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2	Fatty acid profiles of feeding and fasting bears: Estimating calibration coefficients,
3	the timeframe of diet estimates, and selective mobilization during hibernation
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5	Gregory W. Thiemann*, Karyn D. Rode, Joy A. Erlenbach, Suzanne M. Budge, Charles
6	T. Robbins
7	
8	G.W. Thiemann: Faculty of Environmental and Urban Change, York University,
9	Toronto, ON Canada; ORCiD 0000-0002-1888-900X
10	K.D. Rode: US Geological Survey, Alaska Science Center, Anchorage, AK USA;
11	ORCiD 0000-0002-3328-8202
12	J.A. Erlenbach: School of Biological Sciences, Washington State University, Pullman,
13	WA USA; ORCiD 0000-0003-0347-3711. (Current address: Kodiak National Wildlife
14	Refuge, 1390 Buskin River Rd, Kodiak, AK USA)
15	S.M. Budge: Process Engineering and Applied Science, Dalhousie University, Halifax,
16	NS Canada; ORCiD 0000-0003-4984-7344
17	C.T. Robbins: School of the Environment and School of Biological Sciences,
18	Washington State University, Pullman, WA USA; ORCiD 0000-0003-1207-7745
19	
20	*Corresponding author. E-mail: thiemann@yorku.ca
21	RH: Fatty acid metabolism in brown bears

22 Abstract

23 Accurate information on diet composition is central to understanding and conserving 24 carnivore populations. Quantitative fatty acid signature analysis (QFASA) has emerged 25 as a powerful tool for estimating the diets of predators, but ambiguities remain about the 26 timeframe of QFASA estimates and the need to account for species-specific patterns of 27 metabolism. We conducted a series of feeding experiments with four juvenile male brown 28 bears (Ursus arctos) to (1) track the timing of changes in adipose tissue composition and 29 QFASA diet estimates in response to a change in diet and (2) quantify the relationship 30 between consumer and diet FA composition (i.e., determine "calibration coefficients"). 31 Bears were fed three compositionally distinct diets for 90-120 days each. Two marine-32 based diets were intended to approximate the lipid content and composition of the wild 33 diet of polar bears (U. maritimus). Bear adipose tissue composition changed quickly in 34 the direction of the diet and showed evidence of stabilization after 60 days. During 35 hibernation, FA profiles were initially stable but diet estimates after 10 weeks were 36 sensitive to calibration coefficients. Calibration coefficients derived from the marine-37 based diets were broadly similar to each other and to published values from marine-fed 38 mink (*Mustela vison*), which have been used as a model for free-ranging polar bears. For 39 growing bears on a high-fat diet, the temporal window for QFASA estimates was 30-90 40 days. Although our results reinforce the importance of accurate calibration, the 41 similarities across taxa and diets suggest it may be feasible to develop a generalized 42 QFASA approach for mammalian carnivores.

43



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62	

64 Introduction

65	The ability to locate and capture preferred prey is closely tied to the survival and
66	reproductive rates of top predators (Peterson et al. 1998; Fuller and Sievert 2001;
67	Chevallier et al. 2020). Climate warming, and other anthropogenic drivers of
68	environmental change, can disrupt patterns of prey abundance and availability with
69	negative consequences on predator population dynamics (Regehr et al. 2007; Northrup et
70	al. 2012). Accurate information on diet composition and patterns of prey selection is thus
71	central to understanding carnivore ecology and to the design and implementation of
72	effective conservation strategies (Sierro and Arlettaz 1997; Parrish et al. 2002).
73	A variety of methods have been developed to estimate the diet composition of
74	free-ranging predators, including direct observation (Stirling 1974), stomach and fecal
75	content analysis (Barnett et al. 2010; Klare et al. 2011) and, more recently, biochemical
76	tracer methods (Fry 2006; Budge et al. 2006). Quantitative fatty acid signature analysis
77	(QFASA) generates estimates of individual diets by comparing the fatty acid (FA)
78	composition of predator and prey (Iverson et al. 2004). QFASA has emerged as an
79	especially useful tool for estimating the diets of marine (Beck et al. 2007; Budge et al.
80	2012) and Arctic predators (Thiemann et al. 2008; Wang et al. 2010; Haynes et al. 2015),
81	because of the diversity of dietary FA and high lipid content of potential prey,
82	respectively.
83	Accuracy of QFASA is contingent on the use of appropriate calibration
84	coefficients (CCs) that account for FA-specific patterns of metabolism in the predator
85	(Meynier et al. 2010; Budge et al. 2012). CCs are calculated as simple ratios of the
86	abundance of a given FA in the tissue of the predator relative to the abundance in the diet,

87	after tissue-diet equilibration (Iverson et al. 2004). CCs can then be applied to either the
88	predator or prey FA data prior to running the QFASA model (Bromaghin et al. 2015).
89	Because metabolic patterns may be species-specific, and potentially influenced by the
90	gross composition of the diet (Rosen and Tollit 2012), a lack of accurate and appropriate
91	CCs can limit the utility of QFASA as an investigative tool. Bromaghin et al. (2017)
92	developed a model that allows for simultaneous estimation of both predator diet
93	composition and CCs using only predator and prey FA data, which may eliminate the
94	need for empirically derived CCs. However, a single set of CCs may not be appropriate
95	for all groups of predators in a population and a better understanding of the influence of
96	diet composition and nutritional status (i.e., whether an animal is gaining, losing, or
97	maintaining body mass) on CCs and diet estimates is needed to determine how estimated
98	CCs should be applied across groups of animals.
99	The temporal window of QFASA diet estimates also remains uncertain. Iverson et
100	al. (2004) assumed that the blubber of captive gray seals (Halichoerus grypus) reflected
101	diet consumed over the preceding 3-5 months. Budge et al. (2004) showed that
102	radiolabeled FA consumed in the diet were deposited in gray seal blubber within 12
103	hours. Adipose tissue thus represents an integration of recent and long-term diet and most
104	studies using QFASA assume that results reflect diet over a period of "weeks to months"
105	(Beck et al. 2005; Budge et al. 2006; Galicia et al. 2015; McKinney et al. 2017).
106	However, the ambiguity of this timeframe limits ecological insights.
107	The temporal window of QFASA estimates may also depend on the energy
108	balance of the individual. Although few studies have been conducted, the rate of FA
109	turnover in mammalian adipose tissue is likely correlated with the rate of lipid intake

(Anderson et al. 1972), but will also be affected by other physiological functions such as
growth and lactation (Foglia et al. 1994; Nordstrom et al. 2008). A fasting animal will
mobilize stored fat, but if that mobilization is selective (i.e., some FA are preferentially
mobilized or conserved; e.g., Florant et al. 1990; Hill and Florant 1999; Raclot 2003),

