slope waters of the Kerguelen Islands 4 of the Southern Ocean, 18 cephalopod species consumed by teleost, seabird, and 5 elasmobranch predators spanned a continuum of three trophic levels (Cherel & Hobson 6 2005). 7 Because of our poor understanding of deep-sea systems, it is unclear how much of 8 the variation observed in cephalopods across regions is due to differences in trophic roles 9 or collection methods. Specimens were caught at Bear Seamount using standardized 10 survey gear, which has some inherent limitations. Large muscular taxa as well as delicate 11 gelatinous taxa may be under-represented due to their ability to outswim and avoid nets, 12 or because they are badly damaged by sampling gear. For example, Argonauta sp. are 13 rarely captured in midwater nets, yet they are one of the most commonly recovered 14 octopods in the diets of regional large pelagic fishes and are believed to be a key 15 component of offshore food-webs (Staudinger et al. 2013). In comparison, most other 16 studies that have documented deep-sea cephalopod trophic ecology to date have used 17 specimens obtained from the stomachs of marine mammals, seabirds and large pelagic 18 fishes (Clarke 1996, Jackson et al. 2009, Logan et al. 2011, Logan & Lutcavage 2013, 19 Staudinger et al. 2014, Jackson et al. 2009, Seco et al. 2016, Xavier et al. 2018). While 20 information gained from using predators as biological samplers has advanced our 21 understanding of cephalopod diversity and biogeography, results may represent biased 22 selections of species and body sizes that are dependent on predator foraging behavior 23 (e.g., diving depth) and selective abilities (e.g., mouth gape) (Staudinger et al. 2013,

1 Young et al. 2010). The use of beak tissues for analysis in the present study, rather than 2 soft tissues (e.g., mantle), was deliberate and part of a long-term sampling strategy for 3 assessing the ecosystem role of deep-sea cephalopods that takes into account their 4 catchability by direct (i.e., surveys) and indirect (i.e., predator stomachs) sources. 5 An emerging finding across recent studies is that cephalopods occupy a wider range of trophic roles than previously thought (Cherel & Hobson 2005, Navarro et al. 6 7 2013, Golikov et al. 2018). In many systems, particularly offshore habitats, the trophic 8 niches of cephalopods consistently overlap with top predators (Cherel et al. 2009b, Logan 9 et al. 2011, Madigan et al. 2012, Logan & Lutcavage 2013, Navarro et al. 2013). Studies 10 in waters near Bear Seamount, have shown the diets of large pelagic fishes (e.g., tunas, 11 dolphinfish) can comprise substantial amounts of epipelagic and mesopelagic cephalopods, but exhibit similar and sometimes lower  $\delta^{15}$ N values than some of the 12 13 cephalopods examined here (Teffer et al. 2015). In addition, regional studies of deepdiving kogiid whales that forage almost exclusively on mesopelagic squids, exhibited 14  $\delta^{15}$ N values similar to their primary prey (Histioteuthidae, Ommastrephidae, and 15 16 Cranchidae) (Staudinger et al. 2014). Although multiple baselines may be confounding 17 these results (Chouvelon et al. 2012), these results challenge previous assumptions that as 18 invertebrates, cephalopods should be restricted to low-mid trophic levels. Ecosystem 19 models of the Northwest Atlantic (e.g., Ecopath) commonly group all squids together 20 regardless of size and species (Morissette et al. 2006, 2009, Zhang & Chen 2007). 21 Depending on the diversity of cephalopods present in a region, these models may be 22 underestimating trophic redundancy, oversimplifying the guild and failing to accurately 23 depict the breadth of trophic roles represented in a given food-web. This can result in

