TEXT S1

1. Trophic position estimation

Stable isotope techniques can provide an estimation of the trophic position (TP) of an organism to better understand the links between their diet, ecological processes, energy pathways, predation, and competition within the ecosystem (Post 2002). Compound-specific isotope analysis of amino acids (CSIA-AA) is a powerful tool to estimate the TP of organisms while avoiding some of the pitfalls of TP estimated from bulk stable isotope analysis (Chikaraishi et al. 2009). The most used equation to estimate the TP of a consumer is:

$$TP_{Tr\text{-}Sr} = [(\delta^{15}N_{Tr} - \delta^{15}N_{Sr} - \beta) / TDF] + 1$$

where $\delta^{15}N_{Tr}$ and $\delta^{15}N_{Sr}$ represent the nitrogen isotopic values of the trophic and source AA; β represents the difference between the $\delta^{15}N$ values of the trophic AA and the source AA in primary producers (trophic position = 1.0) and TDF (trophic discrimination factor) represents the offset in $\delta^{15}N$ values between the consumers and their diet.

However, uncertainties persist regarding the processes that drive variation in $\delta^{15}N_{AA}$ along the food web (Ramirez et al. 2021) and the universality of the approach (Chikaraishi et al. 2009, Bradley et al. 2015, Nielsen et al. 2015, McMahon & McCarthy 2016, Ramirez et al. 2021). The structure of the equation and the selection of appropriate AA and TDF values still lack consensus (McMahon & Newsome 2019). It is important to choose these factors carefully because TP estimates are highly sensitive to changes in β and TDF (although the relative influence of β values dissipates at higher trophic levels; Nielsen et al. 2015, Ramirez et al. 2021). Recent research indicates that TDF values are not universal, and their accuracy is influenced by the quality of the diet and form of nitrogen excretion (Germain et al. 2013, Nielsen et al. 2015, McMahon & McCarthy 2016). Additionally, there is noticeable variability in TDF values across trophic levels, with lower $TDF_{Glu\text{-}Phe}$ values typically observed in mammals and birds within marine food webs (Lorrain et al. 2009, Germain et al. 2013, McMahon et al. 2015a, Nielsen et al. 2015). Regarding the structure of the equation, recent publications suggest that accurate determination of TP using CSIA-AA necessitates the incorporation of multiple TDF values across trophic levels (Germain et al. 2013, McMahon et al. 2015b, McMahon & McCarthy 2016, Matthews et al. 2020). Additionally, it is still unclear which amino acid pairs are the most accurate in estimation of trophic levels (Chikaraishi et al. 2009). The most commonly used AAs for calculating TP are glutamic acid (Glu) as the trophic AA and phenylalanine (Phe) for the source AA (Chikaraishi et al. 2009). Glu undergoes significant fractionation, making it a robust indicator of trophic transfer. In contrast, Phe exhibit minimal fractionation, closely reflecting the $\delta^{15}N$ at the base of the food web (Chikaraishi et al. 2009, McMahon & McCarthy 2016). However, alternative amino acids have also shown potential for TP estimation in higher trophic level. Proline, for example, has demonstrated less variability in its TDF compared to Glu, making it also a good choice as a trophic AA (McMahon et al. 2015b). Moreover, studies on penguins and seals showed that proline was the most ^{15}N-enriched AA (while it is Glu in lower trophic level organisms) (Germain et al. 2013, Lorrain et al. 2015). Lysine (Lys) can also serve as a reliable source AA, as it undergoes minimal changes across trophic levels (Nielsen et al. 2015, McMahon & McCarthy 2016) and has been found to be the most suitable AA for estimating TP in tuna (Coletto et al. 2022).

Due to these factors, we calculated several seal TPs estimates using a combination of trophic and source AA, β, TDF_1 and TDF_2 (Table S2), with the multi-TDF equation (Germain et al. 2013, McMahon et al. 2019, Feddern et al. 2022) :

$$TP_{Tr\text{-}Sr} = [(\delta^{15}N_{Tr} - \delta^{15}N_{Sr} - TDF_2 - \beta) / TDF_1] + 2$$

where $\delta^{15}N_{Tr}$ and $\delta^{15}N_{Sr}$ represent the nitrogen isotopic values of the trophic and source AA in the consumer; TDF_1 represents the trophic discrimination for lower trophic levels (Table S2), TDF_2 represents the $TDF_{Tr\text{-}Sr}$ for higher trophic levels (Table S2) and β is the difference between the $\delta^{15}N$ values of trophic and source AA in primary producers (Table S2). Borrell et al. (2012) suggested that TDFs remain relatively consistent among taxonomically closely related species, thus we selected the TDF values from Harbour seal (*Phoca vitulina*; Germain et al. 2013) due to the absence of a species-specific TDF for the Antarctic fur seal (*Arctocephalus gazella*; AFS). While the $TDF_{Glu\text{-}Phe}$ is explicitly cited in the manuscript, we derived additional TDFs using the $\delta^{15}N$ serum values from this publication (Table S2). These were calculated using the following equation:

$$TDF_{Tr\text{-}Sr} = \Delta^{15}N_{Tr} - \Delta^{15}N_{Sr} = (\delta^{15}N_{Tr,HarbourSeal} - \delta^{15}N_{Tr,Fish}) - (\delta^{15}N_{Sr,HarbourSeal} - \delta^{15}N_{Sr,Fish})$$

We also calculated the average TP ($TP_{Average}$) using the weighted mean $\delta^{15}N$ values of trophic (Ala, Val, Asx, Leu, Glu, Pro) and source (Phe, Lys) AAs, with the equation (McMahon & Newsome 2019, Coletto et al. 2022):

$$TP_{Tr\text{-}Sr} = [(\delta^{15}N_{Tr\_average} - \delta^{15}N_{Sr\_average} - \beta_{Tr\_average - Sr\_average}) / TDF] + 1$$

where $\delta^{15}N_{Tr\_average}$ and $\delta^{15}N_{Sr\_average}$ represent the average stable nitrogen isotope values of trophic AAs and source AAs, respectively; $\beta_{Tr\_average - Sr\_average}$ represents the difference in average $\delta^{15}N$ between trophic AAs and source AAs of marine primary producers (3.0 ± 1.0 ‰ for non-vascular marine autotrophs; Ramirez et al. 2021), and $TDF_{Avg\text{-}TrAA - Avg\text{-}SrAA}$ represents the average TDF for marine consumers (3.4 ‰; McMahon & McCarthy 2016).

Following the recommendation from Ramirez et al. (2021), we employed the *propagate* package in R to propagate the error associated with each factor value used in the TP calculations to enhance the accuracy of TP estimation. We included analytical (using standard deviation from the replicates) and methodological error (standard deviation of β and TDFs).

Our findings revealed similar patterns in AFS TPs across the three colonies, with Marion Island showing higher TP values than Cape Shirreff, and Cape Shirreff having higher TP values than Bird Island (Figure S2). TP estimates using the Leu-Phe trophic-source AA pair were the more realistic (3.0 < TP < 5.3), given that, as secondary and tertiary consumers (depending on their diet), it is ecologically impossible for AFS to have a TP < 3.0. Moreover, Marion Island summer average $TP_{Leu\text{-}Phe}$ estimation (4.7 in summer and 4.8 in winter) is close to TP_{bulk} estimated for female AFSs from the Kerguelen Islands (4.8 ± 0.1; Cherel et al.

2010), which have a similar diet, and forage within the same ocean basin. As a result, we decided to include the $TDF_{Leu\text{-}Phe}$ in the manuscript, along the commonly used $TDF_{Glx\text{-}Phe}$.

2. Complementary information on $\delta^{15}N_{bulk}$ and $\delta^{13}C_{bulk}$ values

The $\delta^{15}N_{bulk}$ values ranged between 7.4 and 13.3 ‰, while the $\delta^{13}C_{bulk}$ values ranged between -24.5 and -18.6 ‰ across all colonies and seasons (Fig. S1). Bulk $\delta^{13}C_{bulk}$ values varied between the three regions and seasons (Table 1; Fig. S1). In summer, $\delta^{13}C_{bulk}$ values were significantly higher for Bird Island compared to the two other colonies (Tukey HSD, p-value <0.001), and higher for Marion Island compared to Cape Shirreff (Tukey HSD, p-value < 0.0001). Cape Shirreff $\delta^{13}C_{bulk}$ values were significantly higher than Marion Island in winter (Tukey HSD, p-value = 0.0329; Table 1, Table S4). Within location comparison between seasons in $\delta^{13}C_{bulk}$ values revealed no significant differences for Bird Island, higher values in winter for Cape Shirreff (Tuckey, p<0.0001) and higher values in summer for Marion Island (Tukey, p=0.000488). Two outlier values were observed among females from Bird Island, with higher $\delta^{15}N_{bulk}$ and $\delta^{13}C_{bulk}$ values compared to the rest of the population. Tracking data revealed that those females are foraging at lower latitudes, over the Patagonian shelf break. This neritic region is known for exhibiting higher $\delta^{15}N_{baseline}$ values (Espinasse et al. 2019, St John Glew et al. 2021).