114 QFASA estimates may not accurately reflect integrated diet composition.

115 Polar bears (Ursus maritimus) are wide-ranging top predators that rely on annual 116 sea ice for access to their marine mammal prey (Stirling and McEwan 1975; Stirling and 117 Archibald 1977; Thiemann et al. 2008). Polar bear population dynamics have been 118 negatively affected by climate warming, primarily mediated by disruptions in prey 119 availability (Derocher et al. 2004; Regehr et al. 2007; Lunn et al. 2016; Pagano et al. 120 2018). Thus, accurate information on polar bear diet composition is central to 121 understanding the ecological effects of Arctic climate warming (McKinney et al. 2013; 122 Rode et al. 2014; Pilfold et al. 2015). Given the vast distribution and low density of polar 123 bear populations, as well as their high-fat, marine-based diet, QFASA has emerged as an 124 especially powerful tool in understanding polar bear foraging ecology (Iverson et al. 125 2006; Thiemann et al. 2008; Galicia et al. 2016; Bourque et al. 2020). Controlled feeding 126 studies of polar bears are often limited by small sample sizes and logistical constraints 127 associated with housing polar bears in zoos and aquaria (Rode et al. 2016). Thus, studies 128 of polar bears using QFASA have largely relied on data from model species, primarily 129 mink (*Mustela vison*), fed a known marine-based diet (Thiemann 2006; Galicia et al. 130 2015; McKinney et al. 2017). However, the validity of the mink model for polar bears 131 has rarely been tested (but see Bromaghin et al. 2017)

132 Brown bears (U. arctos) are biologically similar to polar bears in many respects, 133 owing to their close evolutionary relationship (Welch et al. 2014; Cahill et al. 2015, 134 2018). Where ecological circumstances allow, the two species may use shared resources 135 (Miller et al. 2006; Doupe et al. 2007; Barnas et al. 2020) and even interbreed (Pongracz 136 et al. 2017). Brown bears may therefore serve as a more appropriate model than mink for 137 understanding patterns of metabolism relevant to dietary analysis in polar bears. 138 We conducted a series of controlled feeding studies using 4 juvenile brown bears, 139 with the following objectives: (1) quantify the relationship between diet and predator FA 140 for bears on a diet nutritionally similar to that of wild polar bears; (2) develop CCs to 141 improve QFASA diet estimation for free-ranging bears; (3) estimate the timeframe for 142 QFASA derived diet estimates; (4) determine changes in FA profiles during 143 fasting/hibernation (e.g., selective mobilization or conservation of specific FA).

144

145 Materials and methods

146 *Captive feeding and fasting trials*

We conducted controlled feeding experiments using four juvenile male brown bears at the Washington State University Bear Research, Education, and Conservation Center. Juvenile bears in a dedicated research center allowed us to isolate the bears from alternative food items (i.e., plants) that are often present within the exhibits of captive bears and allowed us to obtain tissue samples at regular intervals, a sampling protocol that would not be compatible with the husbandry requirements of older bears or those in zoos.

154	Beginning in May 2011, all bears were fed the same series of three diets over two
155	years (Table 1). The Trial 1 diet consisted of dry dog food (Science Diet, Hill's Pet
156	Nutrition, Inc., Topeka, KS) enriched with calcium, vitamin E and minerals. The diets
157	used in Trials 2 and 3 were comprised of dry dog food supplemented with oil derived
158	from salmon (JEdwards International Inc., bulk wild Alaskan salmon oil) and anchovy
159	(Engraulis ringens; JEdwards International, Inc., omega-3 fish oil), respectively. Trial 4
160	was a fasting period during which bears were in hibernation. Trials 1 and 2 occurred in
161	year 1 when the males were first-year cubs (age 5 months at Trial 1 start) and Trials 3 and
162	4 occurred in year 2 when the males were yearlings (age 1.5 years at Trial 3 start). Oil-
163	supplemented diets were prepared in batches by homogenizing dog food pellets and
164	marine fish oil at a wet weight ratio of ca. 2:1. Marine fish oil accounted for 82% and
165	81% of the dietary lipid for Trials 2 and 3, respectively (Table 1). These diets were
166	constructed to approximate the lipid content and FA composition of the wild diet of polar
167	bears while meeting the animals' micronutrient requirements. Wild polar bears
168	preferentially consume the blubber of seals (Stirling 1974; Stirling and Archibald 1977),
169	and captive studies have suggested that polar bears will selectively consume up to 80%
170	blubber (unpublished data cited in Best 1985). Nevertheless, polar bears on the sea ice
171	also scavenge prey remains and will consume some seals almost entirely (Stirling and
172	Archibald 1977). It is thus difficult to estimate the lipid content of the typical wild diet.
173	We used a total lipid content of ca. 40% in Trials 2 and 3 because it was the maximum
174	achievable while still producing a homogenous mixture. The 3 different experimental
175	diets provided an opportunity to calculate CCs for diets with different FA profiles and
176	different lipid contents (Budge et al. 2020).

177	Bears were fed ad libitum during all trials. The bears were fed the Trial 1 diet for
178	90 days and then immediately switched to the Trial 2 diet for another 90 days. The
179	experiment was stopped, and bears were fed a mixed diet prior to winter hibernation.
180	Trial 3 was initiated when bears emerged from hibernation in spring 2012 and were fed
181	dog food supplemented with anchovy oil. Trial 3 lasted 120 days to increase the chances
182	bear FAs would equilibrate with the diet, after which bears were again fed a mixed diet
183	for 4 weeks prior to winter hibernation (Trial 4; see Table 1). All food was withdrawn at
184	the beginning of Trial 4, but bears had access to water ad libitum.

186 Sample collection

187 Diet samples were collected at the beginning of each feeding trial. One sample of 188 dog food was collected from each batch of homogenized pellets (one in 2011, two in 189 2012) and a sample of marine fish oil was collected from each barrel used (one for 190 salmon, two for anchovy). Bears were immobilized with Telazol (tiletamine HCl and 191 zolazepam HCl; Fort Dodge, IA) prior to collecting adipose tissue samples using a 6 mm 192 biopsy punch inserted through a small incision in the skin, approximately 15 cm lateral to 193 the base of the tail. We collected an adipose tissue biopsy from each bear 30-45 days after 194 the initiation of a feeding trial and at the beginning of the fasting/hibernation period in 195 2012. Sampling was repeated ca. every 2 weeks during feeding trials and every 21-65 196 days during hibernation. Final samples were collected at the end of each trial. Samples 197 were stored at -80°C until analysis. All sampling and handling procedures were reviewed 198 and approved by the Washington State University Institutional Animal Care and Use 199 Committee.

201 Laboratory analysis

202 Lipid was quantitatively extracted from adipose tissue biopsies and dog food 203 samples using 2:1 chloroform:methanol according to Folch et al. (1957) as modified by 204 Iverson et al. (2001). FA methyl esters (FAME) were prepared from lipid extracts and 205 dietary oil samples using H₂SO₄ as a catalyst (Budge et al. 2006) and analyzed in 206 duplicate on a Perkin Elmer Autosystem II Capillary gas chromatograph fitted with a 207 flame ionization detector and a flexible fused silica column (30 m x 0.25 mm ID) coated 208 with 50% cyanopropyl polysiloxane (0.25 µm film thickness; Agilent Technologies, DB-209 23; Palo Alto, CA, USA). We inspected each chromatogram manually and corrected any 210 erroneously identified peaks. FAs were measured as the mass percent of all FAs in the 211 extracted lipid sample and are described according to carbon chain length:number of 212 double bonds and location (n-x) of the first double bond relative to the terminal methyl 213 group.

