Supplementary Methods to Respiratory and Olfactory Turbinate Dimensions in

Aquatic and Terrestrial Carnivorans

Please see Supplementary Table S4 for a list of the skulls scanned and their museum identification numbers.

Phylogenetic Reconstruction

 A reliable phylogenetic tree with branch length information, preferably in units of evolutionary time, is essential for phylogenetic comparative analyses. Rather than using an existing phylogeny, we simultaneously inferred phylogeny and divergence times for taxa present in our study using the program BEAST v1.5.4 (Drummond and Rambaut 2007).

We obtained six previously published nuclear loci for all species represented in our study, plus one out-group (the gray wolf *Canis lupus*) from GenBank. This resulted in a total alignment of 4055 bp. Accession numbers and source studies for each sequence used are provided in Table S1. The tropical monk seal *Monachus tropicalis* is recently extinct (Adam 2004) and, as yet, no genetic material from this species has been obtained. In order to include the species in our phylogenetic comparative analyses, we substituted sequence data for the Hawaiian monk seal *M. schauinslandi.* We stress that this does not represent a statement regarding the phylogentic affinities of *M. tropicalis*. Rather, as the monophyly of *Monachus* has not, to our knowledge, been questioned, the use of sequence

1   data from either of the two extant species should be sufficient to resolve the phylogenetic

2   placement of genus and its divergence time from other phocid lineages.

3

4   We identified nine fossil taxa from the literature that represent the minimum age for

5   crown clades represented in our sample (Table S2). We used the ages of these fossils as

6   minimum age calibrations for a relaxed molecular clock, as implemented in BEAST

7   (Drummond and Rambaut, 2007). Fossil calibrations were used to generate log-normally

8   distributed prior ranges on divergence times for their respective nodes. In each case, the

9   minimum age of the fossil was used as the offset value. If a range of ages was given, the

10   mid-point of that range was used to set the median of the log-normal distribution. If no

11   range was given, we placed the median point one million years from the offset. We then

12   adjusted the standard deviation of the distribution so that the 95% range encompassed the

13   minimum fossil age at the next node towards the root. In some cases, we used additional

14   knowledge of the carnivoran fossil record to adjust distributions. For example, the

15   minimum age reported for remains of the American black bear, *Ursus americanus,* is

16   1.8mya (Cassiliano 1999) but the next node for which we had a fossil calibration point is

17   the split between Ursidae and other arctoids (*Parictis*, 37 mya; Hunt 1998). Instead of

18   specifying a fat-tailed distribution, we used the first occurrence of the genus *Ursus* (*U.*

19   *boecki* at 5.3mya; Montoya et al. 2006) as the 95% cut-off. Full details of nodes

20   calibrated, fossil taxa, and age ranges allocated as prior ranges are provided in Table S2.

21

22   We partitioned our alignment by locus, with each allocated an HKY+Γ model of

23   sequence evolution. We ran our analysis for 50 million generations, sampling every 1000

1   generations. After ensuring that parameters had satisfactorily converged based on trace

2   plots of samples from the posterior distribution, we discarded the first 20% of trees as

3   burn-in and produced a maximum-clade credibility tree from the remaining trees. Our

4   tree (see main text) agreed well with previously published time-calibrated phylogenies

5   (e.g. Eizerik et al. 2010; Fulton and Strobeck 2010, Koepfli et al. 2007, 2008) and was

6   subsequently used in comparative analysis.

7

8   ***Phylogenetic Independent Contrasts***

9

10   Regressions of phylogenetic independent contrasts of turbinate surface areas on contrasts

11   of size measures (mass, skull length and chamber volume) are plotted in Figure S1, with

12   regression statistics provided in Table S3. Contrasts for turbinate areas were positivized

13   on size measurements, and regressions fit without intercepts following Garland et al.

14   (1992). In all cases, results are broadly similar to regressions using species' values as data

15   points.

16

1   ***Supplementary Literature Cited***

2

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Supplementary Tables

Table S1: Genbank accession numbers for sequences used in this study. Superscripts refer to references for original sequences (see footnote to table)