The difference in $\delta^{13}C_{bulk}$ values in summer can be linked to their restricted foraging habitat at this time, as female AFSs take regular foraging trips close to their colony during the breeding season to take care of their pups (Boyd et al. 1998, Wege et al. 2019, Borrás-Chávez 2020), the values reflecting the large latitudinal difference in colonies. In winter, the overlap in bulk $\delta^{13}C$ values reflected the extensive movements of females, as they integrate isotopic values across multiple oceanic fronts, resulting in similar $\delta^{13}C_{bulk}$ values (Table 1, Fig. S3).

3. Complimentary information on $\delta^{15}N$ values of amino acids

We measured $\delta^{15}N_{AA}$ from 11 AAs, aligning with findings from prior CSIA-AA studies on Southern Ocean pinnipeds, including the Weddell (*Leptonychotes weddellii*), crabeater (*Lobodon carcinophaga*), Ross (*Ommatophoca rossii*; Brault et al. 2019) and the southern elephant seal (*Mirounga leonina*; Lübcker et al. 2020).

Serine (Ser) and glycine (Gly) are challenging AAs to classify (McMahon & McCarthy 2016, McMahon & Newsome 2019), and our results confirmed their complex patterns. Serine was the only AA with $\delta^{15}N$ values that did not differ between basins in summer, however, it was one of only a few AAs with Lys and Thr that displayed basin-specific discrimination during the winter months (Table S5). In the past, Ser and Gly were classified as source AAs, but they are now categorized as “trophic/source” because of their substantial variation in $\delta^{15}N$ depending on the consumer. The differences observed between $\delta^{15}N_{Gly}$ and $\delta^{15}N_{Ser}$ values can be attributed to $\delta^{15}N_{Gly}$ being more affected by microbial activity (McCarthy et al. 2007, Calleja et al. 2013). Further studies are required to better understand the metabolism and isotopic discrimination patterns of these particular AAs in the context of animal movement and foraging ecology (McMahon et al. 2013, Nielsen et al. 2015). No differences between years were detected for source AA ($\delta^{15}N_{Phe}$ and $\delta^{15}N_{Lys}$) within each colony.

Among all the trophic AAs, Asx exhibited the lowest $\delta^{15}N$ values, a pattern similarly observed in Weddell (*Leptonychotes weddellii*), crabeater (*Lobodon carcinophaga*), Ross (*Ommatophoca rossii*; Brault et al. 2019) and southern elephant seals (*Mirounga leonina*; Lübcker et al. 2020).

Values in $\delta^{15}N_{Thr}$ showed negative fractionation, with values decreasing with each trophic level rather than increasing. The biomolecular mechanism leading to this pattern remains unclear, but it may potentially be related to transamination processes (Whiteman et al. 2019), or its role at an organismal rather than cellular level (Wallace & Hedges 2016). Our findings align with recent publications categorizing Thr as a “metabolic” amino acid (O'Connell 2017, Lübcker et al. 2020), diverging from the previous classification as a “source” amino acid (Nielsen et al. 2015).

Table S1. Number of whole blood samples from adult female Antarctic fur seals analysed per colony, season and year.

Site	Summer			Winter		
	2008	2009	2010	2008	2009	2010
Bird Island	11	11	19	0	8	0
Cape Shirreff	0	0	12	7	10	9
Marion Island	9	4	8	9	6	4

Table S2. Trophic Discrimination Factor (TDF) and β used for Trophic Position (TP) estimations from compound specific stable isotope analysis, with phenylalanine (Phe) or lysine (Lys) as the 'source' amino acid, and alanine (Ala), Aspartic acid (Asx), glutamic acid (Glx), leucine (Leu), proline (Pro) or Valine (Val) as the 'trophic' amino acid.

	β[1]	TDF_1 [1]	TDF_2 [2]
TP Ala/Phe	2.8 ± 2.2 ‰	6.8 ± 2.2 ‰	2.5 ± 2.9 ‰
TP Asp/Phe	1.8 ± 2.9 ‰	5.4 ± 1.8 ‰	3.5 ± 1.8 ‰
TP Glx/Phe	2.9 ± 2 ‰	6.3 ± 0.4 ‰	3.5 ± 2.4 ‰
TP Leu/Phe	1.1 ± 2.5 ‰	5.7 ± 1.9 ‰	1.9 ± 3.2 ‰
TP Pro/Phe	2.7 ± 2.1 ‰	5.0 ± 1.8 ‰	5.5 ± 3.4 ‰
TP Val/Phe	3.4 ± 2.9 ‰	4.6 ± 3.4 ‰	7.5 ± 3.7 ‰
TP Ala/Lys	4.5 ± 4.5 ‰	6.0 ± 2.2 ‰	0.1 ± 2.7 ‰
TP Asp/Lys	4.6 ± 3.2 ‰	3.2 ± 1.6 ‰	1.1 ± 3.8 ‰
TP Glx/Lys	4.5 ± 3.3 ‰	4.9 ± 1.7 ‰	1.0 ± 3.7 ‰
TP Leu/Lys	2.0 ± 2.4 ‰	4.8 ± 2.2 ‰	-0.5 ± 3.2 ‰
TP Pro/Lys	4.5 ± 3.5 ‰	3.2 ± 2.0 ‰	3.0 ± 3.6 ‰
TP Val/Lys	5.0 ± 3.9 ‰	1.9 ± 3.8 ‰	5.0 ± 4.2 ‰
TP average	3.0 ± 1.0 ‰	3.4 ± 1.7 ‰	na