214

215 Calibration coefficients and diet estimates

The FA composition of Trial 2 and 3 diets was calculated by combining the FA values of the dog food and marine fish oil samples according to their relative lipid contributions (Table 1). Direct measurement of the FA composition of combined dog food and fish oil was precluded by separation of lipid and non-lipid components in homogenized diet samples. We identified up to 70 FA in the samples, but some FA were present in only trace amounts. We therefore limited analyses to FA identified in at least one diet at > 0.1% of the total (as per Budge et al. 2012). This full FA set included 45 FAs that accounted for a mean of 98.9% (range: 98.2 to 99.5%) of total bear FA. The full
FA set was rescaled to sum to 100% across all diets and bears.

225 Calibration coefficients were calculated by dividing the percentage of a given FA 226 in each bear by the percentage of the same FA in the diet, averaged across all 4 bears 227 (Iverson et al. 2004). We used the final (i.e., day 90 or 120) FA value for each bear to 228 calculate CCs. Thus, we generated a separate set of CCs for each of the 3 experimental 229 diets. We also compared our results to two sets of CCs generated from studies of captive 230 mink; one set from mink fed a controlled diet supplemented with herring, seal oil or 231 poultry (n = 37, hereafter called "Mink (all)"), and another set using only those mink fed 232 herring or seal oil (n = 21, hereafter called "marine-fed mink"). Both mink sets have been 233 used previously to estimate the diets of polar bears (see Thiemann 2006 and Thiemann et 234 al. 2008 for details).

235 We used QFASA (Iverson et al. 2004) to generate diet estimates for each bear 236 every time they were sampled. Briefly, QFASA models the FA composition of a predator 237 as a linear mixture of potential prey signatures and estimates diet composition by 238 minimizing the distance between the observed and modeled predator, after applying CCs. 239 We used the Aitchison distance measure and generated estimates in the prey space (see 240 (Bromaghin et al. 2015). We could not use a single set of FA to estimate the diets of all 241 bears in the study because some FA were not present in one or more of the experimental 242 diets or the mink CC sets (Table 2). Therefore, diets of bears in Trial 1 were estimated 243 using the Full FA set, minus those FA < 0.1% in either the Trial 1 diet or Trial 1 bears, 244 yielding a set of 18 FA. For bears in Trials 2, 3, and 4, we used a modeling set of 22 FA 245 that was patterned after Florko et al.'s (2020) set of 29 FA, minus 7 FA that were not

246	present in our data set (i.e., < 0.1%; 16:2n-6, 16:4n-3, 16:4n-1, 18:3n-1, 20:3n-3, 22:1n-7,
247	22:4n-3). Although the choice of FA could potentially affect the performance of QFASA,
248	our goal was to develop CCs and test their performance under standardized conditions.
249	Other studies have found little difference in diet estimates generated from different FA
250	sets (Meynier et al. 2010; Wang et al. 2010). All QFASA estimates were generated in R
251	(version 4.0.0, The R Foundation for Statistical Computing, 2020) using the qfasar
252	package (Bromaghin 2017).
253	
254	Statistical analysis
255	To assess the accuracy of QFASA diet estimates, we calculated the sums of the
256	absolute differences between the actual and estimated proportions for each food type,
257	following the equation (Budge et al. 2012):
258	sum of differences = $(actual_{dog food} - estimated_{dog food})$
259	+ ($ actual_{salmon oil} - estimated_{salmon oil} $
260	+ ($ actual_{anchovy oil} - estimated_{anchovy oil} $)
261	We constructed a linear mixed model to assess the effect of CC set on the sum of
262	differences for final diet estimates, with CC as a fixed factor and Bear ID as a random
263	factor. We compared QFASA model outputs using CCs from all 3 feeding trials, plus the
264	two mink CC sets described above. The diet estimates for a given feeding trial that were
265	generated using CCs derived from that same trial were used as an idealized benchmark
266	against which other CC sets could be compared. We also used a linear mixed model to
267	investigate whether and how sums of differences changed over time, with sampling date
268	as a fixed factor and Bear ID as a random factor. We used quantile-quantile plots to

269	assess the normality of residuals and, where necessary, sums of differences were log
270	transformed to meet model assumptions. Parameter p-values were generated using Wald
271	tests and we used Tukey post-hoc contrasts to compare group means. All statistical
272	analyses were performed in R (version 4.0.0, The R Foundation for Statistical
273	Computing, 2020). We used the nlme package to construct linear mixed models and the
274	multcomp package to perform post hoc tests with statistical significance set at $\alpha = 0.05$.
275	
276	Results
277	Diet composition
278	The three experimental diets differed in their FA composition. The Trial 1 diet
279	was comprised of dog food (Table 1) and had 10.8% lipid (dry matter basis). The FA
280	composition was dominated by three FA: 16:0, 18:1n-9 and 18:2n-6 accounted for 80.3%
281	of total extractable lipid. The diet for Trial 2 was comprised of dog food supplemented
282	with salmon oil and although it had a similar ratio of
283	saturated:monounsaturated:polyunsaturated FA as Trial 1 (Table 2), its composition was
284	more balanced across FA (Fig 1). The diet used in Trial 3 was comprised of dog food
285	supplemented with anchovy oil and had the highest proportion of polyunsaturated FA,
286	which accounted for >40% of total lipid (Table 2).
287	
288	Changes in bear FA profiles during feeding and fasting
289	The relative abundance of most FA was stable over the course of Trial 1, which
290	reflects the fact that bears were fed dog food prior to the start of the trial. However, some
291	FA did show gradual change over Trial 1 (e.g., 16:1n-7, Fig S1), indicating de novo

synthesis or mobilization. Once switched to the Trial 2 diet, bear FA profiles changedrapidly in the direction of the new diet. The most rapid change occurred between day 1

and day 45, with more gradual change evident in subsequent samples. During Trial 3,

bear FA profiles again changed rapidly in response to the new diet, with large shifts in

FA occurring between day 1 and day 29, with more gradual changes thereafter and

297 evidence of stabilization after day 62 (Fig 2).

298 There was variability in FA patterns during hibernation (Trial 4). FA profiles were

299 generally stable during the first 3 weeks of hibernation, but beyond that some FA

300 increased (e.g., 18:1n-9), some decreased (e.g., 20:5n-3), while others remained stable

301 (e.g., 18:2n-6; see Table 3, Fig. 2). Of the 45 total FA, 20 decreased during hibernation

302 (mean change in % total FA: -0.39 ± 0.76 , range: -2.92 to -0.01) and 25 increased (mean

303 change in % total FA: 0.31 ± 0.73 , range: 0.003 to 3.66). The FA showing the largest

304 proportional changes (i.e., >52%) were only present in small amounts (i.e., <1% of total

305 FA). Of the FA accounting for >1% of total FA, 20:5n-3 showed the greatest proportional

306 change, declining by 51.5% over 140 days of hibernation (Table 3).

307

308 Calibration coefficients

309 Trial 1 yielded CC values for 38 FA, a smaller number than Trial 2 (45 FA) or

310 Trial 3 (44 FA) because of the more limited diversity of FA in the Trial 1 diet. Trial 1

311 CCs were generally comparable with Trial 2 and 3, with some exceptions (Fig 3). CC

312 values from Trials 1 and 2 were virtually identical for 16:1n-9, 18:0, 18:1n-11, and 20:0.

313 In contrast, the calibration for i-17:0 generated from Trial 1 was 37 times higher than the

314 value generated from Trial 2. Trial 1 CCs were consistently higher than either of the other

feeding trials for the long chain polyunsaturated FA 22:4n-6, 22:5n-6, 22:5n-3, and
22:6n-3.

