

Online Resource 1 for:

Iterative habitat transitions are associated with morphological convergence of the backbone in delphinoids

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Contents:

Supplementary analysis I: Habitat transitions of cetaceans

Supplementary analysis II: Small sample size sensitivity analysis

Supplementary analysis III: Tempo of evolution of cetaceans

Figure S1: Habitat transitions during evolutionary history of modern cetaceans

Figure S2: Variable correlations with the two first PCA axes

Figure S3: Correlations between vertebral shape residuals and PC axes of the PTA

Figure S4: Phylorates of habitat transitions and vertebral shape in cetaceans

Figure S5: Morphospace of 500 randomly simulated *T. truncatus* individuals

Table S1: List of specimens used in this study

Table S2: Habitat classification of species included in this study

Table S3: Variance of morphological residuals and their contribution to PCA axes

Table S4: Number and proportion of transitions between each pairs of habitats

Table S5: Results of MANOVAs and pairwise comparisons testing the effect of habitat

Table S6: Results of ANOVAs on individual PCs on specimen values

Table S7: Results of ANOVAs on individual PCs on species-averaged values

Table S8: Results of phylo-ANOVAs and phylo-MANOVAs on incremental number of PCs

Table S9: Vertebral shape convergence

Table S10: Results of phenotypic trajectory analyses

References

Supplementary analysis I: Habitat transitions of cetaceans

1. Material and methods

Patterns of habitat transitions across the entire cetacean phylogeny were investigated with models of discrete trait evolution in order to retrieve the estimated ecological state of the most recent common ancestor of delphinoids. Habitat data for non-delphinoid cetaceans were taken from Gillet et al. (2019). As adaptation to riverine habitat in modern cetaceans is generally considered as secondary transition from marine environment rather than the ancestral state (Cunha et al. 2011; Gatesy et al. 2013; Pyenson et al. 2015), prior probabilities on the ancestral state of the root node were defined as null for the rivers and bays state and equal for each of the three marine states (coasts, mixed, and offshore). Similarly to the methods used for delphinoid ancestral state reconstruction (see Main Text), four different macroevolutionary models were tested using the function *fitMk* from the *phytools* R- package (Revell 2012): an equal rates model (ER), an all rates different (ARD) model, and two different ordered models (ORD1 and ORD2). The model with the highest weighted Akaike information criterion (AIC) was conserved for simulations of the stochastic mapping which was calculated using the *make.simmap* function (R-package *phytools*). The mapping was repeated 1,000 times.

2. Results

The best macroevolutionary model to investigate habitat transitions in cetaceans was the ORD1 model (weighted AIC: ER = 0.046, ORD1 = 0.891, ORD2 = 0.046, ARD = 0.016). The best model had the following transition rates: coasts to rivers & bays = 0.048; coasts to mixed = 0.066; mixed to coasts = 0.077; coasts to offshore = 0.111; offshore to mixed = 0.006; all other transitions = 0. Based on the 1,000 iterations of the stochastic mapping, the probabilities of the estimated ancestral state of the most recent common ancestor of delphinoids were 0.785 for the mixed habitat, 0.21 for the coastal habitat, and 0.005 for the offshore habitat (Fig. S1). These proportions were used as prior probabilities on the ancestral state of the root node of the habitat transition analysis on delphinoids.

Supplementary analysis II: Small sample size sensitivity analysis

To assess the impact of the small sample size for *T. truncatus* on ANOVAs and MANOVAs results, PC scores of 250 coastal and 250 offshore individuals were randomly simulated with a normal distribution (R-function *rnorm*) based on morphological data (PC scores means and standard deviations) of *T. truncatus* specimens from our dataset. Three different scenarios were simulated. First, coastal individuals were simulated with a mean and standard deviation equal to the mean and standard deviation of our three *T. truncatus* coastal ecotypes and offshore individuals were simulated with a mean and standard deviation equal to those of our three *T. truncatus* offshore ecotypes for each PC axis, hence representing a scenario where both ecological groups are almost perfectly separated in the morphospace (Fig. S5a). The second scenario was similar to the first one, but the standard deviation of each group was set as two times the standard deviation of the corresponding ecotypes. This corresponds to a scenario in which both ecological groups largely overlap but a general morphological trend can still be observed (Fig. S5b). Finally, coastal and offshore individuals were all simulated with the same mean and standard deviation based on values from the nine *T. truncatus* specimens from our dataset. This last scenario represents an almost perfect overlap of both groups (Fig. S5c).

The effect of ecological group on all simulated individuals was assessed for each scenario with an ANOVA on the first PC (R-functions *lm* and *anova*) and a MANOVA on the seven first PCs (R-functions *lm.rppp* and *manova.update* with 10,000 iterations). Both analyses found a significant difference between coastal and offshore individuals for the first (ANOVA: $F = 1088.2$; $P < 0.0001$; MANOVA: F (Roy) = 8.908, $Z = 34.322$, $P = 0.0001$) and second scenarios (ANOVA: $F = 232.94$; $P < 0.0001$; MANOVA: F (Roy) = 2.601, $Z = 24.385$, $P = 0.0001$) but not for the third one (ANOVA: $F = 0.055$; $P = 0.8145$; MANOVA: F (Roy) = 0.003, $Z = -2.025$, $P = 0.9801$).

The effect of small sampling size was then assessed by randomly subsampling three individuals in each ecological group to mirror the sampling size of our dataset. The random subsampling was repeated 10,000 times for each scenario and ANOVAs on PC1 and MANOVAs on PCs 1-7 were run on each subsample. For the first scenario (almost complete morphological separation of the two ecological groups), ANOVAs and MANOVAs were significant for 77.38% and 43.32% of subsamplings, respectively. For the second scenario (large overlap of the groups but still significantly different), 25.49% of ANOVAs and 20.75% of MANOVAs found a significant difference between ecological groups. Finally, for the third scenario (complete overlap and no significant difference between group), only 4.78% of ANOVAs and 4.75% of MANOVAs were significant. While the significant difference observed between coastal and offshore *T. truncatus* specimens from our dataset could still be due to chance and sampling bias, this probability is fairly poor (around 5%).

Supplementary analysis III: Tempo of evolution of cetaceans

1. Material and methods

Habitat states and vertebral shape measurements for non-delphinoid cetaceans were retrieved from Gillet et al. (2019), resulting in a dataset of 68 species for which morphological and ecological data were available. Vertebral shapes for all cetaceans (delphinoids and non-delphinoids) were phylogenetically size-corrected and then implemented in a PCA based on the correlation matrix, using the same methods described in the main text for delphinoids.

