Supplemental Materials

Table S2. Phylogenetic ANOVA results from each linear trait. Last three columns summarize pairwise differences between habitat regimes and associated p-values. Bolded habitat comparisons are considered statistically significant ($p < 0.05$).

Trait	Sum sq	R sq	F-value	Z-score	P-value	Habitats	pairwise P-value
Standard length	0.003	0.001	1.7	0.89	0.18	demersal – benthic	0.739
						pelagic – benthic	0.1141
						pelagic – demersal	0.0702
Max body depth	0.006	0.003	4.21	1.56	0.02	demersal – benthic	0.2833
						pelagic – benthic	0.2062
						pelagic – demersal	**0.0076**
Max fish width	0.002	0.001	1.26	0.66	0.27	demersal – benthic	0.1578
						pelagic – benthic	0.7152
						pelagic – demersal	0.36
Head depth	0.033	0.009	14.55	2.48	0	**demersal – benthic**	**1e-04**
						pelagic – benthic	**0.0297**
						pelagic – demersal	**0.0382**
Lower jaw length	0.012	0.001	1.59	0.84	0.19	demersal – benthic	0.0779
						pelagic – benthic	0.1397
						pelagic – demersal	0.799
Mouth width	0.013	0.001	1.08	0.53	0.32	demersal – benthic	0.1534
						pelagic – benthic	0.1952
						pelagic – demersal	0.7225
Min caudalpeduncle depth	0.03	0.002	3.64	1.47	0.03	**demersal – benthic**	**0.0323**
						pelagic – benthic	0.6926
						pelagic – demersal	0.0824
Min caudalpeduncle width	0.022	0.001	1.23	0.63	0.28	demersal – benthic	0.4179
						pelagic – benthic	0.6219
						pelagic – demersal	0.1529

Table S3. Comparisons of two evolutionary model fits for each linear trait averaged over 100 replications. In every case, the multi-rate Brownian motion model (BMS) is a better fit. delta AICc is the difference in AICc between the model and the best-fit model.

Trait	Model	AICc	ΔAICc	lnl	σ_{Benthic}	σ_{Demersal}	σ_{Pelagic}
Head depth	BM1	-2826	22	1415	0.113	0.113	0.113
	BMS	-2848	0	1428	0.125	0.103	0.115
Lower jaw length	BM1	1334	123	-665	0.392	0.392	0.392
	BMS	1211	0	-601	0.260	0.494	0.364
Max body depth	BM1	-4339	103	2171	0.072	0.072	0.072
	BMS	-4442	0	2225	0.094	0.056	0.071
Max fish width	BM1	-4253	42	2128	0.074	0.074	0.074
	BMS	-4295	0	2151	0.085	0.075	0.053
Min caudalpeduncle depth	BM1	1529	452	-763	0.416	0.416	0.416
	BMS	1077	0	-535	0.753	0.261	0.243
Min caudalpeduncle width	BM1	4032	52	-2014	0.879	0.879	0.879
	BMS	3980	0	-1986	1.112	0.800	0.698
Mouth width	BM1	2656	82	-1326	0.583	0.583	0.583
	BMS	2574	0	-1283	0.406	0.638	0.729
Standard length	BM1	-4054	91	2029	0.078	0.078	0.078
	BMS	-4145	0	2076	0.100	0.060	0.086

Table S4. Average independent contrast for habitat transitions and traits that significantly differed from zero ($p < 0.05$) across 100 simmaps. “n” is the number of simmaps in which the trait and transition combination were significant. Results are only reported for those relationships that are significant in over 50% of the simmaps. Negative values of the average contrast indicate that the trait decreased at the transition, more than it increased.