[1]Nielsen et al. (2015),
[2] Germain et al. (2013)

Table S3. Comparative trophic position (TP) estimations (mean, standard deviation, minimum and maximum) from various trophic and source amino acid combinations, with phenylalanine (Phe) or lysine (Lys) as the 'source' amino acid, and alanine (Ala), Aspartic acid (Asx), glutamic acid (Glx), leucine (Leu), proline (Pro) or Valine (Val) as the 'trophic' amino acid.

	Trophic position estimations		
	Mean ± sd	Min	Max
TP Ala/Phe	3.7 ± 0.5	2.6	4.6
TP Asp/Phe	3.6 ± 0.4	2.8	4.3
TP Glx/Phe	3.7 ± 0.5	2.7	4.7
TP Leu/Phe	4.2 ± 0.6	3.0	5.3
TP Pro/Phe	3.5 ± 1.1	1.1	5.3
TP Val/Phe	3.2 ± 0.7	2.0	5.6
TP Ala/Lys	4.1 ± 0.6	2.6	5.3
TP Asp/Lys	4.7 ± 0.9	3.0	7.1
TP Glx/Lys	4.5 ± 0.8	2.7	6.1
TP Leu/Lys	5.1 ± 0.8	3.2	7.0
TP Pro/Lys	4.8 ± 1.7	0.9	7.6
TP Val/Lys	5.6 ± 2.2	0.7	12.1
TP average	4.8 ± 0.9	2.9	6.6

Table S4. Results of linear mixed models (LMM) on bulk $\delta^{15}N$ ($\delta^{15}N_{bulk}$), $\delta^{13}C$ ($\delta^{13}C_{bulk}$), trophic position (TP) and relative trophic position (RTP). Models are presented as follows: Response Variable ~ Fixed Factors + (Random Factor). Fixed factors: season = summer or winter; site = Bird Island or Cape Shirreff or Marion Island. Random factor: year = 2008, 2009 or 2010.