Tempo of habitat transitions and morphological evolution were investigated following the same protocol used for delphinoids. However, for computational purposes, only models with up to four partitions (three rate shifts) were fitted, conversely to delphinoids for which models with up to five partitions (four rate shifts) were fitted. Although an ordered model with varying rates between each transition was selected as the best model for habitat transition mapping of cetaceans (see supplementary analysis I), all habitat transition rates were forced as equal in the same partition in this analysis as more complex models would have been too computationally heavy. For vertebral shape data, the 3 first PCs of the cetacean PCA, representing 75.17% of the total variance, were used as proxy for backbone morphology.

2. Results

For habitat transitions, 47,972 single and multirate models were fitted. Only two models individually accounted for more than 1% of the total Akaike weight, the best model accounting for 2.57%. These two best models are both four partition models. The highest transition rates were found in Phocoenidae and some Delphininae while the lowest rates were found in Ziphiidae (beaked whales) (Fig. S4). Regarding phenotypic evolutionary rates, 9,920 models were fitted, among which 9,482 converged. Four models accounted for more than 1% of the total Akaike weight with 34.47%, 29.55%, 25.34%, and 8.79%, respectively. The average phylorate of vertebral shape shows that all delphinoids have higher evolutionary rates than any other extant cetacean species (Fig. S4).

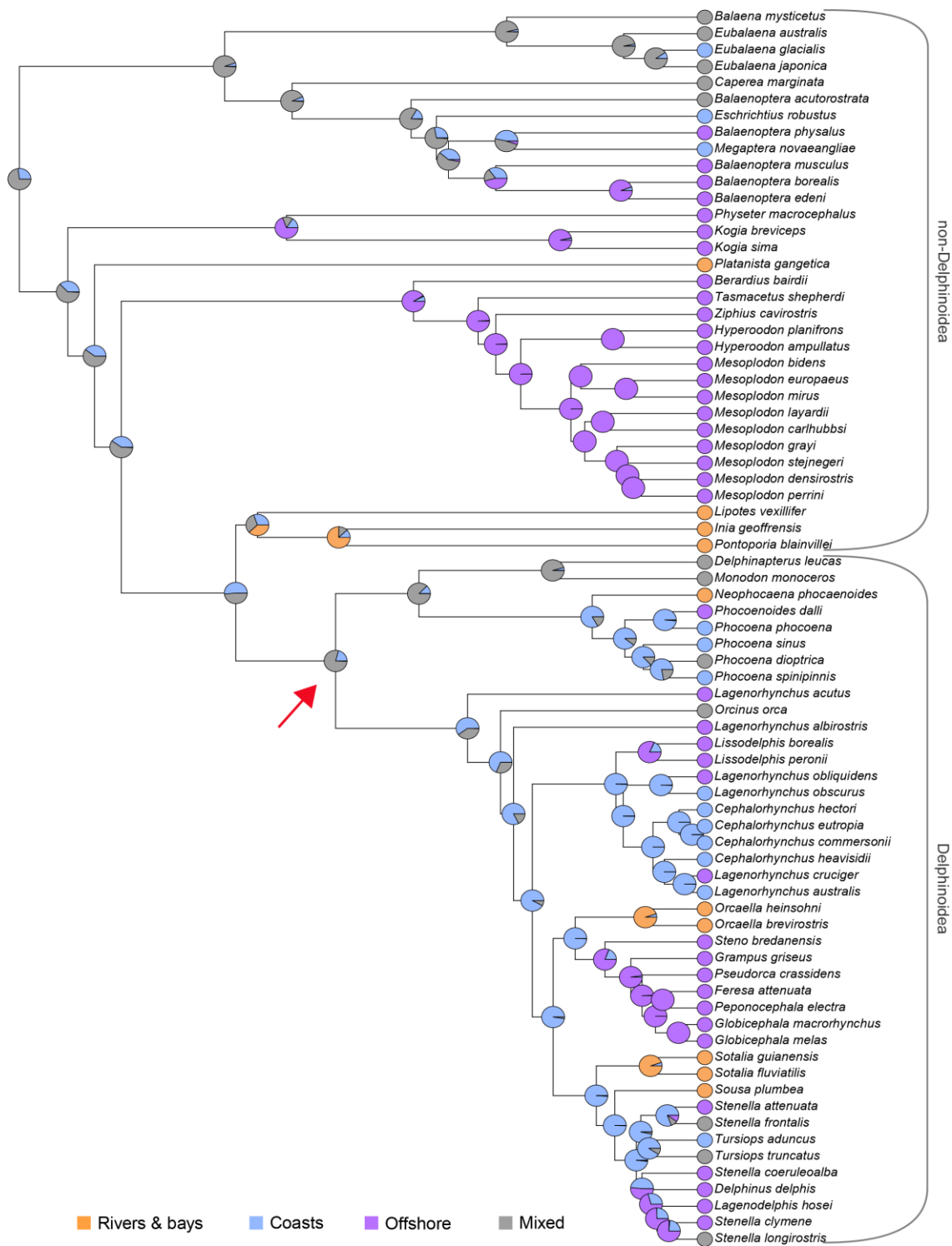


Figure S1. Habitat transitions during evolutionary history of modern cetaceans. Ancestral state reconstruction performed using an ordered model (model ORD1) stochastic mapping and plotted on the cetacean time-calibrated tree from (McGowen et al. 2020). Posterior probabilities (based on 1,000 simulations) of each node state are indicated by pie charts. The node corresponding to the most recent common ancestor of delphinoids is indicated by the red arrow.