1	decreased estimates of ecosystem stability and poor overall understanding of resilience to
2	environmental and anthropogenic stressors such as climate change and fishing pressure
3	(Madigan et al. 2012). Cephalopods are increasingly being recognized as a key forage
4	resource (National Coalition for Marine Conservation; Lenfest Forage Fish Task Force),
5	yet additional attention is still needed to capture and resolve the full range of their
6	potential functional ecology as competitors as well as mid to high-level predators.
7	In conclusion, this study provides novel information on a wide range of deep-sea
8	cephalopods – an important taxonomic group in global oceans; however, many questions
9	remain unresolved. A multifaceted approach using a range of observational and
10	molecular techniques is perhaps the only way we will be able to ascertain the full breadth
11	of trophic roles and delineate separate but inter-locked vertical food-webs of deep-sea
12	cephalopods. Ideally, data from predator diets, survey gear, and in situ feeding
13	observations from Remotely Operated Vehicles (ROVs) (Choy et al. 2017), would be
14	integrated with molecular tools such as metabarcoding, and compound-specific stable
15	isotopes to resolve isotopic baselines, to clarify food habits and to obtain sufficient
16	samples on poorly known species. Simultaneous sampling and/or comparisons with apex
17	predators would also help resolve whether trophic positions of cephalopods, large pelagic
18	fishes and marine mammals are truly equivalent or influenced by different (e.g., deep vs.
19	surface water) $\delta^{15}N$ baselines. Nonetheless, emerging information on the spectrum and
20	diversity of ecological roles within the cephalopod group is compelling and deserves
21	more attention in the future.

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## 5. ACKNOWLEDGEMENTS

1	We thank the Captain and crew of the NOAA Ship Pisces, and all of the participants on
2	this cruise for their efforts in collecting specimens, samples, and data. We greatly
3	appreciate the constructive comments received by three anonymous reviewers, which
4	helped strengthen this manuscript. V. H. Dimkovikj was supported as part of an
5	undergraduate research opportunity with Coastal Carolina University, NSF REU Site
6	EAR-1062692, as well as through a Natural History Research Experiences summer
7	internship at the Smithsonian Institution.
8	
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**Table 1**: Summary of  $\delta^{13}$ C (‰) and  $\delta^{15}$ N (‰) values  $\pm$  SD measured in cephalopod beaks. All measured isotopic values are reported. A correction factor of 3.5‰ was applied to raw  $\delta^{15}$ N values following Cherel et al. (2009a, b). N indicates sample sizes; when two values are separated by a comma, the first number indicates sample size for  $\delta^{13}$ C (‰) and the second indicates sample size for  $\delta^{15}$ N (‰). Length indicates mantle lengths (mm)  $\pm$  SD. Trophic Position (TP) was estimated using the approach from Post (2002). \* indicates species where TP was estimated using a bottom / benthopelagic baseline.

