

Dataset	Sample	Phylogeny	Phylogenetic Comparative Method (PCM)	R ²	F	Z	P-value	AIC
Pooled-sex	Felidae	Piras et al. 2018	BM PGLS	0,332	9,455	3,823	<u>0,001</u>	-117,702
			RR PGLS	0,275	7,213	3,756	<u>0,001</u>	-123,161
		Faurby et al. 2019	BM PGLS	0,331	9,398	4,023	<u>0,001</u>	-122,937
			RR PGLS	0,372	11,238	4,304	<u>0,001</u>	-125,713
Female	Felidae	Piras et al. 2018	BM PGLS	0,239	5,954	3,540	<u>0,001</u>	-106,126
			RR PGLS	0,195	4,614	3,457	<u>0,001</u>	-109,781
		Faurby et al. 2019	BM PGLS	0,240	6,015	3,630	<u>0,001</u>	-107,716
			RR PGLS	0,270	7,041	4,059	<u>0,001</u>	-109,968
Male	Felidae	Piras et al. 2018	BM PGLS	0,243	6,100	3,446	<u>0,001</u>	-99,304
			RR PGLS	0,162	3,686	2,757	<u>0,002</u>	-97,081
		Faurby et al. 2019	BM PGLS	0,239	5,978	3,655	<u>0,001</u>	-103,747
			RR PGLS	0,256	6,554	3,778	<u>0,001</u>	-102,496

Table S4: Allometric regressions comparing pooled-sex, male and female datasets performed on the 10L 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.