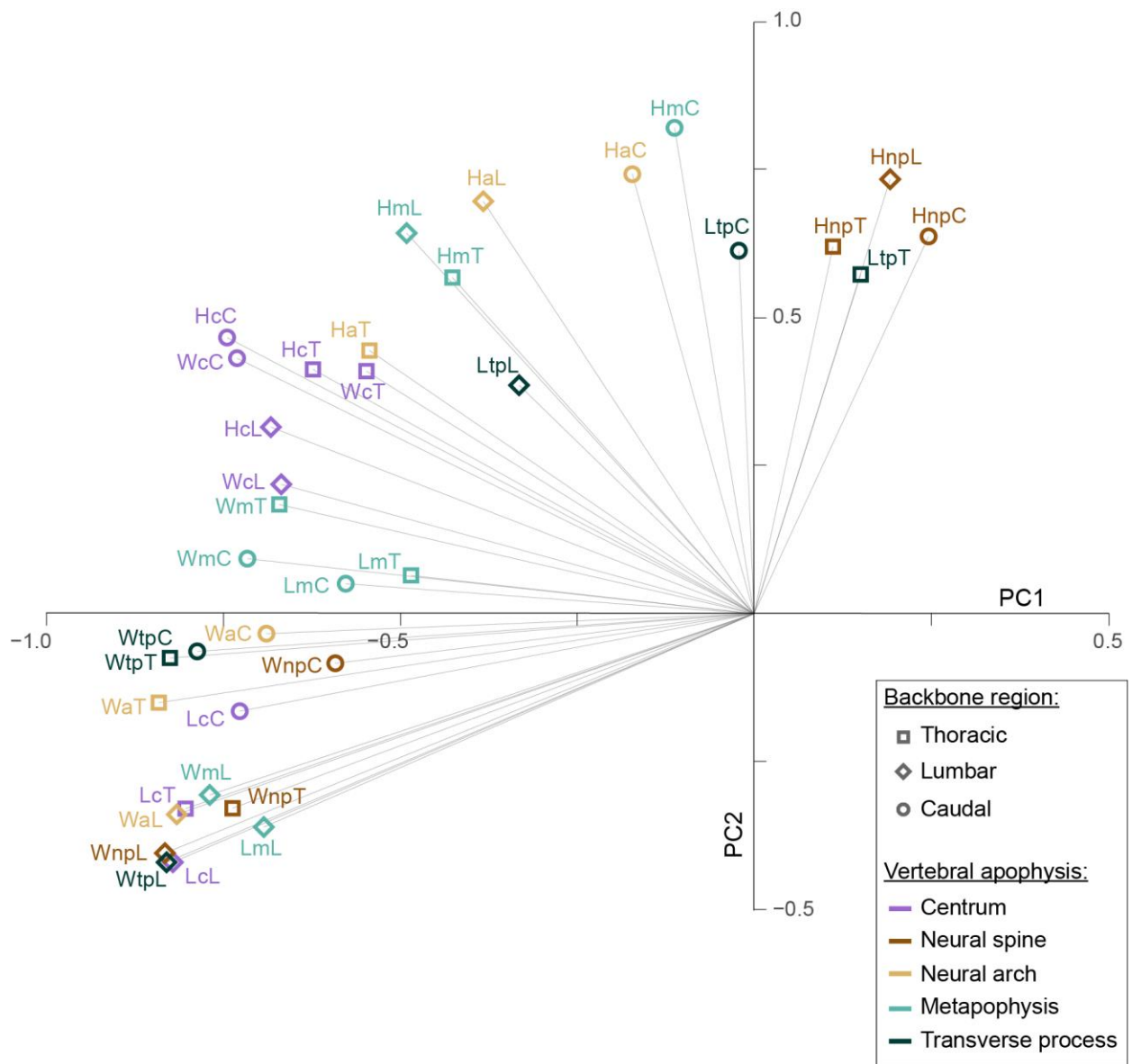


Figure S2. Variable correlations with the two first PCA axes. Variable names coded as follow: the first capital letter corresponds to the type of measurement (*L*: length, *H*: height, *W*: width), the following lowercase letters correspond the vertebral part (*c*: centrum, *np*: neural process, *na*: neural arch, *m*: metapophysis, *tp*: transverse process), and the last capital letter corresponds to the vertebral region (*T*: thoracic, *L*: lumbar, *C*: caudal).

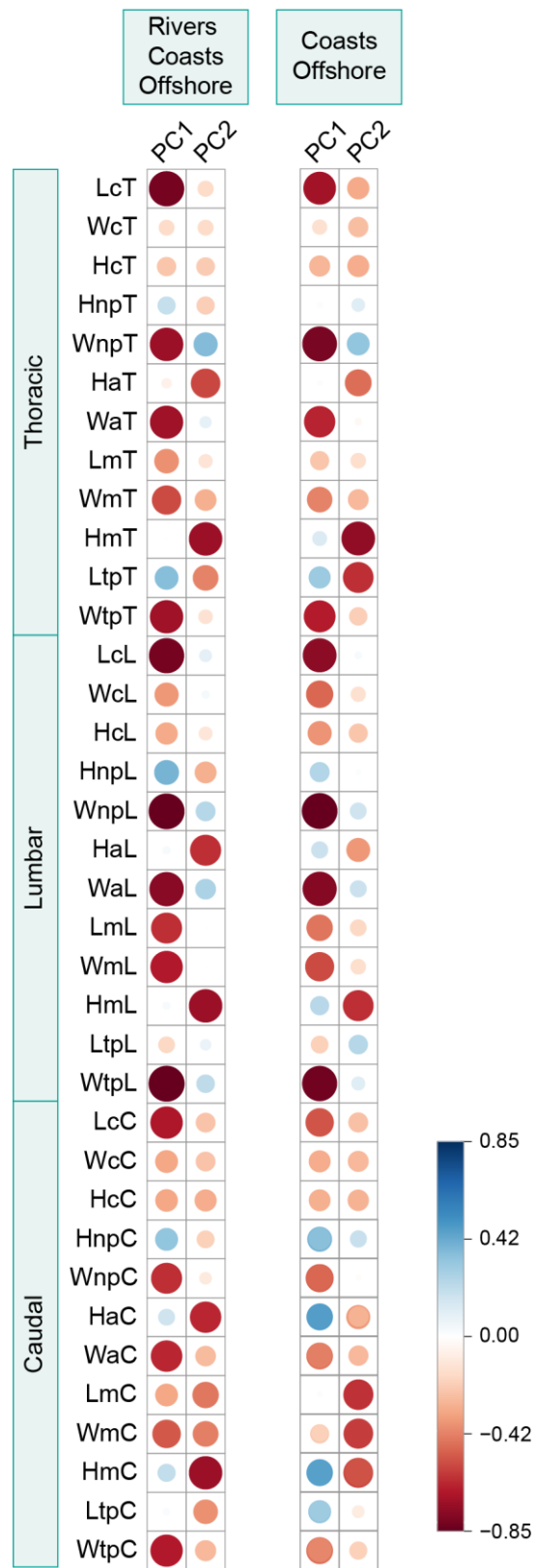


Figure S3. Correlations between vertebral shape residuals and PC axes of the phenotypic trajectory analysis. Variable names coded as in Figure S2.