Taxon	CHRNA1	FES	GHR	IRBP	RAG1	RHO1
Canis lupus	DQ205757[c]	DQ205795[c]	DQ205836[c]	DQ205906[c]	AB371339[l]	DQ205869[c]
Ursus americanus	DQ205726[c]	DQ205766[c]	DQ205799[c]	AY303837[i]	DQ240717[h]	DQ205840[c]
Ursus arctos	GU931041[a]	AM748322[i]	GU931134[a]	AY303842[i]	AB109361[l]	-
Ursus maritimus	DQ205725[c]	DQ205765[c]	DQ205798[c]	AY303843[i]	-	DQ205839[c]
Hydrurga leptonyx	DQ205744[c]	-	DQ205818[c]	DQ205895[c]	GU167539[d]	DQ205857[c]
Mirounga angustirostris	DQ205746[c]	DQ205785[c]	DQ205820[c]	DQ205897[c]	GU167540[d]	DQ205859[c]
Monachus schaluinslandi	DQ205747[c]	DQ205786[c]	DQ205821[c]	DQ205898[c]	GU167542[d]	DQ205860[c]
Zalophus californianus	AB365084[n]	AB365085[n]	GU931126[a]	AY750612[b]	AB302263[m]	AB365087[n]
Mephitis mephtis	DQ205733[c]	-	DQ205805[c]	AB109331[k]	AB109358[k]	DQ205846[c]
Procyon lotor	AF498152[e]	AF498183[e]	AF498207[e]	AB082981[j]	AB109359[k]	AF498231[c]
Potos flavus	DQ205731[c]	DQ205770[c]	DQ205803[c]	DQ205880[c]	DQ660264[f]	DQ205845[c]
Taxidea taxus	AF498148[e]	AF498179[e]	AF498203[e]	DQ205885[c]	DQ660271[f]	AF498227[c]
Gulo gulo	AF498143[e]	AF498170[e]	AF498198[e]	AB082962[j]	AB109340[k]	AF498222[e]
Mustela frenata	AF498139[e]	AF498171[e]	AF498194[e]	DQ205886[c]	EF472412[g]	AF498218[c]
Neovison *vison*	AF498140[e]	AF498163[e]	AF498195[e]	AB082977[j]	DQ660268[f]	AF498219[c]
Lontra canadensis	AF498132[e]	AF498162[e]	AF498187[e]	DQ205884[c]	EF472403[g]	AF498211[e]
Enhydra lutris	AF498131[e]		AF498186[e]	AB082978[j]	GU167549[d]	AF498210[e]

Sources*: a* Eizerik et al. (2010); *b* Flynn et al. (2005); *c* Fulton and Strobeck (2006); *d* Fulton and Strobeck (2010); *e* Koepfi and Wayne (2003); *f* Koepfli et al. (2007); *g* Koepfli et al. (2008); *h* Lindblad-Toh et al. (2005); *i* Pages et al. (2008); *j* Sato et al. (2003); *k* Sato et al. (2004); *l* Sato et al. (2009); *m* Yonezawa et al. (2007); *n* Yonezawa et al. (2009); *o* Yu et al. (2004)

Table S2: Fossil calibrations used in BEAST analysis, with distribution parameters. All priors were log-normally distributed.

clade	fossil taxon	offset	median	95%
Caniformia	*Hesperocyon* sp	40	41.5	50
Arctoidea	*Parictis* sp.	37	38	40
Ursus	*Ursus americanus*	1.8-2.9	2.9	5.3
Ursus maritimus/*arctos*	*Ursus maritimus*	0.17	1.13	5.3
Pinnipedia+ Musteloidea	*Enaliarctos tedfordi*	28	29	33
Crown Pinnipedia	*Allodesmus kernensis*	20.5	23	28
Lobodon+*Mirounga*	*Acrophoca* sp.	5	7	17.3
Procyonidae,Mustelidae	*Broiliana* sp.	24	25	28
Lutrinae+Mustelinae	Lutrinae indet./*Vishnuonyx chinjiensis*	13.7	15	16

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Table S3: Regression statistics for independent contrasts of turbinate areas on contrast of three size measures (in italics).

Regression	DF	Slope	r^2	p
Body mass				
TSA	14	0.62	0.82	<0.001
RSA	14	0.69	0.73	<0.001
OSA	14	0.50	0.60	<0.001
Skull length				
TSA	14	1.95	0.76	<0.001
RSA	14	2.27	0.75	<0.001
OSA	14	1.63	0.59	<0.001
Chamber Volume				
TSA	14	0.84	0.83	<0.001
RSA	14	0.95	0.83	<0.001
OSA	14	0.71	0.70	<0.001

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| Table S4. Specimens scanned. M, male; F, female; U, unknown. Museum or source abbreviations as follows: H, Illinois State Museum; LACM, Museum of Natural History, Los Angeles; MVZ, Museum of Vertebrate Zoology, Berkeley; SO, Southwest Fisheries; UCLA; UCLA, Donald R. Dickey Collection, UCLA; USNM, United States National Museum.			
Genus	Species	Sex	ID NUM
Mephitis	*mephitis*	M	USNM 47553
Mephitis	*mephitis*	F	UCLA JXS001
Enhydra	*lutris*	M	SO 2951-98
Enhydra	*lutris*	F	SO 2853-97
Gulo	*gulo*	M	USNM 314885
Gulo	*gulo*	F	USNM 157327
Lontra	*canadensis*	F	UCLA 18958
Lontra	*canadensis*	M	UCLA 15275
Mustela	*frenata*	F	USNM 95054
Mustela	*frenata*	M	USNM 52702
Neovison	*vison*	M	UCLA 8488
Taxidea	*taxus*	M	UCLA 14841
Taxidea	*taxus*	F	LACM 45012
Zalophus	*californianus*	M	UCLA 252
Zalophus	*californicus*	F	LACM 95730
Hydrurga	*leptonyx*	F	USNM 269533
Hydrurga	*leptonyx*	M	USNM 270326
Mirounga	*angustirostris*	F	MVZ 184140
Monachus	*tropicalis*	F	USNM 102527
Monachus	*tropicalis*	M	USNM 100358
Potos	*flavus*	F	USNM 337630
Potos	*flavus*	M	USNM 291066
Procyon	*lotor*	M	LACM 52261