317	CCs generated from Trials 2 and 3 were generally similar, again with some
318	exceptions. The largest difference was in the CC for 20:1n-11, which was more than 20
319	times larger from Trial 3 than from Trial 2. The CCs generated from captive brown bears
320	were also comparable to those generated from captive mink, also fed a marine based diet
321	(Fig 3), with a few exceptions. For example, the CC value for 18:1n-13 generated from
322	Trial 3 was 3.6 times larger than the marine-fed mink value, whereas the marine-fed mink
323	CC for 18:1n-11 was 3.8 times larger than the value from Trial 2.

324

325 *QFASA estimates across CC*

326 We used sums of differences between actual and estimated diets to assess the 327 accuracy of QFASA diet estimates generated at the end of each feeding trial. The CC set 328 used in QFASA modelling had a significant effect on the accuracy of diet estimates 329 (linear mixed model, Trial 1: $F_{5,15} = 314.2$, p < 0.001; Trial 2: $F_{4,12} = 229.0$, p < 0.001; Trial 3: $F_{4,12} = 49.4$, p < 0.001). The diet composition for bears at the end of Trial 1 was 330 331 most accurately estimated using Trial 3 CC (mean sum of diff: 0.012 ± 0.004); however, 332 Trial 1 final diets were well-estimated regardless of the CC used (Fig 4). The accuracy of 333 estimates using mink (all) did not differ from using no CC, but all other comparisons 334 were significantly different from each other (Tukey contrasts, all p < 0.001; Fig S2). The 335 diet composition for bears at the end of Trial 2 was most accurately estimated using Trial 336 2 CC (mean sum of diff: 0.080 ± 0.052) but did not differ significantly from the estimates using marine-fed mink CC (0.152 ± 0.110 ; p = 0.481; Fig 4). Sums of differences from 337

338	all other CC sets were significantly different from each other (Tukey contrasts $p < 0.001$;
339	Fig S2). The diet composition for bears at the end of Trial 3 was most accurately
340	estimated using Trial 3 CC (mean sum of diff: 0.040 ± 0.014). Marine-fed mink CCs
341	provided the second most accurate estimates (0.371 ± 0.131), although they were less
342	accurate than Trial 3 CC ($p < 0.001$) and were not significantly better than mink (all) CC
343	$(0.420 \pm 0.131; p = 1.000; Fig 4)$. There was also no difference in accuracy between mink
344	(all) and Trial 2 (0.545 \pm 0.181; p = 0.108). Sums of differences from all other CC sets
345	were significantly different from each other (Tukey contrasts $p < 0.01$; Fig S2).
346	
347	QFASA estimates across sampling day
348	We also used sums of differences to examine how the accuracy of QFASA diet
349	estimates changed as a function of sampling date, including diet estimates from
350	hibernating bears (Trial 4; see next section). Because marine-fed mink CCs produced the
351	second-most accurate estimates in Trials 2 and 3 (see above), we compared results across
352	sampling day using two sets of CCs for each trial: (1) CCs generated from that same trial
353	and (2) CCs from marine-fed mink (Fig 5).
354	For bears in Trial 1, QFASA estimates showed relatively little variation across
355	sampling day, regardless of which CC set was used (Fig 5 and 6). However, the accuracy
356	of QFASA estimates from Trial 1 CCs varied across sampling date ($F_{3,9}$ = 4.54, p =
357	0.033; Fig 6a), whereas those from marine-fed mink CCs did not ($F_{3,9} = 0.85$, p = 0.499;
358	Fig 6c). For Trial 1 CCs, QFASA accuracy was lower (i.e., sum of differences was
359	higher, Fig S3) on day 45 than on day 75 (Tukey contrasts $p = 0.006$) or day 89 (d =

360 0.017). Sums of differences did not differ among any other sampling days (p > 0.05; Fig
361 S3).

362	Bears in Trial 2 received their new diet immediately after Trial 1, and diet
363	estimates responded with a rapid change between day 1 and day 45. More gradual change
364	was evident beyond day 45, a pattern that was consistent across both CC sets (Fig 5).
365	Likewise, the accuracy of QFASA estimates improved by day 45 (Fig 6), with sampling
366	day having a significant effect on sums of differences for both Trial 2 CC ($F_{3,9}$ = 323.7, p
367	< 0.001) and marine-fed mink CC ($F_{3,9} = 187.0$, p < 0.001). For both CC sets, there was
368	no difference in accuracy between day 75 and 95 (Tukey contrasts $p > 0.50$). All other
369	comparisons were significant ($p < 0.05$; Fig S3).

370 The Trial 3 diet was given to the bears following winter hibernation and an 371 interim recovery period during which they were fed dog food and allowed to graze on 372 vegetation. Thus, diet estimates changed rapidly in response to the new dog food/anchovy 373 oil diet (Fig 5) and became more accurate (Fig 6) as the trial progressed from day 1 and 374 day 29. Sampling day had a significant effect on sums of differences for both Trial 3 CC 375 $(F_{6,18} = 174.6, p < 0.001)$ and marine-fed mink CC $(F_{6,18} = 61.57, p < 0.001; Fig 6)$. The 376 accuracy of day 1 diet estimates was significantly worse than all subsequent sampling 377 days (Tukey contrasts p < 0.001). Accuracy improved beyond day 29, with significant 378 differences between day 29 and day 75 and beyond (Tukey contrasts p < 0.002). 379 Accuracy on day 62 was lower than day 120 (p = 0.039) when using marine-fed mink 380 CCs. No differences in accuracy were evident beyond day 75 with either set of CCs (p >381 0.767; Fig S3).

QFASA estimates during hibernation

384	Trial 4 began when bears entered hibernation, following a 4-week interim period
385	after Trial 3. We used the Trial 3 diet as a benchmark to detect changes in sums of
386	differences because it was the last known diet consumed prior to hibernation. Trial 4 diet
387	estimates generated using Trial 3 CC showed only slight changes over time, although
388	more change was evident when we used marine-fed mink CC (Fig 5). Using marine-fed
389	mink CCs, the estimated contribution of anchovy oil declined 14.7% (from 71.3% to
390	56.6%) over the 140-day period, whereas estimated dog food and salmon oil
391	contributions increased 3.0% and 11.7%, respectively (Fig 5). These patterns were
392	reflected in sums of differences, which were not affected by sampling day when Trial 3
393	CC were used ($F_{4,12} = 1.568$, p = 0.245) but did change over time when we used marine-
394	fed mink CC ($F_{4,12}$ = 10.270, p < 0.001; Fig 6). In the latter case, accuracy declined
395	significantly on the final sampling day, with differences between day 318 and all 4 earlier
396	samples (Tukey contrasts $p < 0.040$; Fig S3).
397	
398	Discussion
399	Information on diet composition is fundamental to understanding animal ecology.
400	Recent and emerging methods of predator diet estimation, including FA and stable
401	isotope analyses, are premised on a predictable and quantifiable relationship between the
402	biochemical composition of a predator's tissue and that of its composite diet. However,
403	these biochemical relationships may be complex and are poorly understood in many taxa.
404	Our results directly address this knowledge gap and provide a response to calls in the