BULK SIA			
Spatial variability (within a season)			
	Variable	**Model**	**p-values**
Summer	$\delta^{15}N$	~ 1 + colony + (1 | year)	MI>BI (p<0.0001); MI>CS (p<0.0001)
	$\delta^{13}C$	~ 1 + colony + (1 | year)	BI>MI (p=0.000128); BI>CS (p<0.0001); MI>CS (p<0.0001)
Winter	$\delta^{15}N$	~ 1 + colony + (1 | year)	-
	$\delta^{13}C$	~ 1 + colony + (1 | year)	CS>MI (p=0.00329)
Seasonnal variability (within a colony)			
Bird Island	$\delta^{15}N$	~ 1 + season + (1 | year)	Winter > Summer (p=0.0335)
	$\delta^{13}C$	~ 1 + season + (1 | year)	-
Cape Shirreff	$\delta^{15}N$	~ 1 + season + (1 | year)	Winter > Summer (p<0.0001)
	$\delta^{13}C$	~ 1 + season + (1 | year)	Winter > Summer (p<0.0001)
Marion Island	$\delta^{15}N$	~ 1 + season + (1 | year)	-
	$\delta^{13}C$	~ 1 + season + (1 | year)	Summer > Winter (p=0.000488)
TROPHIC POSITION ESTIMATION AND RELATIVE TROPHIC POSITION			
Spatial variability (within a season)			
	Variable	**Model**	**p-values**
Summer	$TP_{Glx-Phe}$	~ 1 + colony + (1 | year)	MI>BI (p<0.0001); MI>CS (p<0.0001); CS>BI (p=0.0158)
	$TP_{Leu-Phe}$	~ 1 + colony + (1 | year)	MI>BI (p<0.0001); MI>CS (p<0.0001); CS>BI (p<0.0001)
	$TP_{Average}$	~ 1 + colony + (1 | year)	MI>BI (p<0.0001); MI>CS (p<0.0001); CS>BI (p=000437)
	$RTP_{Glx-Phe}$	~ 1 + colony + (1 | year)	MI>BI (p<0.0001); MI>CS (p<0.0001); CS>BI (p=0.00146)
	$RTP_{Leu-Phe}$	~ 1 + colony + (1 | year)	MI>BI (p<0.0001); MI>CS (p<0.0001); CS>BI (p<0.0001)
Winter	$TP_{Glx-Phe}$	~ 1 + colony + (1 | year)	MI>BI (p=0.00599); MI>CS (p=0.04150)
	$TP_{Leu-Phe}$	~ 1 + colony + (1 | year)	MI>BI (p<0.0001); CS>BI (0.00185)
	$TP_{Average}$	~ 1 + colony + (1 | year)	MI>BI (p=00111); CS>BI (0.03813)
	$RTP_{Glx-Phe}$	~ 1 + colony + (1 | year)	MI>BI (p=0.0599); MI>CS (p=0.04154)
	$RTP_{Leu-Phe}$	~ 1 + colony + (1 | year)	MI>BI (p<0.0001); CS>BI (0.00185)
Seasonnal variability (within a colony)			
Bird Island	$TP_{Glx-Phe}$	~ 1 + season + (1 | year)	Winter > Summer (p<0.0001)
	$TP_{Leu-Phe}$	~ 1 + season + (1 | year)	Winter > Summer (p<0.0001)
	$TP_{Average}$	~ 1 + season + (1 | year)	Winter > Summer (p=0.000384)
	$RTP_{Glx-Phe}$	~ 1 + season + (1 | year)	Winter > Summer (p<0.0001)
	$RTP_{Leu-Phe}$	~ 1 + season + (1 | year)	Winter > Summer (p<0.0001)
Cape Shirreff	$TP_{Glx-Phe}$	~ 1 + season + (1 | year)	Winter > Summer (p<0.0001)
	$TP_{Leu-Phe}$	~ 1 + season + (1 | year)	Winter > Summer (p<0.0001)
	$TP_{Average}$	~ 1 + season + (1 | year)	Winter > Summer (p=0.00064)
	$RTP_{Glx-Phe}$	~ 1 + season + (1 | year)	Winter > Summer (p<0.0001)
	$RTP_{Leu-Phe}$	~ 1 + season + (1 | year)	Winter > Summer (p<0.0001)
Marion Island	$TP_{Glx-Phe}$	~ 1 + season + (1 | year)	-
	$TP_{Leu-Phe}$	~ 1 + season + (1 | year)	-
	$TP_{Average}$	~ 1 + season + (1 | year)	-
	$RTP_{Glx-Phe}$	~ 1 + season + (1 | year)	-
	$RTP_{Leu-Phe}$	~ 1 + season + (1 | year)	-

Table S5. Results of linear mixed models (LMM) on $\delta^{15}N_{AA}$. Models are presented as follows: Response Variable ~ Fixed Factors + (Random Factor). Fixed factors: season = summer or winter; site= Bird Island or Cape Shirreff or Marion Island. Random factor: year 2008 or 2009 or 2010.