Mantle length							
Species	N	(mm)	$\delta^{13}$ C (‰)	$\delta^{15}N$ (‰)	C:N	TP	
Oegopsida							
Cranchiidae							
Leachia atlantica	7,1	$61.1  \pm 10.5$	$-17.9 \pm 0.4$	8.5	3.46	3.52	
Megalocranchia sp.	9	$98.8  \pm 60.0$	$-18.3 \pm 1.2$	$9.7 \pm 3.1$	3.52	3.90	
Taonius pavo	22,21	$180.0 \pm 50.6$	$-18.1 \pm 0.6$	$10.5~\pm~1.1$	3.53	4.14	
Chiroteuthidae							
Chiroteuthis mega*	9	$81.4 \pm 25.2$	$-18.2 \pm 0.4$	$11.1 ~\pm~ 1.4$	3.49	3.10	
Chiroteuthis spoeli*	4	$92.3 \pm 12.7$	$-18.0 \pm 0.2$	$10.2 ~\pm~ 1.2$	3.52	2.84	
Chiroteuthis veranyi*	3	$49.5  \pm  7.8$	$-17.7 \pm 0.6$	$11.8~\pm~1.8$	3.63	3.31	
Enoploteuthidae							
Abraliopsis morisii	12,13	$27.7  \pm 8.0$	$-18.3 \pm 0.4$	$7.9 \pm 1.0$	3.30	3.37	
Histioteuthidae							
Histioteuthis bonnellii*	5	$36.2  \pm 33.7$	$-18.3 \pm 0.4$	$9.7 \pm 0.3$	3.50	2.69	
Histioteuthis corona	4	$42.3  \pm 6.4$	$-18.1 \pm 0.2$	$9.8 \pm 0.6$	3.53	3.91	
Histioteuthis meleagroteuthis	8	$50.1 \pm 10.9$	$-18.2 \pm 0.3$	$8.9 \pm 0.8$	3.50	3.66	
Histioteuthis reversa	8,7	$60.3 \pm 50.1$	$-17.8 \pm 0.2$	$11.4 ~\pm~ 1.1$	3.43	4.40	
Stigmatoteuthis arcturi	3,4	$31.8 \pm 7.1$	$-18.6 \pm 0.2$	$9.4 \pm 0.7$	3.50	3.81	
Joubiniteuthidae							
Joubiniteuthis portieri*	5	$60.7 \pm 3.2$	$-17.1 \pm 0.3$	$12.6 \pm 0.3$	3.44	3.55	
Mastigoteuthidae							
Mastigoteuthis agassizii*	7	$76.9 \pm 16.4$	$-17.7 \pm 0.2$	$13.5~\pm~0.4$	3.49	3.83	
Mastigopsis hjorti*	3	63.0	$-17.5 \pm 0.2$	$11.3 \pm 1.5$	3.45	3.18	
Mastigoteuthis magna*	15	$129.9 \pm 75.5$	$-17.4 \pm 0.3$	$12.7 \pm 0.9$	3.44	3.58	
Octopoteuthidae							
Octopoteuthis sicula	14	$74.6 \pm 46.1$	$-17.8 \pm 0.4$	$10.9 \pm 2.3$	3.71	4.25	
Ommastrephidae							
Illex illecebrosus	4	$256.3 \pm 48.7$	$-17.8 \pm 0.4$	$11.7~\pm~0.8$	3.41	4.49	
Ommastrephes bartramii	6	$138.8 \pm 19.3$	$-17.6 \pm 0.4$	$5.8 \pm 0.7$	3.54	2.75	
Ornithoteuthis antillarum	11,7	$49.9 \pm 20.5$	$-19.0 \pm 0.4$	$7.3 \pm 0.6$	3.53	3.19	
Sthenoteuthis pteropus	11	$75.2 \pm 31.7$	$-18.9 \pm 0.7$	$6.4 \pm 0.7$	3.45	2.92	
Onychoteuthidae							
Onychoteuthis banksii	8,5	$31.6 \pm 14.5$	$-18.7 \pm 0.1$	$7.2 \pm 1.1$	3.53	3.16	
Pyroteuthidae	,						
Pyroteuthis margaritifera	8,2	$24.0 \pm 7.3$	$-18.8 \pm 0.6$	$9.0 \pm 0.2$	3.32	3.68	
Octopodiformes							
Argonautoidea							
Argonauta sp.	9	±	$-18.9 \pm 0.3$	$8.6 \pm 0.3$	3.55	3.57	
Haliphron atlanticus	11	$88.4 \pm 17.0$	$-18.0 \pm 0.2$	$10.2 \pm 0.3$	3.67	4.02	
Bolitaenidae						-	
Bolitaena pygmaea	6,4	$37.8 \pm 14.0$	$-18.3 \pm 0.8$	$8.1 \pm 0.9$	3.60	3.43	
Vampyroteuthidae	,						
Vampyroteuthis infernalis*	9	$37.6 \pm 19.5$	$-17.5 \pm 0.3$	$12.0~\pm~0.7$	3.55	3.38	

**Table 2:** Among family differences in  $\delta^{15}$ N and  $\delta^{13}$ C (‰) values using a Kruskal-Wallis One Way Analysis of Variance on ranks and pairwise multiple comparisons tests (Dunns). Different letters show similarities and differences among families. SIBER analysis results show core isotopic trophic niche width (SEAc), and overall niche diversity (TA) measurements in beak tissues. Values correspond to bayesian ellipses (SEAc) and convex hulls (TA) in Figure 7. Bolitaenidae and Pyroteuthidae were excluded from SIBER analyses due to low paired sample sizes.

Family	${f N}$	$\delta^{15}$ N (‰)	$\delta^{13}$ C (‰)	ML	<b>SEAc</b>	TA
Argonautoidea	20	D	F	88.4	0.71	1.74
Bolitaenidae	4	C	Н	37.8	-	-
Chiroteuthidae	16	D	Н	83.1	1.96	5.04
Cranchiidae	29	D	Н	139.9	4.01	13.77
Enoploteuthidae	12	В	F	28.8	0.76	1.54
Histioteuthidae	27	D	Н	45.3	1.21	3.67
Joubiniteuthidae	5	A	E	60.7	0.31	0.24
Mastigoteuthidae	25	A,C	E	110.9	1.03	2.77
Octopoteuthidae	14	D	G	74.6	2.96	5.25
Ommastrephidae	27	В	F	100.3	4.86	14.18
Onychoteuthidae	5	В	F, G	34.5	0.55	0.47
Pyroteuthidae	2	D	F,G	25.4	-	-
Vampyroteuthidae	9	A	Е	37.6	0.70	1.03

**Table 3:** The percentage of shared isotopic niche space for all pair-wise comparisons of cephalopod families. Values in parentheses indicate the directional percent overlap of family A (column) with family B (row).