405	literature for additional experimental studies to improve the accuracy and utility of
406	nutrient-tracking approaches to estimating predator diets (e.g., Bowen and Iverson 2013).
407	This study provides direct estimates of the timeframe represented by FA-based
408	diet estimates in a terrestrial carnivore. Ambiguity about the timeframe of FA turnover
409	has limited the ecological interpretation of QFASA diet estimates. Thus, our results will
410	improve the utility of QFASA as an ecological tool. Our controlled diets were designed to
411	mimic the lipid content and composition of polar bear diets to the degree possible, so our
412	results are most relevant to polar bears, but are also applicable to wild brown bears
413	feeding on marine-based foods (e.g., spawning salmon).
414	The Trial 1 diet was compositionally simple and largely consistent with the
415	maintenance diet the bears received after weaning and prior to the start of the experiment.
416	Consequently, the bears' FA profiles did not noticeably change over the course of Trial 1.
417	QFASA diet estimates were similarly consistent during Trial 1 and estimates were highly
418	accurate, regardless of sampling day or the CC used. The high accuracy was likely
419	influenced by the simple "prey library" (Budge et al. 2006; Bromaghin 2017) of only
420	three potential foods. The clear difference between the compositionally simple dog food
421	(i.e., dominated by ca. six FA) and the two more complex fish oils (Fig. 1) presumably
422	reduced the potential for confounding prey types. However, the similarity of the two fish
423	oils may have impaired diet estimates, as discussed below.
424	When bears were started on a new diet (i.e., Trial 2 and 3), their FA profiles
425	abruptly shifted in the direction of the new diet. Some FAs were more variable across
426	individual bears, as reflected in differences in SD (Table 2), but individual variability was
427	generally low. With only four bears in this study, our sample size was small (a common

428 limitation of large-carnivore experiments); however, the limited individual variation 429 suggests that a larger sample size would not have substantively altered our results. The 430 relationship between bear and diet FA was variable across diets (Fig 2), as reflected in 431 differences in CC values across feeding trials (Fig 3). For some FA (e.g., 18:2n-6, 22:1n-432 11; Fig 2), bears had values that were higher or lower than their composite diet, 433 depending on the feeding trial. For instance, 22:1n-11 had a Trial 2 CC value of 0.38 (i.e., 434 the FA was higher in the diet than in the bears) but a Trial 3 CC value of 2.42 in (i.e., the 435 FA was higher in the bears than in the diet; Table 2). 436 In Trials 2 and 3, CCs had an important effect on QFASA diet estimates (Fig 4) 437 and our study adds to existing evidence that CCs are to some extent diet-specific. For 438 instance, the diets of bears in Trial 2 were not accurately estimated using CCs from Trial 439 3 (Fig 4), even though they were the same bears with some common dietary components 440 (i.e., dog food was present in both diets). In fact, Trial 3 CCs produced the worst 441 estimates of Trial 2 diet among the five CC sets we compared. Differences in CC values 442 for some FA in Trials 2 and 3 (e.g., 22:1n-11, see above) could have contributed to the 443 reduced accuracy of diet estimates compared to the marine-fed mink CCs. The similarity 444 of the fish oil components in the Trial 2 and Trial 3 diets may also have contributed to the 445 poor performance of Trial 3 CCs in estimating the diets of Trial 2 bears. The dog food 446 component of the diet was relatively accurately estimated by all CC sets aside from mink 447 (all) and none. The Trial 3 CC set had difficulty resolving the two types of fish oil, which 448 suggests the anchovy oil used in Trial 3 predisposed the Trial 3 CCs to estimate that 449 dietary component. Similarly, the Trial 2 CCs led to misallocation of Trial 3 diets to 450 salmon oil.

451	Given apparent differences among CC sets derived from different diets, the
452	numerical (Fig 3) and functional (Fig 4) similarity between CCs derived from marine-fed
453	mink (Iverson et al. 2004, Thiemann 2006, Thiemann et al. 2008) and the CCs derived
454	from Trials 2 and 3 was surprising. Marine-fed mink CCs generated the second-most
455	accurate estimates of diet for bears in both Trial 2 and 3. Marine-fed mink CCs also
456	performed well in Trial 1, although better estimates were generated from mink (all) and
457	no CCs. Estimating the diet composition of individual predators using CCs generated
458	from that same diet and those same predators is obviously not feasible in wildlife
459	research and is mathematically circular, i.e., the predator FA profile is used to calculate
460	the CC, which is then applied to the predator FA profile. We used these idealized, same-
461	trial CCs as a benchmark against which other CCs could be tested and, in that context,
462	marine-fed mink CCs emerged as the top performer. This finding is encouraging in a
463	couple of ways; first, it suggests that the marine-fed mink CCs that have been used in
464	previous studies of polar bear diet composition perform as well as those generated from
465	species more closely related to polar bears; second, it suggests that CC sets may have
466	relatively broad applicability across taxa for similar (e.g., marine-based) diets.
467	Most of the values for marine-fed mink CCs were similar to, or within the range
468	of, values derived in the current study, with a few exceptions, including 18:1n-13, 18:1n-
469	11, 20:1n-11, and 20:5n-3. Of those, only 20:5n-3 was used in QFASA modelling. The
470	two 18:1 isomers showed inverse trends (Fig 3) as the marine-fed mink value for 18:1n-
471	11 (5.47) was higher than Trial 2 (0.95 ± 0.09) or Trial 3 (2.78 ± 0.55), but the value for
472	18:1n-13 (0.45) was lower than Trial 2 (1.78 ± 0.11) or Trial 3 (1.64 ± 0.00). This pattern
473	may reflect some degree of mis-identification, as it can be difficult to resolve these two

474	isomers as their peaks may overlap with each other and with the adjacent 18:1n-9 in
475	chromatographic analysis. The CC value for 20:1n-11 derived from marine-fed mink
476	(4.52) was substantially higher than the value derived from Trial 1 (1.25 \pm 0.10) or Trial
477	2 (0.68 \pm 0.03), but lower than Trial 3 (14.63 \pm 3.17), suggesting the metabolism of this
478	FA is especially sensitive to diet and it thus may not be a useful dietary tracer. Indeed,
479	Bromaghin et al. (2015) found that modelled predator values using mink (all) CCs for this
480	FA were outside the range of prey values (i.e., the FA could not be modelled realistically)
481	and other studies have identified 20:1n-11 as an unreliable dietary indicator (Galicia et al.
482	2015; Goetsch et al. 2018). It is unclear why the marine-fed mink CC value for 20:5n-3
483	(0.14) was lower than either Trial 2 (0.34 \pm 0.02) or Trial 3 (0.34 \pm 0.04), but this FA
484	may be especially metabolically active. It showed the largest change in concentration
485	during hibernation of any $FA > 1\%$.
486	That the marine-fed mink CCs performed well is also consistent with the results
487	of Bromaghin et al. (2017) who found that CCs derived mathematically from Chukchi
488	Sea polar bear and prey data were similar to those derived from the mink feeding trial
489	(see their Fig 8). Our results thus add to growing evidence that diet-specific variation can
490	be more important than species-specific differences in estimating CCs. Thus, whenever
491	possible, deriving CCs on diets similar to the predator of interest, even if in a model
492	species, may aid in producing the most accurate diet estimates. Estimation of CCs
493	mathematically, as proposed by Bromaghin et al. (2017), provides an alternative
494	approach for diet estimation from FA in which direct estimate of CCs are not required,

495 but feeding trials can continue to be useful in determining when separate CCs need to be

496 generated for different groups of predators.