Trait	$Habitat_{From}$	$Habitat_{To}$	Average PIC	n
Head depth	demersal	benthic	-0.0209	87
Min caudalpeduncle depth	demersal	benthic	-0.0338	65
Head depth	benthic	demersal	0.0085	96
Max body depth	demersal	pelagic	-0.0051	88
Max fish width	benthic	pelagic	-0.0134	67
Standard length	demersal	pelagic	0.0052	91

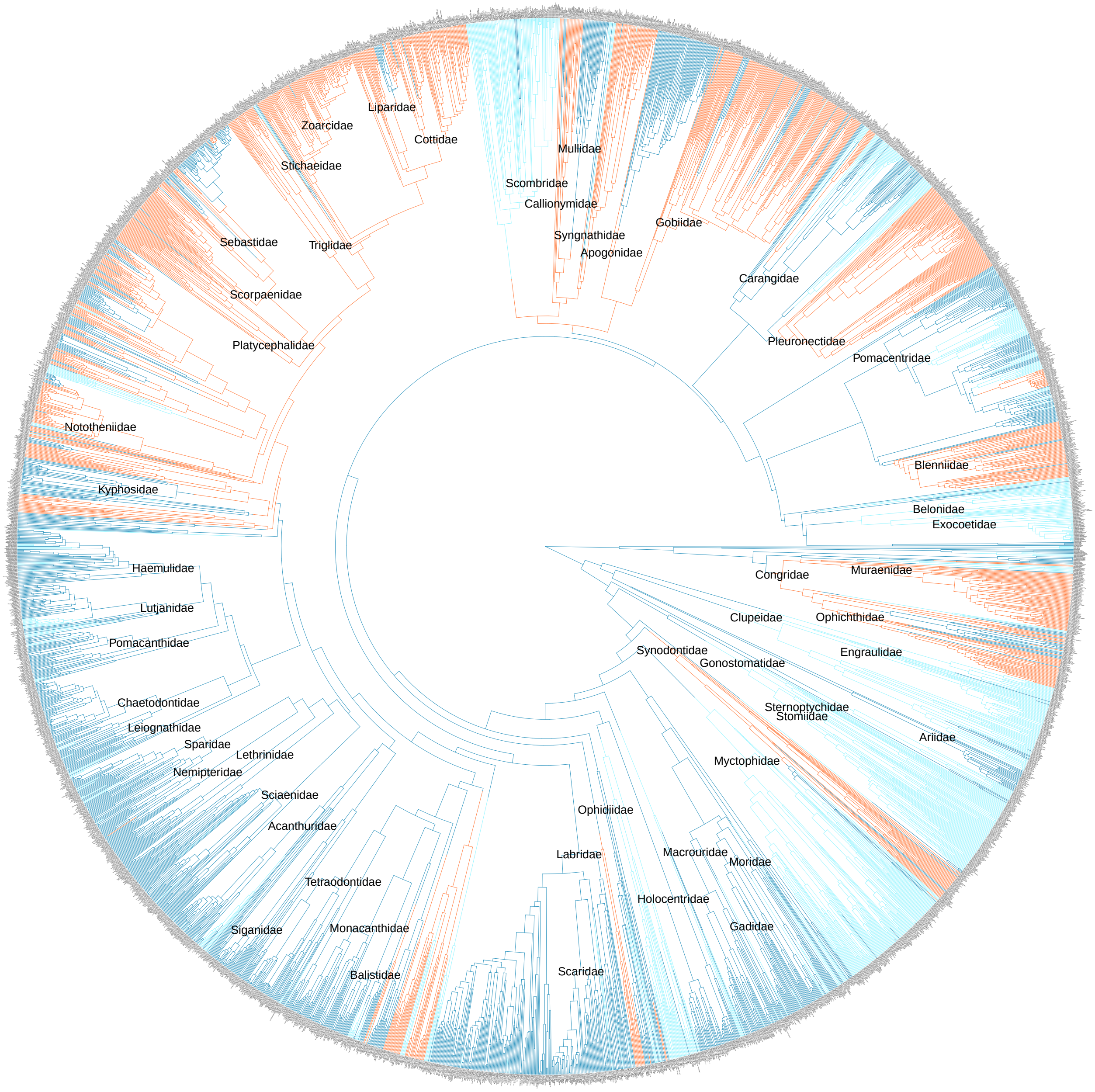

Figure S1: Representative stochastic character reconstruction showing habitat transitions across the phylogeny (benthic: orange; demersal: dark blue; pelagic: light blue). Names of families with more than 15 species present are printed at the node corresponding to the most recent common ancestor.