	Argonautoidea	Chiroteuthidae	Cranchiidae	Enoploteuthidae	Histioteuthidae	Joubiniteuthidae	Mastigoteuthidae	Octopoteuthidae	Ommastrephidae	Onychoteuthidae
Chiroteuthidae	20 (75, 27)									
Cranchiidae	15 (100, 18)	32 (97, 47)								
Enoploteuthidae	14 (29, 27)	17 (24, 62)	16 (18, 98)							
Histioteuthidae	27 (44, 74)	35 (56, 91)	23 (30, 100)	28 (72, 45)						
Joubiniteuthidae	0	8 (9, 56)	7 (8, 100)	0	5 (6, 23)					
Mastigoteuthidae	7 (18, 12)	25 (38, 73)	18 (23, 88)	<1 (2, 1)	15 (28, 33)	18 (78, 24)				
Octopoteuthidae	12 (62, 15)	35 (87, 57)	31 (55, 74)	14 (66, 17)	25 (86, 35)	7 (74, 8)	25 (98, 34)			
Ommastrephidae	13 (100, 15)	20 (70, 28)	30 (67, 56)	14 (100, 16)	19 (96, 24)	<1 (13, 1)	6 (36, 8)	24 (64, 39)		
Onychoteuthidae	13 (23, 30)	9 (11, 40)	9 (11, 77)	27 (46, 63)	18 (26, 56)	0	0	6 (7, 35)	10 (11, 100)	
Vampyroteuthidae	9 (18, 18)	23 (30, 86)	15 (17, 100)	<1 (2, 2)	18 (28, 48)	22 (72, 33)	39 (65, 97)	19 (23, 99)	7 (8, 55)	0

**Table 4:** Within family differences in isotopic values for a subset of groups with  $\ge 3$  species using one-way ANOVA (F) or Kruskal-Wallis One Way Analysis of Variance (H) depending on whether the assumption of normality was upheld. Kruskal-Wallis test results are in bold. Different letters show results of pairwise multiple comparisons (Tukey Test) for parametic and (Dunns) for non-parametric tests. NS = non-significant within family differences.

	$\delta^{13}$ C (‰)		$\delta^{15}$ N	(‰)	
Family and species	F, <b>H</b>	p	F, <b>H</b>	p	
Cranchiidae	0.07	NS	1.85	NS	
Chiroteuthidae	2.04	NS	1.09	NS	
Histioteuthidae	7.22	< 0.001	18.99	< 0.001	
Histioteuthis bonnellii	В				
Histioteuthis corona	A, B, C				
Histioteuthis meleagroteuthis	B, C				
Histioteuthis reversa	A				
Stigmatoteuthis arcturi	C				
Mastigoteuthidae	3.62	0.04	6.152	0.003	
Mastigoteuthis agassizii	A				
Mastigopsis hjorti	В				
Mastigoteuthis magna	A,B				
Ommastrephidae	9.9	< 0.001	68.33	< 0.001	
Illex illecebrosus	A				
Ommastrephes bartramii	В				
Ornithoteuthis antillarum	C				
Sthenoteuthis pteropus	C, B				
Argonautoidea	61.84	< 0.001	170.5	< 0.001	
Argonauta sp.					
Haliphron atlanticus					

### Figure legends

**Figure 1:** Map of the Northwest Atlantic region, the New England Seamount chain, and Bear Seamount, which is highlighted in the red box. Detailed station locations are shown in the inset map. Station locations represent tow start locations and additional information on all midwaters tows can be found in Appendix 1.

**Figure 2**: Mean and standard deviations of stable (A) nitrogen and (B) carbon isotope values measured in the beaks of 26 cephalopod species from waters of the Bear Seamount.