497 Our study is one of the few to examine changes in FA profiles over time in 498 individual carnivores and thus provides important new insights into the temporal window 499 of QFASA diet estimates. In a controlled feeding study of juvenile harbor seals (*Phoca* 500 vitulina), Nordstrom et al. (2008) sampled individual seals three times over 42 days and 501 estimated that blubber FA would have equilibrated with the diet at 50-65 d. Bowen and 502 Iverson (2013) cite unpublished data that QFASA diet estimates for captive juvenile 503 Steller sea lions (*Eumetopias jubatus*) were most accurate between 56 d and 84 d. We 504 found that bear FA profiles responded rapidly to a change in diet and QFASA estimates 505 were reasonably accurate within about 30 days of a dietary switch (Fig 5 and 6). Bears 506 came to maximally resemble their diets after about 90 days and sampling beyond 90 days 507 provided no improvement in accuracy. Thus, for these growing brown bears on a 508 relatively high-fat diet, the temporal window for QFASA estimates was essentially 90 509 days. Samples taken before that day still captured some pre-trial diet. This timeframe is 510 longer than the estimates from captive pinnipeds (Kirsch et al. 2000; Nordstrom et al. 511 2008; Bowen and Iverson 2013), but corresponds well to the general "weeks-to-months" 512 timeframe often cited in QFASA studies. Understanding the timeframe of diet estimates 513 will also help in interpreting QFASA results in the context of seasonal food availability. 514 This could be especially important for highly seasonal foragers like polar bears (Galicia 515 et al. 2020). Although our estimates of turnover are for young, growing bears, rates of fat 516 deposition and mobilization are more likely to be influenced by nutritional status than by 517 age since fat stores are mobilized when dietary intake is insufficient to meet energetic 518 needs, rather than as a function of metabolic rate which would vary with age or size.

519 This is also the first study to examine progressive changes in the FA profiles of 520 fasting carnivores. While estimating the diets of hibernating animals may not be 521 ecologically insightful, our results are relevant to non-hibernating, fasting carnivores. 522 Polar bears are able to go prolonged periods without food while maintaining activity; a 523 state that has previously been characterized as "walking hibernation" (Nelson et al. 524 1983). More recent studies have suggested this metabolic state is equivalent to fasting in 525 other mammals (Robbins et al. 2012; Whiteman et al. 2015), but it remains a common 526 occurrence in polar bears, especially during the ice-free season when ice-associated seals 527 are largely unavailable (Derocher et al. 1990; Atkinson and Ramsay 1995; Atkinson et al. 528 1996). Polar bears may also fast during winter and during the spring breeding season, 529 when adult males are focused on securing mates (Ramsay et al. 1991; Cherry et al. 2009; 530 Rode et al. 2018). Pregnant female polar bears may fast for up to 8 months, including the 531 ice-free period and subsequent maternity denning (Ramsay and Stirling 1986; Atkinson 532 and Ramsay 1995). Our results suggest that diet estimates generated from fasting animals 533 may have to be interpreted cautiously and may be particularly sensitive to inaccurate 534 CCs. When idealized CCs were used, QFASA diet estimates remained highly accurate 535 during the entire fasting period (Fig 6b). However, using marine-fed mink CCs, accuracy 536 declined significantly after 74 days of fasting. It seems unlikely that wild polar bears 537 would undergo such a prolonged fast on the sea ice, but it may be increasingly common 538 during the ice free-period (Molnár et al. 2020). It is possible that fasting, non-hibernating 539 polar bears would mobilize energy reserves, and alter FA stores, more rapidly than 540 hibernating bears because of higher energetic demands (Whiteman et al. 2015). Studies of

- 541 free-ranging polar bears in which animals are sampled on shore in summer and fall or
- 542 immediately after denning will need to take this into account.

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Feeding	Diet	Lipid from	Lipid from	Total lipid (%	Trial
trial		dog food (%)	fish oil (%)	dry matter)	duration (d)
Trial 1	Dog food	100	0	10.8	90
Trial 2	Dog food + salmon oil	18.3	81.7	39.8	90
Trial 3	Dog food + anchovy oil	19.0	81.0	40.2	120
Trial 4	None (hibernation)	-	-	-	140

Table 1 Duration and composition of diets fed to four juvenile male brown bears during four experimental feeding trials. Lipid proportions are on an as-fed basis (% wet matter)

		Trial 1 - Dog food					Trial 2 - Dog food + salmon oil				Trial 3 - Dog food + 30% fish oil					
		Final B	ear FA	C	C		Final Be (%	ear FA	CC	_	Final B	ear FA	C	С		
Fatty acid	Diet (%)	Mean	SD	Mean	SD	Diet (%)	Mean	SD	Mea n SD	Diet (%)	Mean	SD	Mean	SD	Mink CC	Mink (marine) CC
Saturated																
14:0*	0.71	0.86	0.05	1.22	0.06	4.33	2.25	0.12	0.52 0.03	6.06	3.20	0.22	0.53	0.04	1.37	0.81
i-15:0	0.00	0.37	0.02	-	-	0.17	0.48	0.04	2.74 0.24	0.18	0.51	0.03	2.86	0.15	0.70	0.63
15:0	0.06	0.28	0.01	4.79	0.23	0.40	0.43	0.01	1.09 0.02	2 0.43	0.48	0.02	1.11	0.05	0.80	0.78
16:0*	19.79	17.51	0.56	0.88	0.03	14.31	16.58	0.63	1.16 0.04	17.26	17.34	0.89	1.00	0.05	0.96	1.06
i-17:0	0.03	0.71	0.03	24.61	1.17	0.21	0.66	0.09	3.15 0.43	3 0.17	0.47	0.05	2.72	0.31	-	-
ai-17:0	0.02	0.08	0.01	3.93	0.47	0.09	0.11	0.01	1.25 0.10	6 0.18	0.14	0.01	0.79	0.04	0.75	0.70
17:0*	0.22	0.50	0.01	2.23	0.06	0.30	0.42	0.04	1.38 0.13	5 0.48	0.38	0.01	0.78	0.02	0.77	0.85
18:0*	7.90	5.55	0.81	0.70	0.10	3.40	2.66	0.42	0.78 0.12	2 4.38	2.63	0.24	0.60	0.06	0.72	0.79
20:0*	0.19	0.14	0.01	0.72	0.07	0.15	0.11	0.00	0.74 0.02	2 0.26	0.13	0.02	0.51	0.07	0.75	0.71
Monounsaturated																
16:1n-11	0.04	0.04	0.00	0.88	0.03	0.43	0.26	0.02	0.60 0.00	5 0.38	0.23	0.02	0.59	0.05	0.91	0.95
16:1n-9*	0.29	0.35	0.02	1.20	0.05	0.27	0.30	0.02	1.13 0.07	0.26	0.30	0.02	1.16	0.08	0.99	1.13
16:1n-7*	2.71	5.21	0.59	1.92	0.22	5.28	8.92	0.79	1.69 0.13	5 8.17	10.86	0.21	1.33	0.03	1.44	1.24
16:1n-5	0.03	0.09	0.01	2.58	0.34	0.31	0.24	0.02	0.77 0.03	5 0.18	0.19	0.01	1.05	0.04	0.79	0.73
17:1b	0.00	0.01	0.00	-	-	0.33	0.15	0.01	0.45 0.03	3 0.20	0.16	0.01	0.78	0.05	0.90	0.88
17:1*	0.15	0.49	0.05	3.23	0.33	0.31	0.60	0.05	1.92 0.1	0.18	0.60	0.05	3.37	0.28	1.17	1.16
18:1n-13	0.03	0.06	0.01	2.09	0.20	0.12	0.21	0.01	1.78 0.1	0.09	0.04	0.07	1.64	-	0.72	0.45
18:1n-11*	0.12	0.12	0.02	0.99	0.13	0.77	0.74	0.07	0.95 0.09	0.11	0.31	0.06	2.78	0.55	3.65	5.47
18:1n-9*	33.34	43.39	1.01	1.30	0.03	17.47	30.85	0.60	1.77 0.03	3 13.90	27.64	1.35	1.99	0.10	1.41	1.64
18:1n-7*	2.01	2.51	0.16	1.25	0.08	3.07	2.94	0.12	0.96 0.04	4 3.10	2.99	0.07	0.97	0.02	1.33	1.40
18:1n-5	0.09	0.15	0.02	1.62	0.22	0.54	0.43	0.04	0.80 0.0	0.12	0.21	0.02	1.70	0.20	0.96	0.87
20:1n-11	0.06	0.07	0.01	1.25	0.10	5.46	3.70	0.14	0.68 0.02	0.12	1.70	0.37	14.63	3.17	4.39	4.52