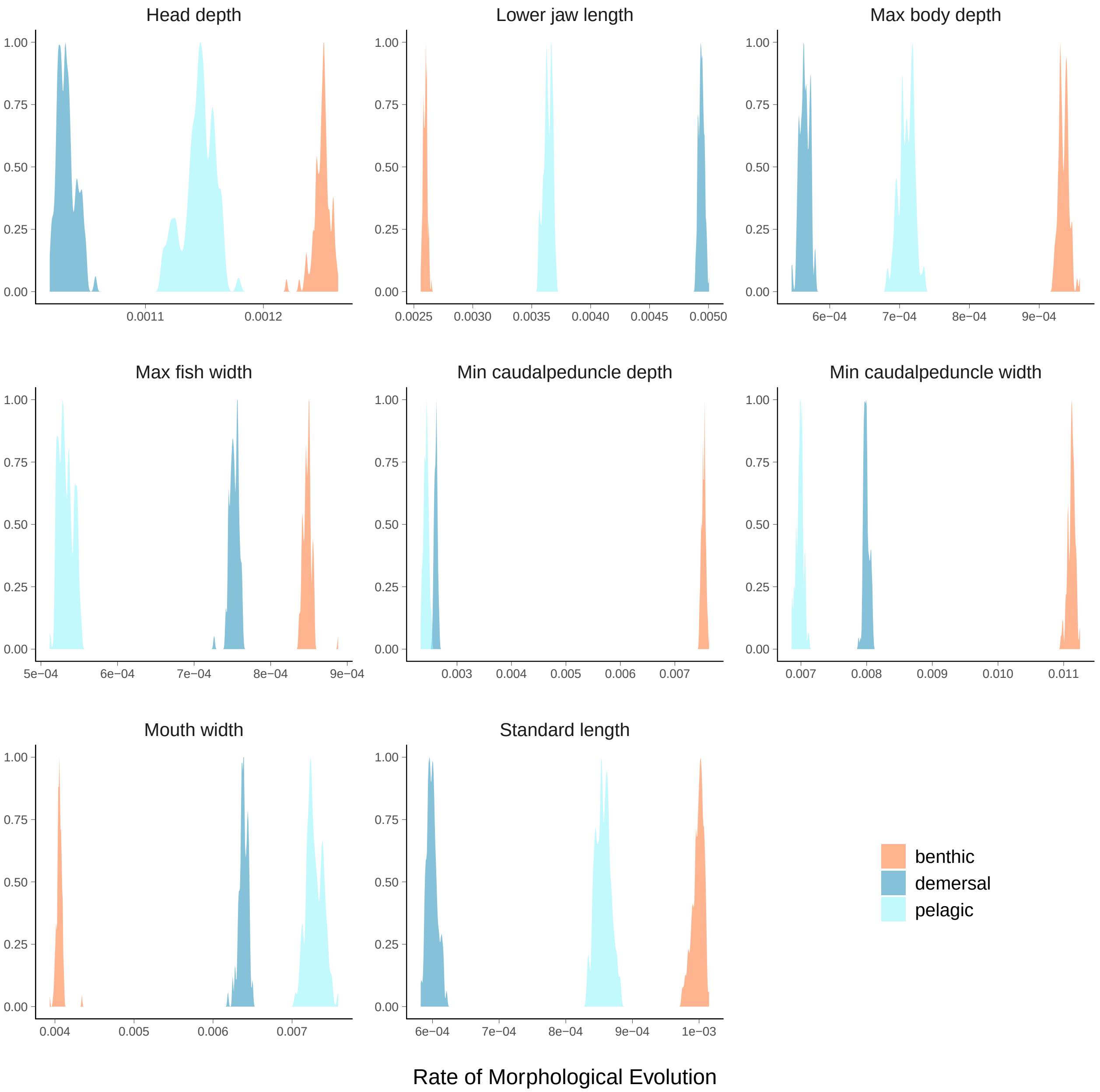

Figure S2: Plot summarizing the rate estimates from the OUwie analysis for each habitat and trait under the best fit model (BMS) across the 100 stochastic character maps.