Figure 3: Stable isotope A) bi-plot and B) SIBER ellipses of δ<sup>13</sup>C (‰, VPDB) and δ<sup>15</sup>N (‰, air) values for 13 cephalopod families from Bear Seamount. Bi-plots show mean ± SD for all individuals with paired measurements. Standard ellipses corrected for small sample sizes (SEAc) (solid lines) represent the core niche area of each family, and convex hulls of overall niche diversity (dotted lines) encompass all data points. In order of most enriched δ<sup>15</sup>N values, Mastigoteuthidae (MAST), Joubiniteuthidae (JOUB), Vampyroteuthidae (VAMP), Octopoteuthidae (OCT), Chiroteuthidae (CHIR), Cranchiidae (CRA), Histioteuthidae (HIST), Argonautoidea (ARG), Pyroteuthidae (PYR), Bolitaenidae (BOL), Enoploteuthidae (ENO), Ommastrephidae (OMM), and Onychoteuthidae (ONY). Note that sample sizes were not large enough for Pyroteuthidae and Bolitaenidae to be included in the SIBER analysis.

**Figure 4:** Plots show changes in A) trophic position and B) habitat use across the cephalopod assemblage of the Bear Seamount as a function of mantle length (ML). Note that only species

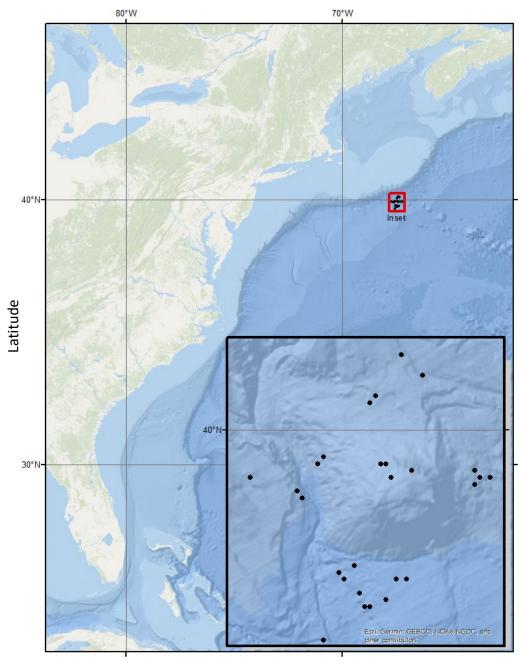
with reliable measurements of ML (from relatively intact specimens) were included in this analysis.

**Figure 5**: Overall range of mean species-specific values for A) mantle length (mm), and B) trophic position, ordered from smallest to largest.

Figure 6: Within family stable isotope bi-plots of  $\delta^{13}$ C (‰, VPDB) and  $\delta^{15}$ N (‰, air) values for A) Ommastrephidae , B) Mastigoteuthidae, C) Histioteuthidae, and D) Argonautoidea. Bi-plots show mean  $\pm$  SD. Note scaling on all axes varies with family group.

Figure 7: Ontogenic shifts in  $\delta^{15}$ N (‰, air) values as a function of mantle length (mm) were found to be significant in the species A) *Abraliopsis morisii*, B) *Octopoteuthis sicula*, C) four species within the family Ommastrephidae: *Illex illecebrosus* (circle), *Ommastrephes bartramii* (square), *Ornithoteuthis antillarum* (triangle), and *Sthenoteuthis pteropus* (diamond); D) *Taonius pavo* (triangle), and E) *Histioteuthis corona* (square). Data for additional species within the families Cranchiidae and Histioteuthidae are shown for context in D) *Megalocranchia* sp. (diamond) and *Leachia atlantica* (circle), and E) *H. reversa* (X), *H. bonellii* (circle), *H. meleagroteuthis* (triangle), *Stigmatoteuthis arcturi* (diamond).