Table 2 FA composition of diets and bears and resulting calibration coefficients calculated from 3 controlled feeding studies of 4 juvenile brown bears

20:1n-9*	0.50	0.49	0.02	0.98	0.04	2.72	1.77	0.06	0.65 0.02	0.85	1.20	0.15	1.40	0.18	1.69	1.27
20:1n-7	0.03	0.04	0.01	1.30	0.20	0.34	0.21	0.02	0.62 0.05	0.25	0.19	0.01	0.73	0.04	1.78	1.20
22:1n-11	0.00	0.01	0.01	-	-	7.62	2.87	0.24	0.38 0.03	0.42	1.01	0.25	2.42	0.60	0.67	0.33
22:1n-9	0.09	0.03	0.00	0.32	0.03	0.83	0.34	0.02	0.41 0.03	0.18	0.14	0.03	0.78	0.15	0.60	0.54
24:1	0.02	0.02	0.01	1.20	0.62	0.67	0.18	0.03	0.27 0.05	0.32	0.00	0.00	-	-	0.17	0.16
Polyunsaturated																
16:2n-4	0.00	0.00	0.00	-	-	0.35	0.19	0.01	0.53 0.04	0.90	0.45	0.02	0.51	0.03	0.89	0.50
16:3n-4	0.01	0.00	0.00	-	-	0.26	0.03	0.01	0.11 0.04	1.11	0.15	0.02	0.14	0.01	0.52	0.25
18:2n-6*	27.15	17.50	1.31	0.64	0.05	6.29	8.32	0.68	1.32 0.11	6.09	8.42	0.62	1.38	0.10	1.12	1.29
18:2n-4	0.02	0.01	0.01	0.96	0.66	0.14	0.08	0.01	0.61 0.05	0.31	0.17	0.01	0.57	0.03	2.03	0.73
18:3n-6	0.10	0.21	0.02	2.09	0.21	0.09	0.11	0.02	1.29 0.24	0.31	0.21	0.02	0.67	0.05	0.71	0.75
18:3n-4	0.03	0.06	0.01	2.16	0.18	0.12	0.22	0.02	1.91 0.17	0.15	0.47	0.04	3.14	0.30	1.61	1.56
18:3n-3*	3.09	1.60	0.12	0.52	0.04	1.38	1.16	0.04	0.84 0.03	1.16	1.13	0.07	0.98	0.06	0.62	0.70
18:4n-3	0.02	0.04	0.01	2.87	0.57	2.13	0.64	0.03	0.30 0.01	2.11	0.77	0.07	0.37	0.03	0.48	0.30
18:4n-1	0.06	0.05	0.01	0.83	0.15	0.17	0.27	0.04	1.55 0.22	0.22	0.65	0.09	3.03	0.40	0.60	0.48
20:2n-6*	0.35	0.31	0.02	0.89	0.06	0.37	0.30	0.00	0.80 0.01	0.30	0.34	0.02	1.14	0.06	0.93	0.92
20:3n-6*	0.12	0.20	0.01	1.64	0.05	0.12	0.14	0.01	1.19 0.08	0.21	0.16	0.01	0.75	0.03	0.72	0.73
20:4n-6*	0.34	0.47	0.04	1.36	0.12	0.49	0.38	0.02	0.78 0.05	1.06	0.59	0.06	0.55	0.06	0.37	0.44
20:4n-3	0.00	0.04	0.01	-	-	1.08	0.98	0.10	0.91 0.09	0.67	0.68	0.05	1.01	0.07	0.76	0.51
20:5n-3	0.06	0.05	0.00	0.82	0.06	7.97	2.73	0.14	0.34 0.02	15.09	5.15	0.65	0.34	0.04	0.19	0.14
21:5n-3	0.00	0.01	0.01	-	-	0.36	0.19	0.01	0.53 0.02	0.61	0.30	0.02	0.49	0.03	0.70	0.46
22:4n-6*	0.12	0.20	0.01	1.68	0.12	0.09	0.11	0.00	1.27 0.01	0.16	0.13	0.01	0.81	0.06	0.89	0.97
22:5n-6	0.02	0.03	0.00	1.26	0.16	0.09	0.08	0.00	0.88 0.05	0.28	0.13	0.01	0.48	0.04	0.70	0.81
22:5n-3	0.05	0.09	0.01	1.88	0.17	1.59	1.41	0.13	0.89 0.08	1.67	1.53	0.06	0.92	0.04	0.87	0.88
22:6n-3	0.04	0.05	0.02	1.28	0.41	7.03	4.25	0.20	0.60 0.03	9.37	5.52	0.36	0.59	0.04	0.64	0.59
\sum Saturated	28.93	26.00				23.35	23.70			29.41	25.29					
\sum Monounsaturated	39.51	53.09				46.54	54.72			28.83	47.75					
\sum Polyunsaturated	31.57	20.91				30.11	21.58			41.76	26.96					
TOTAL (%)	100	100				100	100			100	100					

* denotes the 18 fatty acids used to generate QFASA estimates for bears in Trial 1 Bold type denotes the 22 fatty acids used to generate QFASA estimates for bears in Trial 2-4

Table 3 Initial, final and change in concentration of fatty acids in the adipose tissue of four juvenile brown bears during a 140 d period of hibernation. Change values reflect mean changes within each bear. Fatty acids in bold type are also plotted in Fig. 3