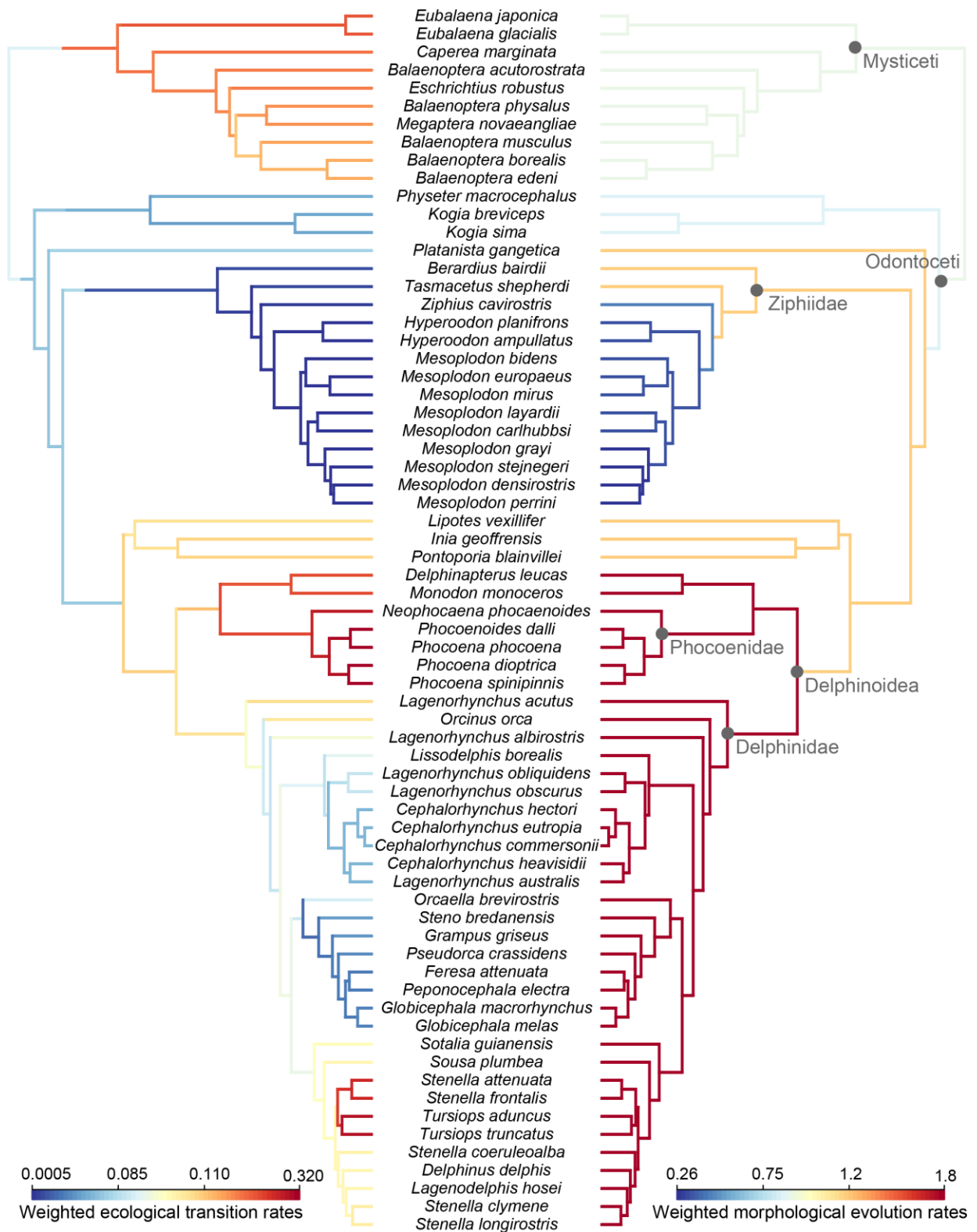


Figure S4. Phylorates of cetaceans. Weighted evolutionary rates of habitat transitions (left) and vertebral shape (right) of delphinoids averaged from single and multirate models.

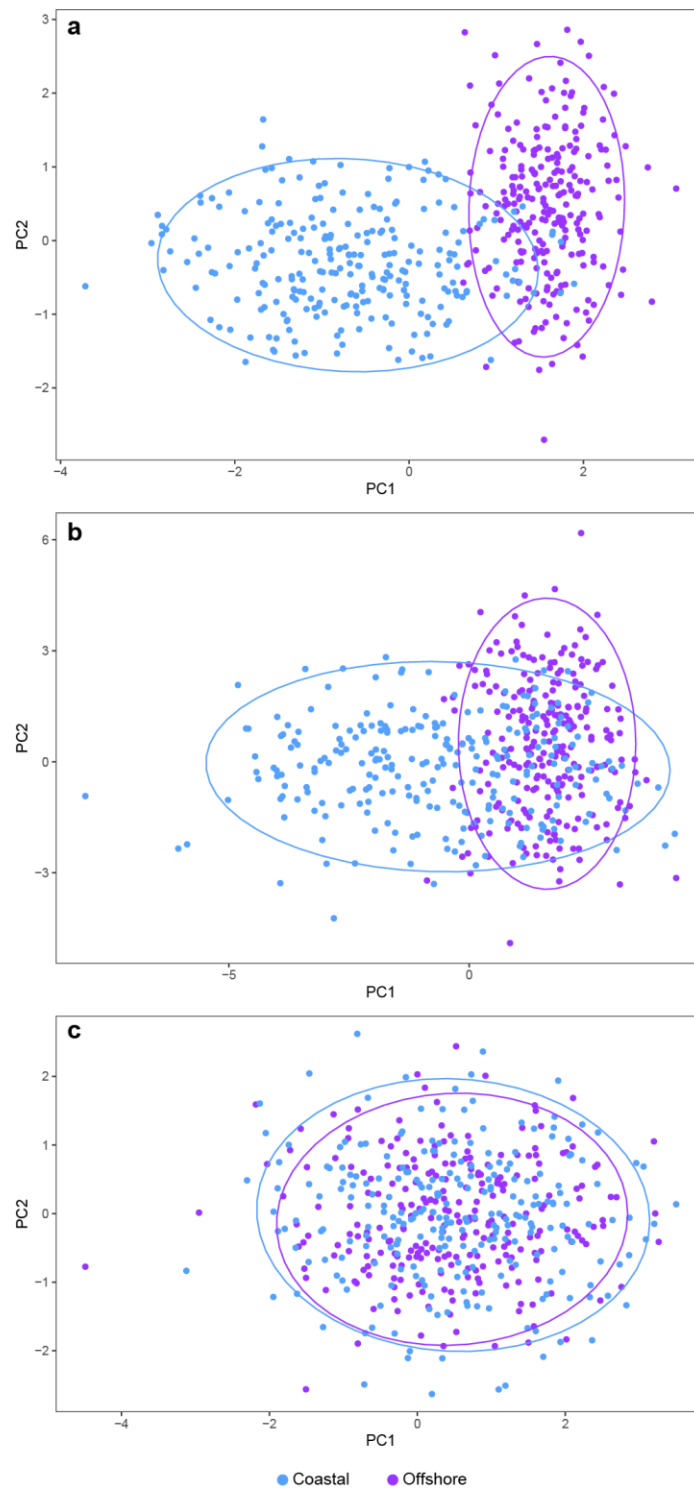


Figure S5. Morphospace of 500 randomly simulated *T. truncatus* individuals (250 coastal and 250 offshore) following a normal distribution. Ellipses correspond to the 95% confidence for each ecological group. (a) First scenario with almost perfect segregation of ecological groups. (b) Second scenario with large overlap but still a significant difference between the two groups. (c) Third scenario with almost complete overlap and no significant difference between the two groups.