Procyon	*lotor*	F	LACM 07241
Ursus	*americanus*	F	USNM 211397
Ursus	*americanus*	M	USNM 227070
Ursus	*arctos*	M	USNM 82003
Ursus	*arctos (skull)*	F	USNM 98062
Ursus	*maritimus*	M	H 001-05
Ursus	*maritimus*	U	USNM 275072

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Supplementary Figures

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3
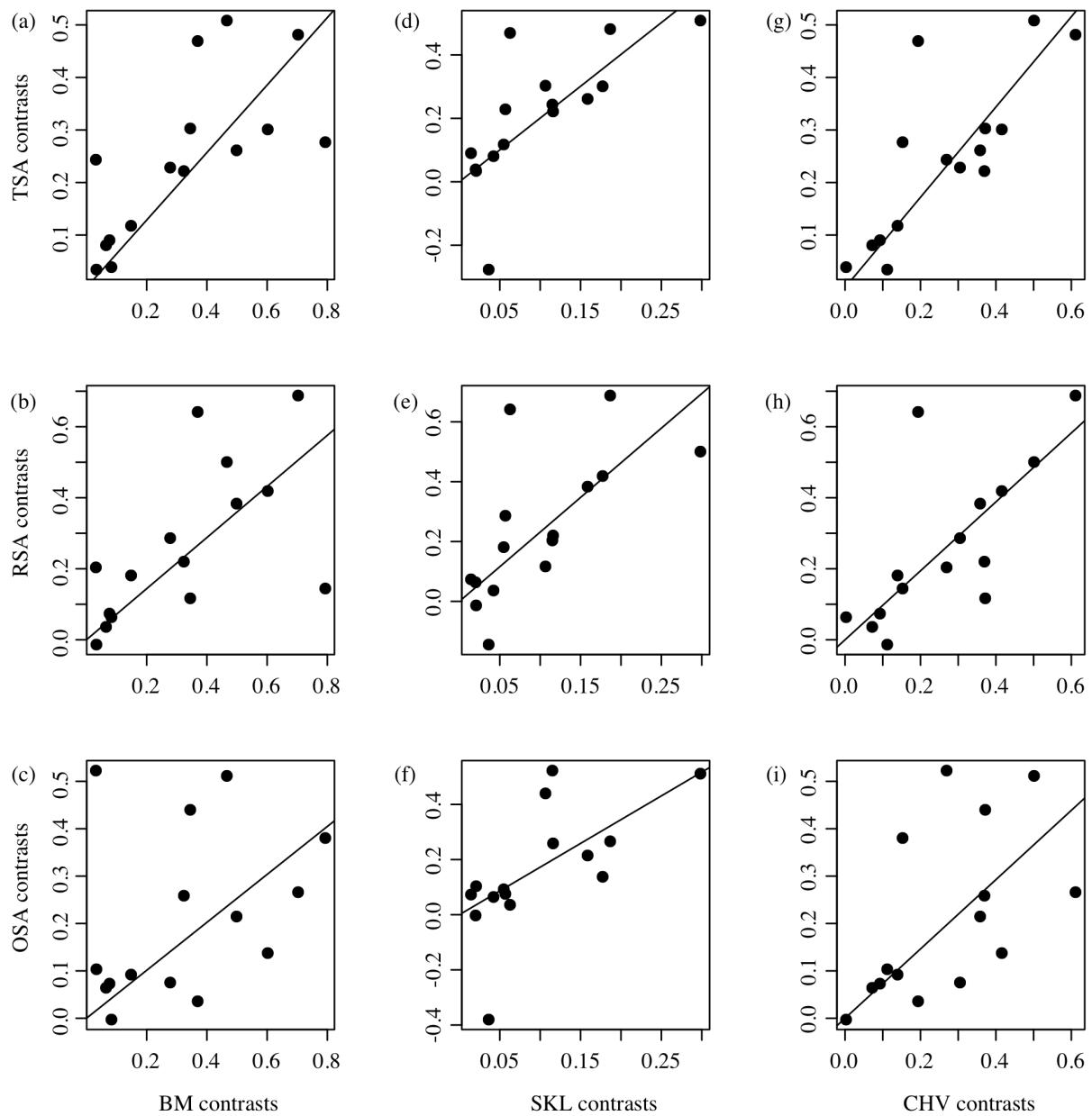
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5

6 Figure S1. Regressions of phylogenetic independent contrasts of total turbinate surface
7 area (TSA, top row), respiratory surface area (RSA, middle row), and olfactory surface
8 area (OSA, bottom row) on contrasts for body mass (BM, left column), skull length
9 (SKL, middle column), and chamber volume (CHV, right column). All measures were
10 natural log (ln) transformed prior to computation of contrasts.

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