	Start con	centration	Final Con	centration	Total indi	vidual	Percent individual			
	(%)		(%	6)	chang	ge	change (%)			
Fatty acid	Mean	SD	Mean	SD	Mean	SD	Mean	SD		
14:0	2.61	0.25	2.35	0.26	-0.27	0.13	-10.12	5.12		
i-15:0	0.50	0.02	0.52	0.05	0.02	0.06	3.65	12.79		
15:0	0.47	0.02	0.42	0.03	-0.05	0.03	-11.50	5.42		
16:0	16.05	1.27	14.88	0.89	-1.16	0.63	-7.11	3.41		
16:1n-11	0.26	0.01	0.23	0.02	-0.03	0.02	-12.67	7.20		
16:1n-9	0.29	0.02	0.32	0.01	0.03	0.01	10.75	2.90		
16:1n-7	10.30	1.24	8.38	1.28	-1.92	1.13	-18.45	9.67		
16:1n-5	0.19	0.02	0.16	0.01	-0.03	0.02	-17.54	10.01		
i-17:0	0.56	0.07	0.57	0.05	0.01	0.05	2.14	8.96		
ai-17:0	0.16	0.01	0.16	0.01	0.01	0.01	4.13	3.19		
17:1b	0.21	0.00	0.22	0.02	0.01	0.02	6.88	9.33		
16:2n-4	0.52	0.02	0.45	0.04	-0.07	0.04	-13.44	8.34		
17:0	0.42	0.05	0.42	0.03	-0.01	0.03	-1.04	6.58		
16:3n-4	0.15	0.01	0.12	0.02	-0.03	0.01	-18.97	6.83		
17:1	0.54	0.08	0.47	0.05	-0.07	0.03	-12.80	5.32		
18:0	2.62	0.58	3.06	0.43	0.45	0.38	18.98	16.52		
18:1n-13	0.12	0.02	0.09	0.02	-0.03	0.03	-24.50	22.78		
18:1n-11	0.33	0.02	0.44	0.04	0.11	0.03	34.18	9.28		
18:1n-9	27.55	1.12	31.21	1.65	3.66	1.66	13.35	6.33		
18:1n-7	3.21	0.18	3.31	0.11	0.09	0.09	2.97	3.21		
18:1n-5	0.22	0.03	0.22	0.01	0.00	0.03	2.42	13.30		
18:2n-6	8.53	0.59	9.41	0.73	0.89	0.49	10.46	5.80		
18:2n-4	0.19	0.01	0.17	0.01	-0.02	0.01	-10.10	3.38		
18:3n-6	0.18	0.01	0.15	0.01	-0.04	0.01	-20.59	4.78		
18:3n-4	0.46	0.05	0.42	0.03	-0.04	0.04	-8.26	8.44		
18:3n-3	1.16	0.05	1.04	0.10	-0.12	0.09	-10.33	8.05		
18:4n-3	0.79	0.06	0.51	0.05	-0.29	0.08	-35.70	8.55		
18:4 n- 1	0.76	0.07	0.42	0.09	-0.34	0.14	-43.56	14.31		
20:0	0.17	0.00	0.27	0.03	0.10	0.03	58.16	16.47		
20:1n-11	1.35	0.17	1.87	0.22	0.52	0.19	38.95	17.14		
20:1n-9	1.20	0.05	1.69	0.10	0.49	0.11	40.81	10.52		
20:1n-7	0.19	0.00	0.29	0.02	0.10	0.02	50.48	13.41		
20:2n-6	0.27	0.01	0.31	0.02	0.04	0.02	16.21	7.55		
20:3n-6	0.18	0.01	0.20	0.02	0.02	0.02	9.96	10.21		
20:4n-6	0.68	0.05	0.52	0.06	-0.15	0.07	-22.60	8.58		
20:4n-3	0.83	0.06	0.71	0.04	-0.13	0.07	-14.86	6.76		
20:5n-3	5.59	0.56	2.68	0.32	-2.92	0.81	-51.50	9.95		

22:1n-11	0.79	0.09	1.10	0.11	0.31	0.06	39.21	9.32
22:1n-9	0.16	0.01	0.24	0.02	0.08	0.02	52.31	11.11
21:5n-3	0.38	0.02	0.38	0.03	0.00	0.02	1.02	5.58
22:4n-6	0.14	0.01	0.20	0.02	0.06	0.03	42.92	20.32
22:5n-6	0.18	0.01	0.25	0.05	0.07	0.04	36.25	21.52
22:5n-3	2.02	0.14	2.38	0.27	0.36	0.31	18.42	15.80
22:6n-3	6.42	0.34	6.66	1.16	0.24	1.03	3.63	15.60
24:1	0.07	0.01	0.13	0.02	0.06	0.02	79.99	25.93
-								

1 Fig. 1 Fatty acid composition of three experimental diets fed to brown bears

2

Fig. 2 Concentration (mass % of total FA) of selected FA in adipose tissue of 4 juvenile 3 4 brown bears during 3 feeding trials, followed by hibernation (Trial 4). Pink circles 5 indicate the FA composition of the experimental diets 6 7 **Fig. 3** Mean calibration coefficients (log scale, \pm SD) calculated from 4 juvenile brown 8 bears at the conclusion of 3 feeding trials. Also shown are calibration coefficients from 9 captive mink fed a marine-based diet (mink data from Thiemann 2006, Thiemann et al. 10 2008) 11 12 Fig. 4 Mean (\pm SD) diet estimates from QFASA for four brown bears sampled at the end 13 of controlled feeding experiments. Horizontal dashed lines indicate true diet composition 14 (see Table 1). Diet estimation used calibration coefficients generated from the feeding 15 trials, from captive mink (Thiemann et al. 2008), or no calibration. Trial 1 calibration 16 coefficients could not be applied to bears in Trial 2 or 3 because of the limited number of 17 FA in Trial 1 18 19 **Fig. 5** Mean $(\pm$ SD) diet estimates for four brown bears sampled intermittently during 20 controlled feeding experiments. See Table 1 for diet composition. Panels A and B: Diet 21 estimation used calibration coefficients generated from the same trial for trials 1-3; trial 4

22 used calibration coefficients from trial 3 (see text for details). Panels C and D: Diet

23	estimation used calibration coefficients generated from captive mink fed a marine-based
24	diet (Thiemann et al. 2008)
25	
26	Fig. 6 Mean (\pm SD) sum of differences between estimated and actual diets for four brown
27	bears sampled intermittently during controlled feeding experiments. See Table 1 for diet
28	composition. Panels A and B: Diet estimation used calibration coefficients generated
29	from the same trial for trials 1-3; trial 4 used calibration coefficients from trial 3 (see text
30	for details). Panels C and D: Diet estimation used calibration coefficients generated from
31	captive mink fed a marine-based diet (Thiemann et al. 2008)
32	
33	Fig S1 Concentration (mass % of total FA) of all 45 FA in adipose tissue of 4 juvenile
34	brown bears over 3 feeding trials, followed by hibernation (Trial 4). Pink circles indicate
35	the FA composition of the experimental diets
36	
37	Fig S2 Sums of differences between actual and estimated diet composition across
38	different sets of calibration coefficients in 3 controlled feeding trials. Boxplots show
39	upper and lower quartiles and maximum, minimum, and median values
40	
41	Fig S3 Sums of differences between estimated and actual diets for four brown bears
42	sampled intermittently during controlled feeding experiments. See Table 1 for diet
43	composition. Diet estimation used calibration coefficients generated from the same trial
44	(top row) or from captive mink fed a marine-based diet (bottom row). Boxplots show
45	upper and lower quartiles and maximum, minimum, and median values



Fig. 1 R1

















Fig. 5 R1



Fig. 6 R1