Table S1. List of specimens used in this study. *Tursiops truncatus* ecotypes are indicated beside the accession number: C: coasts, O: offshore. Museum abbreviations: MNHN: French National Museum of Natural History, Paris; NRM: Swedish Royal Museum of Natural History, Stockholm; PEM: Bayworld Port Elizabeth Museum, Port Elizabeth; QM: Queensland Museum, Brisbane; RBINS: Royal Belgian Institute of Natural Sciences, Brussels; SAM: Iziko South African Museum, Cape Town; SMNS: State Museum of Natural History, Stuttgart; USNM: Smithsonian National Museum of Natural History, Washington D.C..

<u>Monodontidae</u>		<i>Cephalorhynchus heavisidii</i>	SAM ZM 0014
<i>Delphinapterus leucas</i>	MNHN A3246		SAM ZM19943
	NRM 558404		SAM ZM36717
	RBINS 1508	<i>Cephalorhynchus hectori</i>	SAM ZM36182
	USNM 571021		USNM 500864
<i>Monodon monoceros</i>	MNHN A3235	<i>Delphinus delphis</i>	NRM 805172
	NRM 558407		USNM 500273
	USNM 594407		USNM 593770
<u>Phocoenidae</u>		<i>Feresa attenuata</i>	PEM N4762
<i>Neophocaena phocaenoides</i>	SMNS 45679		PEM N4763
	SMNS 45680		USNM 571268
	SMNS 45681	<i>Globicephala macrorhynchus</i>	USNM 22561
	USNM 240002		USNM 593641
<i>Phocoena dioptrica</i>	USNM 571485	<i>Globicephala melas</i>	NRM 558264
	USNM 571486		USNM 21118
<i>Phocoena phocoena</i>	NRM 895156	<i>Grampus griseus</i>	PEM N117
	NRM 20065226		USNM 347613
	NRM 558322		USNM 504328
	NRM 805026	<i>Lagenodelphis hosei</i>	PEM N395
	NRM 815072		PEM N827
	NRM 835011		USNM 571619
	NRM 845002	<i>Lagenorhynchus acutus</i>	USNM 504153
	NRM 855083		USNM 504154
	NRM 855196		USNM 504164
	NRM 865039	<i>Lagenorhynchus albirostris</i>	NRM 20065395
	NRM 865044		SMNS 7591
	NRM 875045		USNM 550208
	NRM 875216	<i>Lagenorhynchus australis</i>	USNM 395347
	NRM 875358		USNM 395350
<i>Phocoena spinipinnis</i>	USNM 395751	<i>Lagenorhynchus obliquidens</i>	USNM 504412
	USNM 550782		USNM 504413
	USNM 550785		USNM 504415
<i>Phocoenoides dalli</i>	USNM 396304	<i>Lagenorhynchus obscurus</i>	SAM ZM41890
	USNM 504417		SAM ZM35681
	USNM 504969	<i>Lissodelphis borealis</i>	USNM 484929
<u>Delphinidae</u>			USNM 550026
<i>Cephalorhynchus commersonii</i>	SAM ZM40555	<i>Orcaella brevirostris</i>	RBINS 1512
	USNM 550154	<i>Orcinus orca</i>	NRM 558250
	USNM 550156		NRM 558251
<i>Cephalorhynchus eutropia</i>	NRM 616647		NRM 558401
	USNM 395374		

Table S1 (continued).

<i>Peponocephala electra</i>	SAM ZM38245	<i>Stenella coeruleoalba</i>	PEM N289
	USNM 550399		USNM 504350
	USNM 593799		USNM 504384
	USNM 593941	<i>Stenella frontalis</i>	USNM 21915
<i>Pseudorca crassidens</i>	NRM 558271		USNM 22017
	NRM 558405		USNM 504321
	QM J14210	<i>Stenella longirostris</i>	PEM N1278
<i>Sotalia guianensis</i>	RBINS 20137		USNM 395414
	RBINS 1516		USNM 500017
	USNM 571558	<i>Steno bredanensis</i>	SAM ZM41124
<i>Sousa plumbea</i>	PEM N1179		USNM 504462
	PEM N1266		USNM 504468
	PEM N1582	<i>Tursiops aduncus</i>	SAM ZM38240
	PEM N1593		SMNS 45711
	USNM 550939	<i>Tursiops truncatus</i>	USNM 484529
<i>Stenella attenuata</i>	USNM 395390		USNM 504618 ^o
	USNM 396028		USNM 504726 ^o
	USNM 500122		USNM 504906 ^o
<i>Stenella clymene</i>	USNM 550501		USNM 550225 ^c
	USNM 550511		USNM 550364
	USNM 550532		USNM 550422 ^c
			USNM 550852
			USNM 571388 ^c

Table S2. Classification of species included in this study according to their habitat. Numbers in brackets indicate the number of specimens per species. When considered as a species, *T. truncatus* was classified as a “mixed” species. Mono. Monodontidae, Phoco.: Phocoenidae, Delphi.: Delphinidae.

	<u>Rivers & Bays</u>	<u>Coastal</u>	<u>Mixed</u>	<u>Offshore</u>
<u>Mono.</u>			<i>Delphinapterus leucas</i> (4) <i>Monodon monoceros</i> (3)	
<u>Phoco.</u>	<i>Neophocaena phocaenoides</i> (4)	<i>Phocoena phocoena</i> (14) <i>Phocoena spinipinnis</i> (3)	<i>Phocoena dioptrica</i> (2)	<i>Phocoenoides dalli</i> (3)
<u>Delphi.</u>	<i>Orcaella brevirostris</i> (1) <i>Sotalia guianensis</i> (3) <i>Sousa plumbea</i> (5)	<i>Cephalorhynchus commersonii</i> (3) <i>Cephalorhynchus eutropia</i> (2) <i>Cephalorhynchus heavisidii</i> (3) <i>Cephalorhynchus hectori</i> (2) <i>Lagenorhynchus australis</i> (2) <i>Lagenorhynchus obscurus</i> (2) <i>Tursiops aduncus</i> (2)	<i>Orcinus orca</i> (3) <i>Stenella frontalis</i> (3) <i>Stenella longirostris</i> (3) <i>Tursiops truncatus</i> (9)	<i>Delphinus delphis</i> (3) <i>Feresa attenuata</i> (3) <i>Globicephala macrorhynchus</i> (2) <i>Globicephala melas</i> (2) <i>Grampus griseus</i> (3) <i>Lagenodelphis hosei</i> (3) <i>Lagenorhynchus acutus</i> (3) <i>Lagenorhynchus albirostris</i> (3) <i>Lagenorhynchus obliquidens</i> (3) <i>Lissodelphis borealis</i> (2) <i>Peponocephala electra</i> (4) <i>Pseudorca crassidens</i> (3) <i>Stenella attenuata</i> (3) <i>Stenella clymene</i> (3) <i>Stenella coeruleoalba</i> (3) <i>Steno bredanensis</i> (3)
<u>Total :</u>	4 species (13 specimens)	9 species (33 specimens)	7 species (27 specimens)	17 species (49 specimens)

Table S3. Variance (*Var.*) of morphological residuals and their correlation and contribution (in %) to the two first principal components (PC1 and PC2) of the PCA. Variable names are coded as follow: the first capital letter corresponds to the type of measurement (*L*: length, *H*: height, *W*: width), the following lowercase letters correspond the vertebral part (*c*: centrum, *np*: neural process, *na*: neural arch, *m*: metapophysis, *tp*: transverse process), and the last capital letter corresponds to the vertebral region (*T*: thoracic, *L*: lumbar, *C*: caudal).