AMINO ACID $\delta^{15}N$			
Spatial variability (within a season)			
	Variable	**Model**	**p-values**
Summer	Ala	~ 1 + colony + (1 | year)	MI>BI (p<0.0001) ; MI>CS (p<0.000218)
	Val	~ 1 + colony + (1 | year)	MI>BI (p<0.0001) ; MI>CS (p=0.00104)
	Asx	~ 1 + colony + (1 | year)	MI>BI (p<0.0001) ; MI>CS (p<0.0001)
	Leu	~ 1 + colony + (1 | year)	MI>BI (p<0.0001) ; MI>CS (p<0.0001) ; CS>BI (p=0.0454)
	Glx	~ 1 + colony + (1 | year)	MI>BI (p<0.0001) ; MI>CS (p<0.0001)
	Pro	~ 1 + colony + (1 | year)	MI>BI (p<0.0001) ; MI>CS (p<0.00105)
	Ser	~ 1 + colony + (1 | year)	-
	Gly	~ 1 + colony + (1 | year)	MI>BI (p<0.0001) ; MI>CS (p=0.00686)
	Phe	~ 1 + colony + (1 | year)	MI>BI (p=0.0029)
	Lys	~ 1 + colony + (1 | year)	MI>BI (p=0.00838) ; MI>CS (p=0.02913)
	Thr	~ 1 + colony + (1 | year)	BI>CS (p<0.0001) ; BI>MI (p<0.0001) ; CS>MI (p=0.000139)
Winter	Ala	~ 1 + colony + (1 | year)	-
	Val	~ 1 + colony + (1 | year)	-
	Asx	~ 1 + colony + (1 | year)	-
	Leu	~ 1 + colony + (1 | year)	-
	Glx	~ 1 + colony + (1 | year)	-
	Pro	~ 1 + colony + (1 | year)	-
	Ser	~ 1 + colony + (1 | year)	BI>MI (p=0.007044); CS>MI (p=0.000326)
	Gly	~ 1 + colony + (1 | year)	-
	Phe	~ 1 + colony + (1 | year)	-
	Lys	~ 1 + colony + (1 | year)	BI>CS (p=0.0186); BI>MI (p=0.0160)
	Thr	~ 1 + colony + (1 | year)	BI>CS (p=0.00236) ; BI>MI (p<0.0001)
MANOVA	Ala, Val, Asp, Leu, GLX, Pro, Ser, Gly, Phe, Lys, Thr	~ colony*season*year	colony (p<0.0001); season (p<0.0001); year (p=0.0018058); colony:season (p=0.0007309); colony:year (p<0.0001); season:year (-)
Seasonal variability (within a colony)			
	Variable	**Model**	**p-values**
Bird Island	Ala	~1 + season + (1 | year)	Winter > summer (p=0.00178)
	Val	~1 + season + (1 | year)	Winter > summer (p=0.0017)
	Asx	~1 + season + (1 | year)	Winter > summer (p=0.002885)
	Leu	~1 + season + (1 | year)	Winter > summer (p=0.00118)
	Glx	~1 + season + (1 | year)	Winter > summer (p=0.000685)
	Pro	~1 + season + (1 | year)	Winter > summer (p=0.000303)
	Ser	~1 + season + (1 | year)	Winter > summer (p=0.000107)
	Gly	~1 + season + (1 | year)	-
	Phe	~1 + season + (1 | year)	-
	Lys	~1 + season + (1 | year)	Winter > summer (p=0.000568)
	Thr	~1 + season + (1 | year)	Summer > Winter (p=0.00156)
Cape Shirreff	Ala	~1 + season + (1 | year)	Winter > Summer (p=0.000625)
	Val	~1 + season + (1 | year)	Winter > Summer (p=0.000343)
	Asx	~1 + season + (1 | year)	Winter > Summer (p<0.0001)
	Leu	~1 + season + (1 | year)	Winter > Summer (p<0.0001)
	Glx	~1 + season + (1 | year)	Winter > Summer (p<0.0001)
	Pro	~1 + season + (1 | year)	Winter > Summer (p=0.000869)
	Ser	~1 + season + (1 | year)	Winter > Summer (p<0.0001)
	Gly	~1 + season + (1 | year)	Winter > Summer (p=0.0194)
	Phe	~1 + season + (1 | year)	Winter > Summer (p=0.0135)
	Lys	~1 + season + (1 | year)	Winter > Summer (p<0.0001)
	Thr	~1 + season + (1 | year)	Summer > Winter (p=0.000202)
Marion Island	Ala	~1 + season + (1 | year)	-
	Val	~1 + season + (1 | year)	-
	Asx	~1 + season + (1 | year)	-
	Leu	~1 + season + (1 | year)	-
	Glx	~1 + season + (1 | year)	-
	Pro	~1 + season + (1 | year)	-
	Ser	~1 + season + (1 | year)	-
	Gly	~1 + season + (1 | year)	-
	Phe	~1 + season + (1 | year)	-
	Lys	~1 + season + (1 | year)	-
	Thr	~1 + season + (1 | year)	-