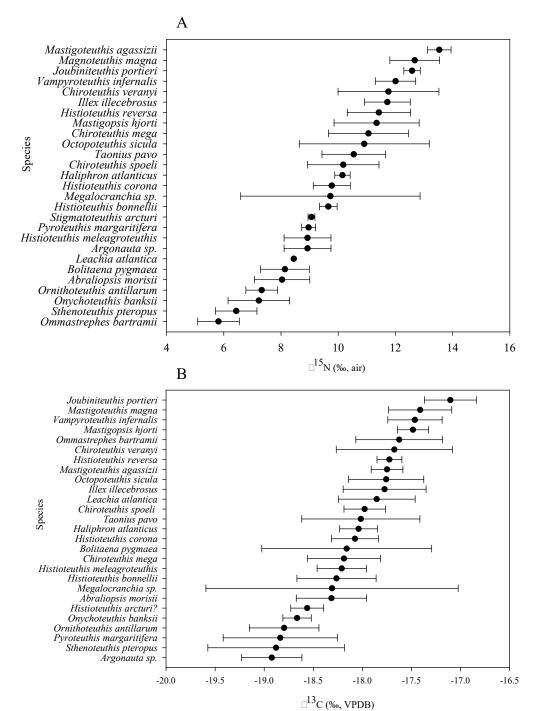


Figure 3

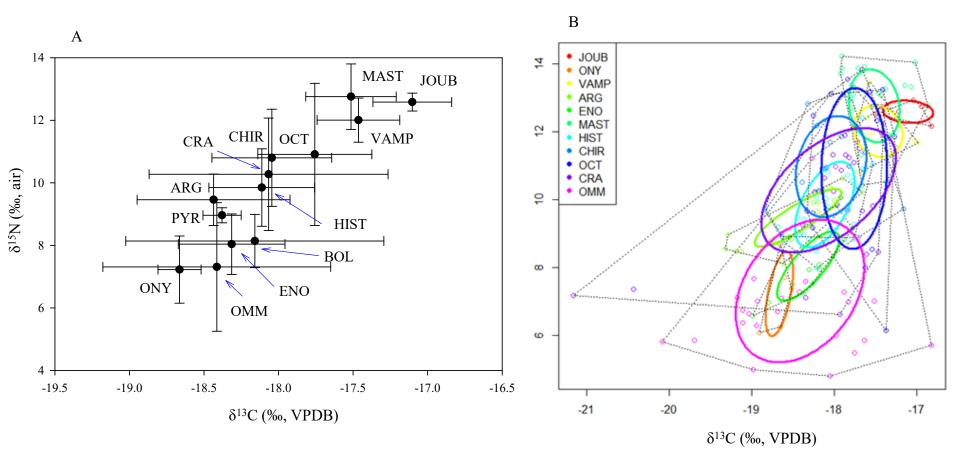


Figure 4

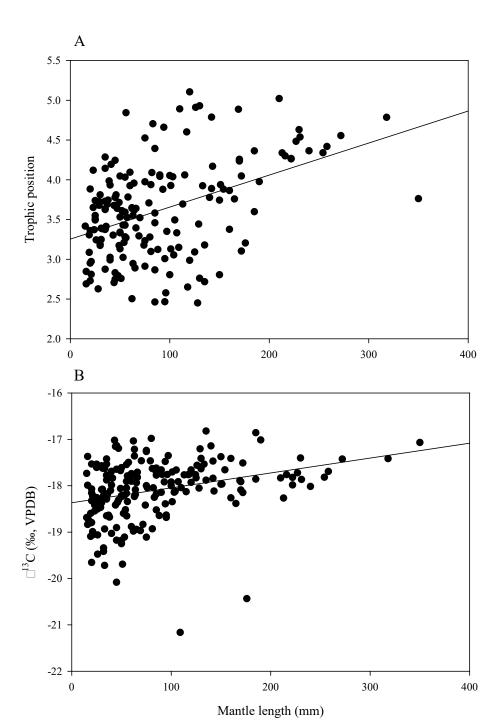


