

Dataset	Sample	Phylogeny	Phylogenetic Comparative Method (PCM)	R ²	F	Z	P-value	AIC
Pooled-sex	Felidae	Piras et al. 2018	BM PGLS	0,321	9,002	3,854	<u>0,001</u>	-105,979
			RR PGLS	0,259	6,641	3,978	<u>0,001</u>	-115,138
		Faurby et al. 2019	BM PGLS	0,311	8,595	3,971	<u>0,001</u>	-112,403
			RR PGLS	0,353	10,383	4,334	<u>0,001</u>	-116,237
Female	Felidae	Piras et al. 2018	BM PGLS	0,230	5,680	3,697	<u>0,001</u>	-99,042
			RR PGLS	0,185	4,326	3,788	<u>0,001</u>	-105,607
		Faurby et al. 2019	BM PGLS	0,230	5,675	3,846	<u>0,001</u>	-103,460
			RR PGLS	0,261	6,711	4,300	<u>0,001</u>	-106,178
Male	Felidae	Piras et al. 2018	BM PGLS	0,275	7,203	3,934	<u>0,001</u>	-100,500
			RR PGLS	0,202	4,820	3,680	<u>0,001</u>	-104,826
		Faurby et al. 2019	BM PGLS	0,261	6,704	4,134	<u>0,001</u>	-105,487
			RR PGLS	0,271	7,060	4,197	<u>0,001</u>	-107,269

Table S3: Allometric regressions comparing pooled-sex, male and female datasets performed on the 30L configuration using Brownian Motion (BM) or phylogenetic ridge regression (RR) PGLS. Significant P-values at $\alpha = 0.05$ are underlined, whereas P-values still significant after applying a Benjamini-Hochberg procedure are in *italics*. Best fitting models according to the Akaike information criterion (AIC) are in bold.