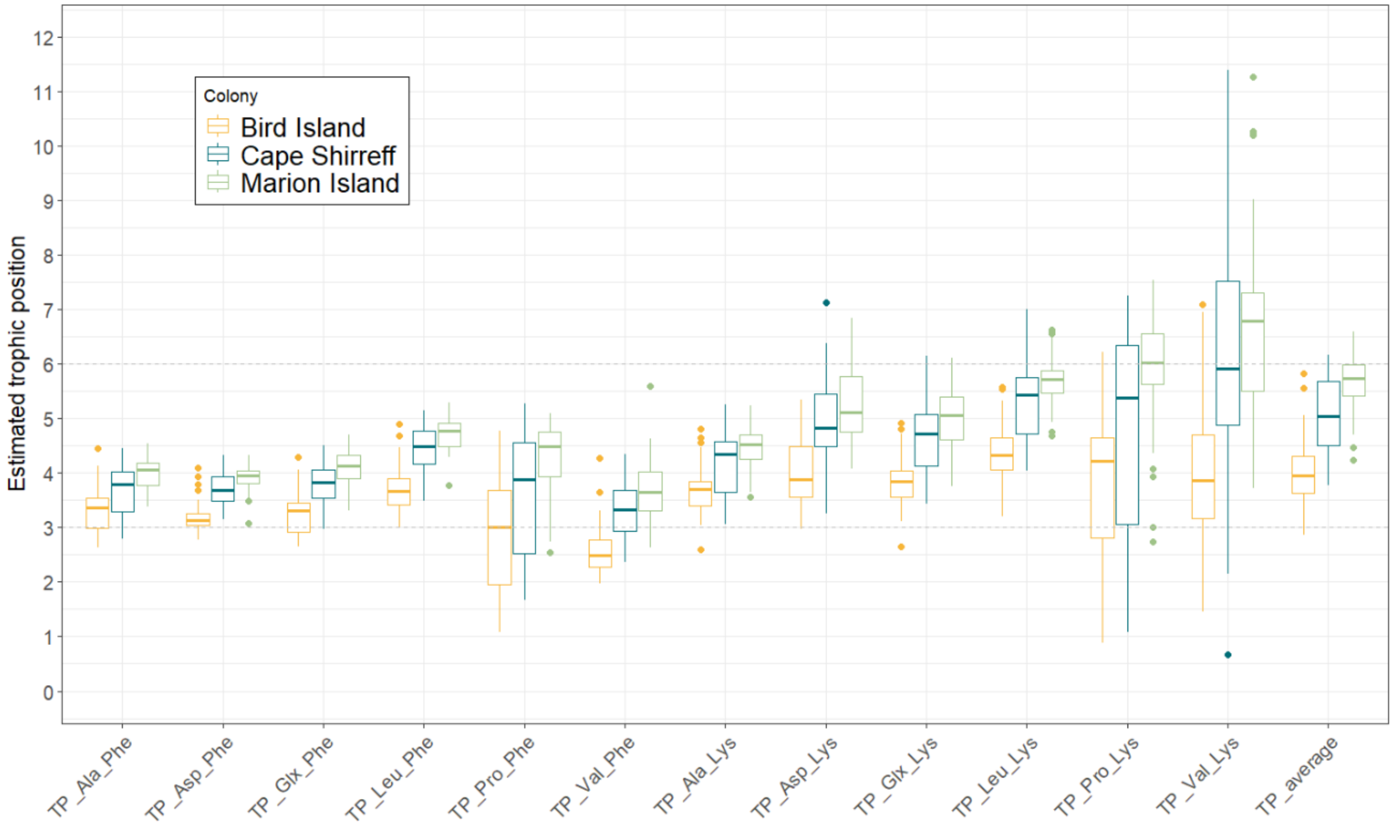

Figure S1. Comparison of the estimated trophic positions (TP) of adult female Antarctic fur seals *(Arctocephalus gazella)* using amino acid $\delta^{15}N$ values. Each colour represents a colony, yellow for Bird Island, blue for Cape Shirreff, and green for Marion Island. All TP estimations use a multiple TDF approach (except $TP_{average}$), with phenylalanine as the 'source' amino acid, and glutamic acid or proline as the 'trophic' amino acid. Dotted lines indicate the TPs that are ecologically plausible for this species.