Figure 5

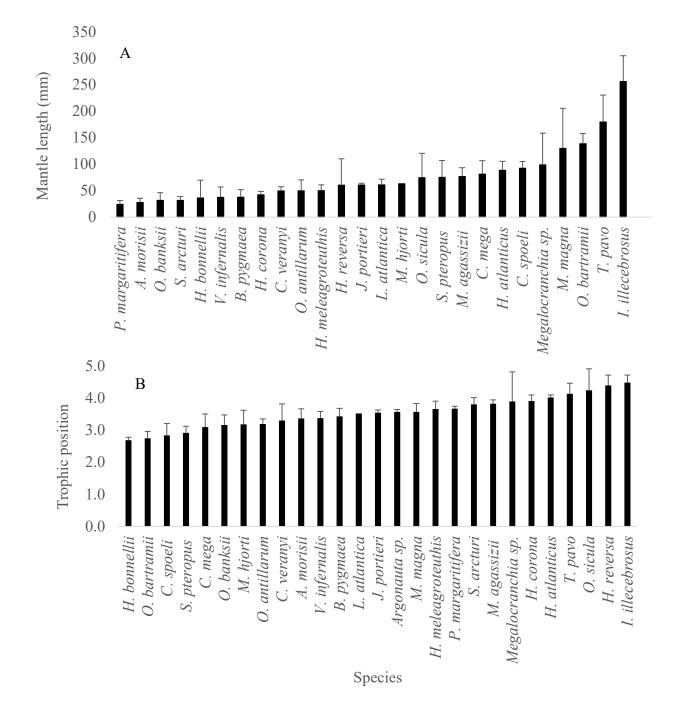


Figure 6

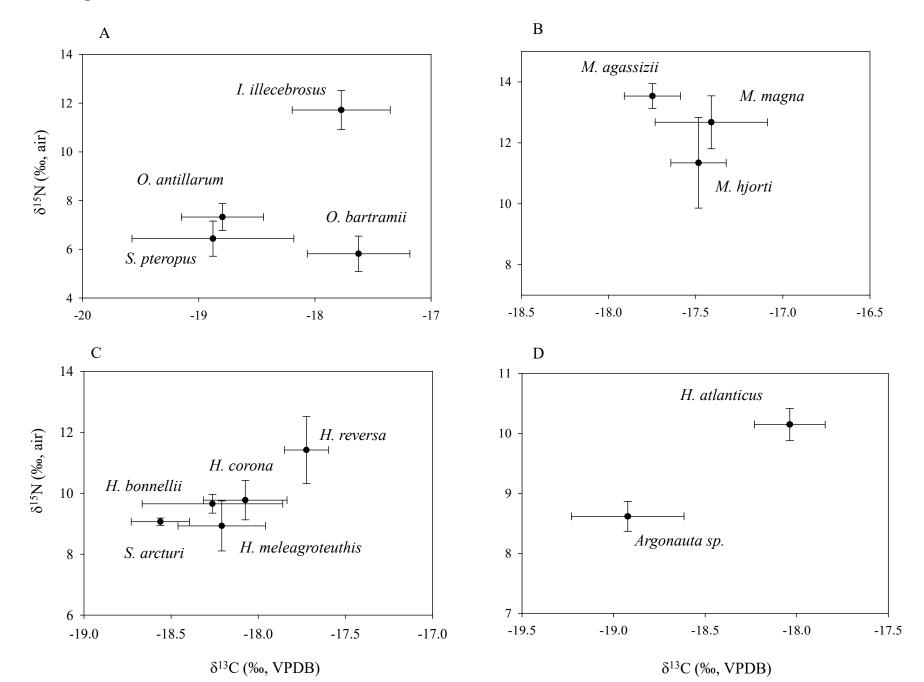
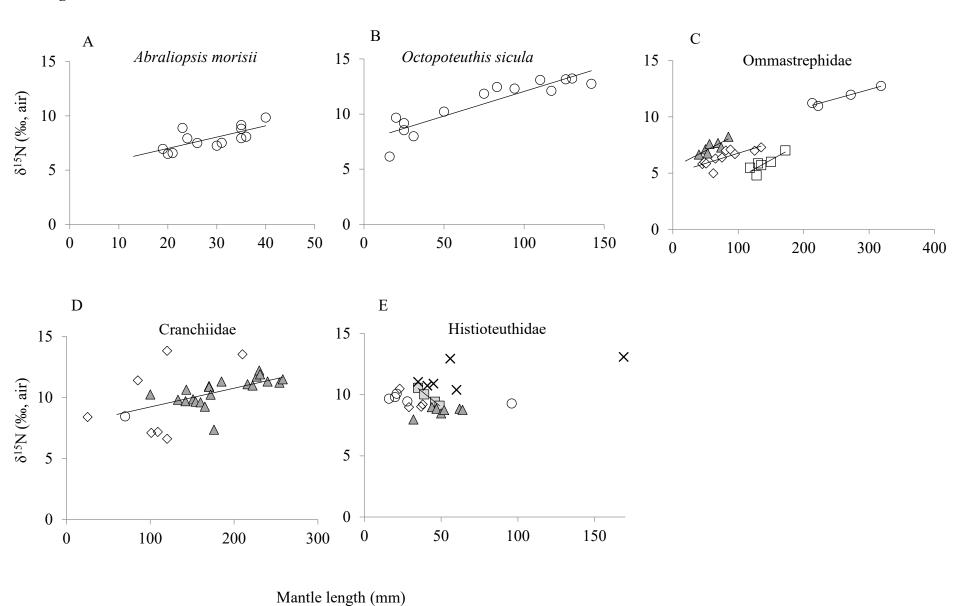