	Variance	Correlation		Contribution	
		PC1	PC2	PC1	PC2
LcT	0.0033	-0.803	-0.329	4.71	1.57
WcT	0.0028	-0.548	0.410	2.19	2.43
HcT	0.0029	-0.623	0.413	2.83	2.47
HnpT	0.0123	0.112	0.620	0.09	5.57
WnpT	0.0116	-0.737	-0.329	3.96	1.56
HaT	0.0055	-0.543	0.445	2.15	2.86
WaT	0.0048	-0.841	-0.150	5.16	0.33
LmT	0.0141	-0.485	0.065	1.71	0.06
WmT	0.0095	-0.671	0.185	3.28	0.49
HmT	0.0049	-0.426	0.568	1.32	4.67
LtpT	0.0083	0.151	0.573	0.17	4.76
WtpT	0.0044	-0.825	-0.075	4.97	0.08
LcL	0.0125	-0.821	-0.420	4.92	2.55
WcL	0.0035	-0.668	0.219	3.25	0.69
HcL	0.0034	-0.683	0.315	3.40	1.44
HnpL	0.01	0.192	0.734	0.27	7.80
WnpL	0.018	-0.832	-0.405	5.05	2.37
HaL	0.0056	-0.383	0.697	1.07	7.03
WaL	0.0101	-0.815	-0.339	4.85	1.67
LmL	0.1487	-0.692	-0.361	3.50	1.88
WmL	0.0852	-0.769	-0.306	4.32	1.36
HmL	0.0072	-0.491	0.643	1.76	5.99
LtpL	0.003	-0.332	0.386	0.80	2.16
WtpL	0.0216	-0.830	-0.420	5.03	2.55
LcC	0.0093	-0.727	-0.165	3.85	0.39
WcC	0.0032	-0.730	0.432	3.89	2.70
HcC	0.0032	-0.744	0.467	4.04	3.15
HnpC	0.0201	0.247	0.638	0.44	5.88
WnpC	0.0109	-0.591	-0.084	2.55	0.10
HaC	0.0115	-0.172	0.743	0.22	7.98
WaC	0.0075	-0.689	-0.034	3.46	0.02
LmC	0.051	-0.577	0.051	2.43	0.04
WmC	0.0219	-0.716	0.093	3.74	0.13
HmC	0.0175	-0.112	0.821	0.09	9.76
LtpC	0.0121	-0.021	0.614	0.00	5.45
WtpC	0.0185	-0.787	-0.064	4.51	0.06

Table S4. Number and proportion (%) of transitions between each pair of habitats. Numbers of shifts are averaged over 1,000 repeated stochastic mapping on the delphinoid tree.

Total number of shifts	Delphinoidea		Phocoenidae		Delphinidae	
	29.01		4.41		19.28	
	Number	%	Number	%	Number	%
Rivers → Coasts	1.16	3.99	0.31	7.01	0.60	3.10
Rivers → Mixed	1.37	4.71	0.13	2.88	0.76	3.93
Rivers → Offshore	1.94	6.68	0.11	2.54	1.58	8.18
Coasts → Rivers	1.47	5.06	0.59	13.36	0.66	3.41
Coasts → Mixed	2.24	7.71	0.94	21.23	0.75	3.89
Coasts → Offshore	3.79	13.07	0.94	21.23	2.58	13.37
Mixed → Rivers	1.55	5.36	0.20	4.56	0.66	3.43
Mixed → Coasts	1.84	6.35	0.37	8.37	0.69	3.58
Mixed → Offshore	2.41	8.32	0.12	2.81	1.41	7.31
Offshore → Rivers	3.39	11.70	0.22	4.90	2.97	15.39
Offshore → Coasts	3.63	12.52	0.38	8.51	3.01	15.58
Offshore → Mixed	4.22	14.53	0.11	2.59	3.63	18.83

Table S5. Results of regular and phylogenetically-corrected MANOVAs and pairwise comparisons testing the effect of habitat in Delphinoidea, Delphinidae, Phocoenidae and *T. truncatus*. Regular MANOVAs were computed on specimen values while phylo-MANOVAs were calculated on species-averaged values. Roy's statistics (Roy), effect sizes (Z) and *p*-values (*P*) are reported. Significant results are in bold.

	Regular MANOVAs			Phylo-MANOVAs		
	Roy	Z	<i>P</i>	Roy	Z	<i>P</i>
Delphinoidea	1.572	8.477	0.0001	1.572	2.631	0.0045
Rivers × Coasts		2.908	0.0015		0.097	0.4539
Rivers × Mixed		0.870	0.1932		0.683	0.2512
Rivers × Offshore		5.384	0.0001		2.542	0.0018
Coasts × Mixed		2.037	0.0213		-1.402	0.9171
Coasts × Offshore		5.269	0.0001		2.533	0.0036
Offshore × Mixed		4.990	0.0001		1.822	0.0364
Delphinidae	2.222	7.495	0.0001	2.734	2.525	0.0066
Rivers × Coasts		2.484	0.0051		0.177	0.4224
Rivers × Mixed		2.184	0.014		1.035	0.1542
Rivers × Offshore		4.429	0.0001		2.241	0.0114
Coasts × Mixed		0.351	0.3637		-0.422	0.658
Coasts × Offshore		3.961	0.0001		1.764	0.0423
Offshore × Mixed		2.191	0.0128		0.139	0.4359
Phocoenidae	62.351	5.562	0.0001	/	/	/
Rivers × Coasts		1.917	0.0409		/	/
Rivers × Mixed		1.052	0.1749		/	/
Rivers × Offshore		3.846	0.0001		/	/
Coasts × Mixed		0.259	0.4128		/	/
Coasts × Offshore		3.433	0.0002		/	/
Offshore × Mixed		2.596	0.0046		/	/
<i>T. truncatus</i>	6.577	1.721	0.0842	/	/	/

Table S6. Results of non-phylogenetic and phylogenetic ANOVAs on specimen values for the 7 first PCs individually. Pairwise test were run for non-phylogenetic ANOVA when a significant effect of habitat was found. Note that phylogenetic ANOVAs cannot be run on *T. truncatus* specimens as their intraspecific phylogenetic relationship is unknown. F- statistic (*F*), non-phylogenetic *P*-value (*P*) and phylogenetic *P*-value based on 10,000 simulations (*phylo-P*) are reported. Significant values are indicated in bold. Proportion of total variance explained by each PC is indicated in between brackets besides each PC.