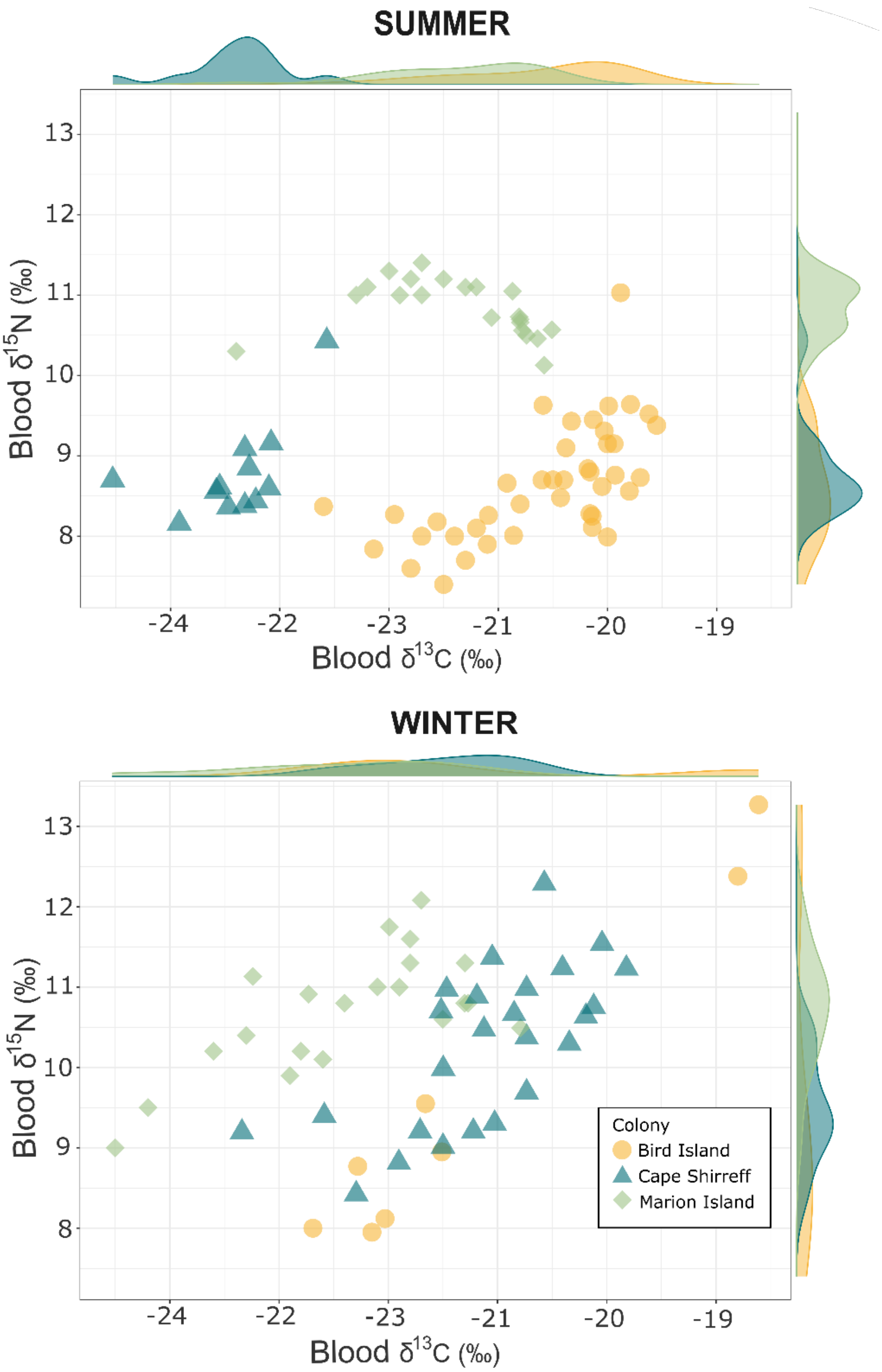

Figure S2. Inter-individual variations in bulk $\delta^{15}N$ and $\delta^{13}C$ values of whole blood from adult female Antarctic fur seals from three colonies: Bird Island, Cape Shirreff, and Marion Island. The colours represent the different colonies, yellow for Bird Island, blue for Cape Shirreff, and green for Marion Island

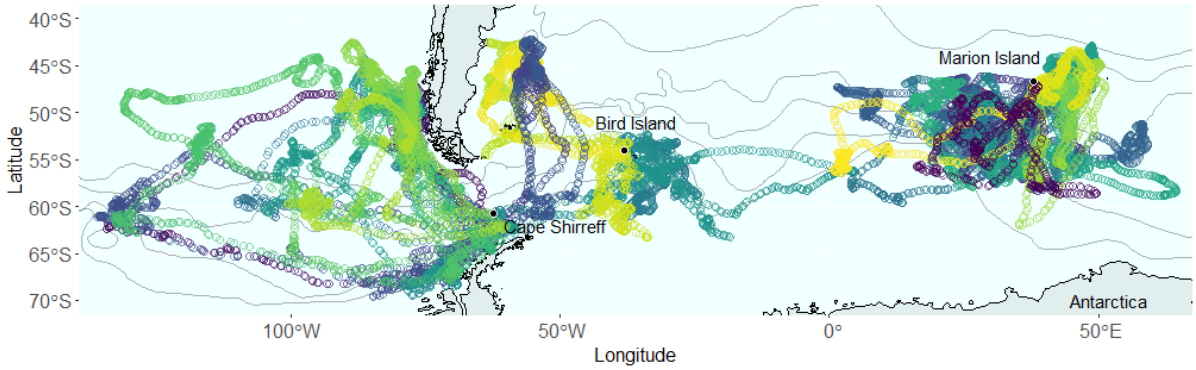

Figure S3. Tracks of adult female Antarctic fur seals from Bird Island, Cape Shirreff and Marion Island, from winter 2008 to 2010, modified from Arthur et al. (2017). Grey lines indicate the oceanic front revealed by SST gradient, from North to South: sub-Tropical Front; sub-Antarctic Front; Polar Front; Southern Antarctic Circumpolar Current Front; Southern Boundary of the Antarctic Circumpolar Current.

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