Figure 7



**Appendix 1:** Summary of midwater trawls conducted during the 2012 National Marine Fisheries Service biodiversity cruise (ID# PC1205) on the NOAA ship Pisces. Latitude and longitude indicate the coordinates at which each tow began. \* indicates that the net did not deploy correctly on those tows; a maximum depth was not determined but specimens were collected.

Date	Depth / time of day	Bottom /midwater	Latitude	Longitude	Maximum depth of net (m)
8/30/2012	Shallow / day	Midwater	39.94	-67.28	602
8/30/2012	Deep / day	Midwater	39.94	-67.28	1,921
8/31/2012	Shallow / night	Midwater	39.92	-67.27	688
8/31/2012	Shallow / night	Midwater	39.93	-67.25	1,220
8/31/2012	•	Midwater	39.93	-67.23 -67.41	969
	Shallow / day				
8/31/2012	Deep / day	Midwater	39.78	-67.43	1,520
9/1/2012	Shallow / night	Midwater	39.75	-67.45	802
9/1/2012	Deep / night	Midwater	39.74	-67.48	1,066
9/1/2012	Shallow / day	Midwater	39.90	-67.61	614
9/1/2012	Deep / day	Midwater	39.93	-67.71	1,290
9/2/2012	Shallow / night	Midwater	39.91	-67.62	750
9/2/2012	Deep / night	Midwater	39.96	-67.57	1,313
9/2/2012	Shallow / day	Midwater	40.04	-67.48	964
9/2/2012	Deep / day	Midwater	40.11	-67.42	1,354
9/3/2012	Shallow / night	Midwater	40.05	-67.47	870
9/3/2012	Deep / night	Midwater	40.08	-67.38	1,332
9/3/2012	Deep / day	Bottom	39.95	-67.46	*
9/3/2012	Deep / day	Bottom	39.95	-67.46	1,297
9/4/2012	Shallow / day	Midwater	39.95	-67.46	790
9/4/2012	Deep / day	Midwater	39.95	-67.58	1,461
9/5/2012	Shallow / night	Midwater	39.93	-67.44	*
9/5/2012	Shallow / night	Midwater	39.95	-67.45	1,052
9/5/2012	Shallow / day	Midwater	39.94	-67.40	1,000
9/6/2012	Deep / night	Midwater	39.74	-67.49	1,217
9/6/2012	Deep / night	Midwater	39.80	-67.51	1,314
9/6/2012	Deep / day	Midwater	39.69	-67.57	1,447
9/6/2012	Deep / day	Midwater	39.79	-67.54	1,446
9/7/2012	Deep / night	Midwater	39.78	-67.53	1,525
9/7/2012	Deep / night	Midwater	39.76	-67.50	1,788

Appendix 2: Density plot showing the confidence intervals of the standard ellipse areas. Black round points correspond to the mean standard ellipse area, red square points to the SEAc, and gray shaded boxed areas reflect the 9%5, 75%, and 50% confidence intervals from lightest to darkest, respectively. Cephalopod families are ordered from smallest to largest SEAc values and correspond to Table 5: Joubiniteuthidae (JOUB), Onychoteuthidae (ONY), Vampyroteuthidae (VAMP), Argonautoidea (ARG), Enoploteuthidae (ENO), Mastigoteuthidae (MAST), Histioteuthidae (HIST), Chiroteuthidae (CHIR), Octopoteuthidae (OCT), Cranchiidae (CRA), Ommastrephidae (OMM).