	PC1 (38.07%)			PC2 (19.20%)			PC3 (11.527%)			PC4 (8.17%)			PC5 (5.38%)			PC6 (3.16%)			PC7 (2.37%)		
	F	<i>P</i>	<i>phylo-P</i>	F	<i>P</i>	<i>phylo-P</i>	F	<i>P</i>	<i>phylo-P</i>	F	<i>P</i>	<i>phylo-P</i>	F	<i>P</i>	<i>phylo-P</i>	F	<i>P</i>	<i>phylo-P</i>	F	<i>P</i>	<i>phylo-P</i>
Delphinoidea	36.68	< 0.0001	0.0006	3.15	0.0277	0.7589	8.12	< 0.0001	0.3172	7.50	0.0001	0.3725	0.24	0.8656	0.9912	1.74	0.162	0.8643	3.74	0.0131	0.7061
Rivers × Coasts		0.0360			1			< 0.0001			0.4819									0.014	
Rivers × Mixed		1			1			0.0558			1									0.405	
Rivers × Offshore		< 0.0001			0.1430			0.0072			1									0.644	
Coasts × Mixed		0.1410			1			0.2156			0.0018									1	
Coasts × Offshore		< 0.0001			0.0620			0.0794			0.0002									0.127	
Offshore × Mixed		< 0.0001			1			1			1									1	
Delphinidae	23.72	< 0.0001	0.0149	2.12	0.1048	0.761	10.54	< 0.0001	0.1733	3.55	0.0183	0.5921	0.66	0.5815	0.9526	0.33	0.8065	0.9776	3.44	0.021	0.6796
Rivers × Coasts		0.6247						< 0.0001			1									0.413	
Rivers × Mixed		0.0733						0.0062			0.196									1	
Rivers × Offshore		< 0.0001						< 0.0001			0.029									1	
Coasts × Mixed		1						0.5558			1									1	
Coasts × Offshore		< 0.0001						0.2012			0.361									0.015	
Offshore × Mixed		0.0059						1			1									1	
Phocoenidae	63.71	< 0.0001	0.1671	38.24	< 0.0001	0.1372	3.03	0.0511	0.609	68.49	< 0.0001	0.1541	3.80	0.0247	0.7437	5.15	0.0075	0.6479	28.06	< 0.0001	0.1986
Rivers × Coasts		0.0006			0.0011						< 0.0001			1			0.0439			< 0.0001	
Rivers × Mixed		0.2262			0.0598						0.9515			0.536			0.083			< 0.0001	
Rivers × Offshore		< 0.0001			< 0.0001						< 0.0001			0.048			0.0087			0.177	
Coasts × Mixed		1			1						0.0006			0.961			1			0.03	
Coasts × Offshore		< 0.0001			< 0.0001						< 0.0001			0.058			0.4975			0.0052	
Offshore × Mixed		< 0.0001			< 0.0001						< 0.0001			1			1			0.0002	
<i>T. truncatus</i>	11.79	0.0265	/	1.09	0.3554	/	37.25	0.0037	/	0.03	0.8681	/	1.43	0.2974	/	3.99	0.1166	/	0.20	0.6763	/

Table S7. Results of non-phylogenetic and phylogenetic ANOVAs on species-averaged values for the 7 first PCs individually. Pairwise test were run when a significant effect of habitat was found. Note that phylogenetic ANOVAs cannot be run on Phocoenidae because the number of species is too small and on *T. truncatus*. F- statistic (*F*), non-phylogenetic *P*-value (*P*) and phylogenetic *P*-value based on 10,000 simulations (*phylo-P*) are reported. Significant values are indicated in bold. Proportion of total variance explained by each PC is indicated in between brackets besides each PC.

	PC1 (38.07%)			PC2 (19.20%)			PC3 (11.527%)			PC4 (8.17%)			PC5 (5.38%)			PC6 (3.16%)			PC7 (2.37%)		
	F	<i>P</i>	<i>phylo-P</i>	F	<i>P</i>	<i>phylo-P</i>	F	<i>P</i>	<i>phylo-P</i>	F	<i>P</i>	<i>phylo-P</i>	F	<i>P</i>	<i>phylo-P</i>	F	<i>P</i>	<i>phylo-P</i>	F	<i>P</i>	<i>phylo-P</i>
Delphinoidea	11.33	< 0.0001	< 0.0001	0.69	0.565	0.781	2.26	0.099	0.316	0.75	0.529	0.770	0.38	0.767	0.902	0.85	0.477	0.732	1.62	0.193	0.422
Rivers × Coasts		1	1																		
Rivers × Mixed		1	1																		
Rivers × Offshore		0.012	0.003																		
Coasts × Mixed		1	1																		
Coasts × Offshore		0.0015	0.048																		
Offshore × Mixed		0.001	0.0102																		
Delphinidae	8.81	0.0004	0.0171	1.27	0.306	0.624	2.36	0.095	0.375	1.05	0.389	0.707	0.32	0.809	0.927	0.21	0.89	0.961	1.09	0.370	0.691
Rivers × Coasts		1	1																		
Rivers × Mixed		1	1																		
Rivers × Offshore		0.0045	0.015																		
Coasts × Mixed		1	1																		
Coasts × Offshore		0.0025	0.225																		
Offshore × Mixed		0.3013	0.4464																		

Table S8. Results of phylogenetically-corrected ANOVAs and MANOVAs testing the effect of habitat in Delphinoidea and Delphinidae on each PC individually (phylo-ANOVAs) and on an incremental number of PCs (phylo-MANOVAs). The proportion of total variance (*% var*), F statistics (*F* and *F-Roy*), effect sizes (*Z*) and *p*-values (*P*) are reported for each test. Significant results are in bold.