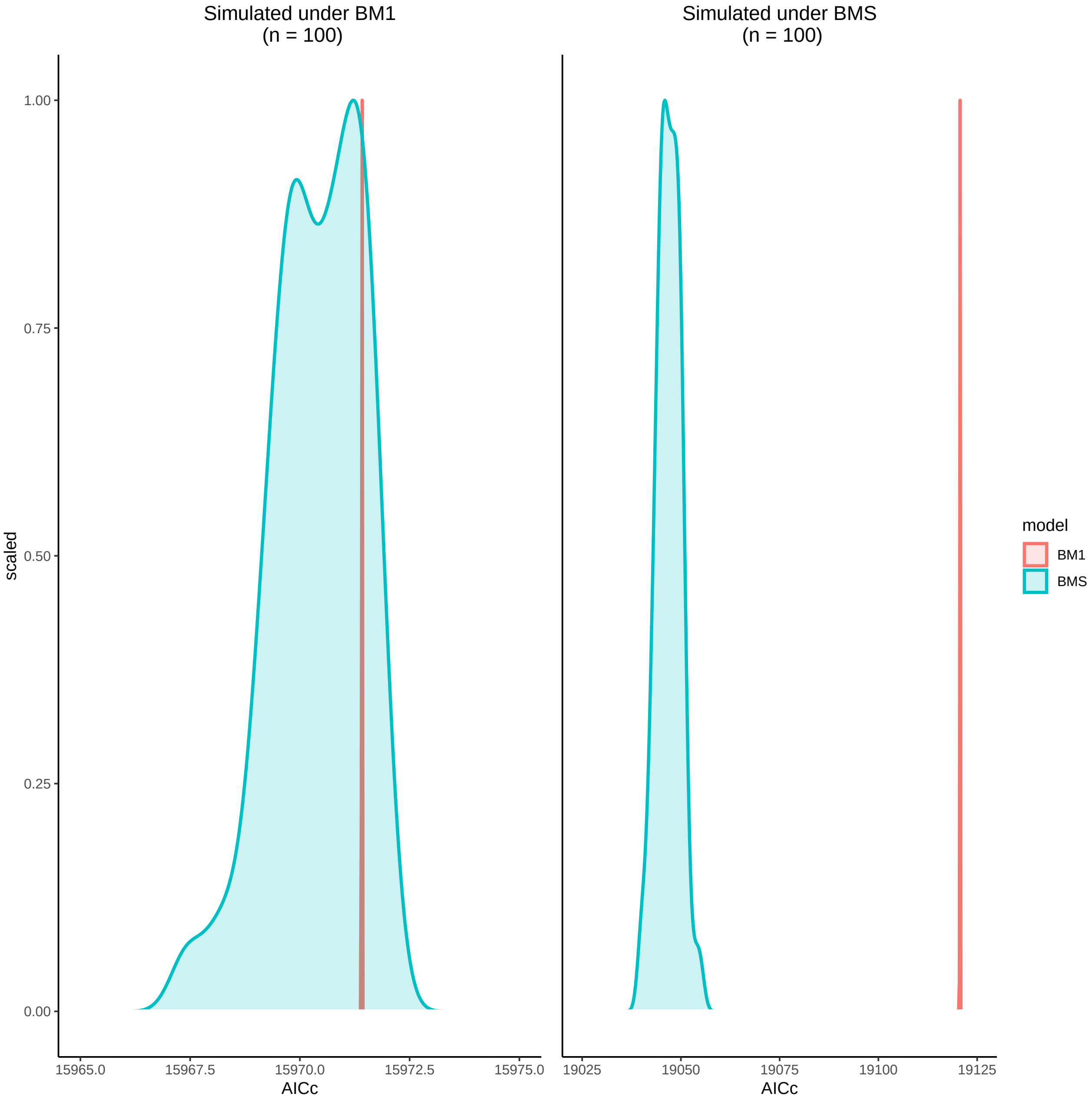

Figure S3: Plot summarizing the AICc estimates from the OUwie simulations under BM1 (left) and BMS (right) across the 100 stochastic character maps.

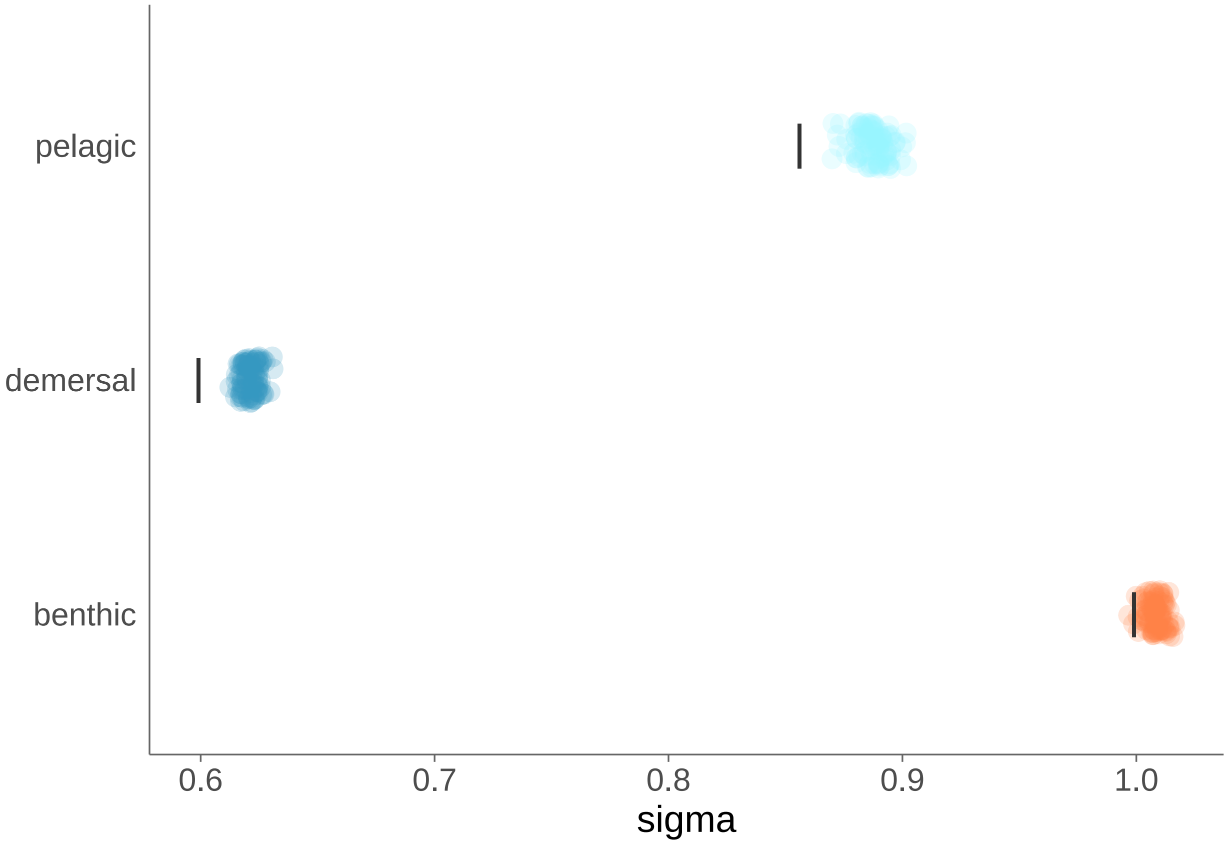

Figure S4: Distribution of sigma values by habitat for best-fit evolutionary models (all BMS) over 100 simulations. The horizontal black lines designate the original sigma under which datasets were simulated.