		Phylo-ANOVAs						Phylo-MANOVAs					
		Delphinoidea		Delphinidae				Delphinoidea			Delphinidae		
<i>PC</i>	<i>% var</i>	<i>F</i>	<i>P</i>	<i>F</i>	<i>P</i>	<i>PCs</i>	<i>% var</i>	<i>F - Roy</i>	<i>Z</i>	<i>P</i>	<i>F - Roy</i>	<i>Z</i>	<i>P</i>
1	38.07	11.331	0.0008	8.807	0.0154	1		See ANOVA			See ANOVA		
2	19.20	0.689	0.7816	1.269	0.624	1-2	57.27	1.088	3.603	0.0001	0.976	2.642	0.0044
3	11.52	2.260	0.3185	2.362	0.3664	1-3	68.78	1.202	3.341	0.0004	1.131	2.296	0.0106
4	8.17	0.752	0.7678	1.047	0.7007	1-4	76.96	1.228	3.021	0.0015	1.131	1.896	0.0293
5	5.38	0.382	0.9033	0.323	0.9292	1-5	82.33	1.235	2.711	0.0037	1.135	1.549	0.0598
6	3.16	0.849	0.7311	0.208	0.9633	1-6	85.49	1.349	2.624	0.0048	2.316	2.523	0.0063
7	2.37	1.624	0.4753	1.094	0.6905	1-7	87.85	1.572	2.631	0.0045	2.734	2.533	0.0062
8	1.80	0.778	0.767	0.929	0.7373	1-8	89.65	1.574	2.291	0.012	2.754	2.250	0.0117
9	1.63	5.913	0.0283	4.310	0.144	1-9	91.28	1.788	2.289	0.0118	2.755	1.936	0.0259
10	1.31	1.999	0.3734	5.678	0.0694	1-10	92.59	2.112	2.390	0.0079	3.477	2.093	0.0182
11	0.96	0.892	0.7094	1.219	0.6394	1-11	93.55	2.165	2.167	0.0149	3.528	1.788	0.036
12	0.78	3.470	0.1406	2.938	0.2835	1-12	94.34	2.251	1.994	0.0233	3.553	1.485	0.0691
13	0.67	0.661	0.794	1.094	0.6842	1-13	95.01	2.401	1.852	0.033	4.468	1.596	0.0534
14	0.65	0.614	0.8126	2.114	0.4165	1-14	95.66	3.091	2.153	0.0165	5.390	1.577	0.0558
15	0.57	1.208	0.6048	1.495	0.5659	1-15	96.23	3.203	1.936	0.0263	5.468	1.258	0.1049
16	0.49	0.049	0.9939	0.193	0.966	1-16	96.72	3.221	1.659	0.0478	5.703	0.980	0.1629
17	0.41	0.232	0.9498	0.106	0.9856	1-17	97.13	3.232	1.347	0.0878	5.941	0.661	0.2525
18	0.38	0.168	0.9706	1.202	0.6517	1-18	97.50	3.247	1.051	0.1458	9.414	1.045	0.1471
19	0.31	0.558	0.8452	0.379	0.9152	1-19	97.81	3.268	0.768	0.2214	9.495	0.654	0.2519
20	0.29	1.063	0.6553	0.798	0.7707	1-20	98.11	3.813	0.796	0.2134	27.902	1.675	0.048
21	0.25	0.145	0.9756	0.257	0.9489	1-21	98.36	4.213	0.693	0.2442	28.253	1.224	0.1124
22	0.23	1.800	0.4225	3.076	0.262	1-22	98.59	4.396	0.470	0.3179	29.004	0.717	0.2402
23	0.20	1.909	0.3996	2.312	0.3796	1-23	98.79	5.278	0.538	0.2928	29.194	0.113	0.4512
24	0.19	0.856	0.722	0.792	0.7825	1-24	98.97	5.335	0.210	0.4176	38.235	-0.311	0.6157
25	0.16	0.349	0.9144	0.896	0.7461	1-25	99.14	5.564	-0.068	0.5263	50.811	-0.921	0.81
26	0.15	1.276	0.5728	1.457	0.5679	1-26	99.28	6.363	-0.179	0.5703	39.587	-0.210	0.5719
27	0.13	0.957	0.6827	1.140	0.669	1-27	99.42	6.577	-0.512	0.6923	35.922	0.030	0.4942
28	0.11	0.453	0.8729	0.707	0.8081	1-28	99.53	9.312	-0.282	0.61	35.481	0.215	0.4146
29	0.10	0.005	0.9997	0.044	0.9962	1-29	99.63	13.484	-0.134	0.5506	27.539	0.591	0.2792
30	0.08	0.963	0.6867	0.776	0.7861	1-30	99.71	13.708	-0.620	0.727	15.640	-0.150	0.5549
31	0.07	1.069	0.6432	1.272	0.635	1-31	99.78	16.418	-0.931	0.823	12.650	0.145	0.4422
32	0.06	2.194	0.3295	1.527	0.5649	1-32	99.85	31.990	-0.787	0.7757	12.394	0.205	0.4213
33	0.05	0.340	0.9153	0.340	0.9236	1-33	99.90	37.737	-1.303	0.9051	11.319	0.605	0.2762
34	0.04	0.163	0.9721	0.552	0.857	1-34	99.94	34.523	-0.847	0.7989	11.320	1.225	0.1079
35	0.03	0.767	0.7582	0.712	0.8071	1-35	99.97	28.941	-0.726	0.7643	11.487	1.287	0.0972
36	0.03	0.942	0.6888	0.617	0.838	1-36	100.00	28.742	-0.051	0.5199	11.487	1.442	0.0734

Table S9. Vertebral shape convergence of delphinoids within each habitat category based on the full dataset and on the subsampled species dataset. C1, C2, C3, C4: distance-based convergence scores. *P*: *P*-values of each convergence score. Significant results are in bold.

	C1	<i>P</i>	C2	<i>P</i>	C3	<i>P</i>	C4	<i>P</i>
Full dataset								
Rivers	0.456	< 0.001	0.555	< 0.001	0.274	< 0.001	0.016	0.012
Coasts	0.375	< 0.001	0.452	< 0.001	0.189	< 0.001	0.013	0.018
Offshore	0.209	< 0.001	0.375	< 0.001	0.135	< 0.001	0.011	< 0.001
Subsampling								
Rivers	0.463	< 0.001	0.651	< 0.001	0.297	< 0.001	0.025	0.008
Coasts	0.292	0.004	0.378	0.002	0.123	0.014	0.015	0.142
Offshore	0.216	< 0.001	0.504	< 0.001	0.145	< 0.001	0.019	0.003

Table S10. Results of phenotypic trajectory analyses. Differences (Δ) in trajectory length, angle and shape, effect size (Z), and P -value (P) are presented for each pairwise comparison among phylogenetic groups. Significant results are in bold.

	Length			Angles			Shape		
	Δ	Z	P	Δ	Z	P	Δ	Z	P
<u>Rivers - Coasts - Offshore</u>									
Delphinidae \times Phocoenidae	5.760	2.531	0.002	59.88	2.847	0.004	0.304	1.721	0.040
<u>Coasts – Offshore</u>									
Delphinidae \times Phocoenidae	6.405	3.118	< 0.001	68.45	2.890	0.001	/	/	/
Delphinidae \times <i>T. truncatus</i>	2.469	0.893	0.191	47.63	1.089	0.144	/	/	/
Phocoenidae \times <i>T. truncatus</i>	8.874	3.212	< 0.001	53.27	0.952	0.174	/	/	/

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