Supplementary material

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Mammalian intestinal allometry, phylogeny, trophic level and climate

María J. Duque-Correa, Daryl Codron, Carlo Meloro, Amanda McGrosky, Christian Schiffmann, Mark S. Edwards, Marcus Clauss*

*correspondence at mclauss@vetclinics.uzh.ch

- Additional thoughts on the very influential publication by Chivers and Hladik (1980)
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Additional thoughts on the very influential publication by Chivers and Hladik [1], where not only a plethora of digestive tracts are given as illustrations, but where digestive tract measures are also submitted to statistical analyses.
In that dataset, the overlap between diet groups is substantial – a fact typically not mentioned when it is cited. Various details of this work might lead to the conclusion that the methods are not robust: There is a dramatic difference in measures between the – ecologically, physiologically and anatomically similar – sheep (*Ovis aries*) and goat (*Capra hircus*) in the dataset, with sheep having less 'fermentation' capacity, tending towards the frugivores (Fig. 17, 18,); the rabbit (*Oryctolagus cuniculus*) is placed on the borderline between frugivores and folivores (Fig. 17, 18); the golden cat (*Profelis aurata*) and the domestic pig (*Sus scrofa*) have similar measures on the border between faunivores and frugivores (Fig. 17), and the domestic cat (*Felis catus*) is classified as more of a frugivore than the domestic pig and dog, which are both classified as fauni-/frugivores (Fig. 18); dietary classifications are not consistent across the analyses, e.g. the group of colobine monkeys is classified as both frugi- and folivorous in one display (Fig. 18) and as only folivorous in another (Fig. 20); whether a surface area of a haustrated structure like the colon of a pig or horse or gorilla can be really approximated using 'length and a series of breadths' (p. 356) appears questionable. Some of these problems are proactively addressed, e.g. in the legend of Fig. 20.

Additional analyses regarding the trophic level proxy. The proportion of animal matter (i.e., the reciprocal of the proportion of all plant matter) in the diet yielded the best fit for the total intestine-body mass relationship in GLS (ΔAIC to models with other diet proxies >8); in PGLS, it was equally supported as the faunivore-omnivore-herbivore classification with the 70% threshold (ΔAIC<2; ΔAIC to models with other diet proxies >3; Table S3). However, in the latter analysis, omnivores were not significantly different from faunivores. The proportion of more readily digestible plant parts (fruits, nectar, seeds), or of the less digestible plant parts (leaves and stems) did not yield a better data fit, and only had a significant effect in GLS but not PGLS (Table S3). Therefore, %faunivory was used as a trophic proxy throughout.

Table S1 Phylogenetic signals (K and λ) in the main datasets of the present study

	All available data					**Consistent species dataset**				
		body mass		intestine length			body mass		intestine length	
	n	K	λ	K	λ	n	K	λ	K	λ
Total intestine	519	0.76	0.99	0.76	0.98	351	0.61	0.99	0.62	0.98
Small intestine	397	0.63	0.99	0.58	0.98	351	0.61	0.99	0.59	0.98
Large intestine	387	0.64	0.99	0.66	0.99	351	0.61	0.99	0.64	0.99
Caecum	352	0.61	0.99	0.34	0.97	351	0.61	0.99	0.34	0.97
Colon	370	0.62	0.99	0.65	0.99	351	0.61	0.99	0.64	0.99

analyses performed in 'phytools' [2] using 9999 simulations per analysis and log-transformed values; all analyses significant at $P < 0.001$

Table S2 Summary statistics for allometric scaling as log(y) = a + b log(body mass), or y = (10^a) BM^b (significant parameters in **bold**)

			GLS				PGLS			
Dependent	**Model**	**n**	**AICc**	**ΔAIC**		**parameter (95%CI)**	**lambda (95%CI)**	**AICc**	**ΔAIC**	**parameter (95%CI)**
All data										
Total intest.	BM	519	-	-	a	**2.26 (2.24 to 2.28)**	0.93 (0.88 to 0.96)	-	-	**2.17 (1.85 to 2.49)**
					b	**0.48 (0.46 to 0.49)**				**0.40 (0.38 to 0.43)**
Small intest.	BM	397	-	-	a	**2.13 (2.11 to 2.15)**	0.93 (0.88 to 0.96)	-	-	**2.04 (1.69 to 2.39)**
					b	**0.46 (0.44 to 0.47)**				**0.40 (0.38 to 0.43)**
Large intest.	BM	387	-	-	a	**1.75 (1.71 to 1.78)**	0.97 (0.95 to 0.99)	-	-	**1.57 (1.09 to 2.06)**
					b	**0.41 (0.39 to 0.44)**				**0.37 (0.34 to 0.41)**
Caecum	BM	352	-	-	a	**0.98 (0.95 to 1.02)**	0.96 (0.94 to 0.98)	-	-	**0.71 (0.23 to 1.20)**
					b	**0.21 (0.18 to 0.24)**				**0.28 (0.25 to 0.32)**
Colon/Rect.	BM	370	-	-	a	**1.65 (1.61 to 1.68)**	0.97 (0.95 to 0.99)	-	-	**1.47 (0.94 to 2.01)**
					b	**0.45 (0.42 to 0.48)**				**0.39 (0.35 to 0.43)**
Consistent data (species for which both small and large intestinal length are available)										
Total intest.	BM	387	-94.9	4.3	a	**2.31 (2.29 to 2.33)**	0.92 (0.86 to 0.96)	-399.8	0.0	**2.20 (1.90 to 2.50)**
					b	**0.44 (0.43 to 0.46)**				**0.40 (0.37 to 0.42)**
Small intest.	BM	387	-99.2	0.0	a	**2.14 (2.11 to 2.16)**	0.94 (0.89 to 0.97)	-349.6	50.2	**2.04 (1.70 to 2.39)**
					b	**0.46 (0.44 to 0.47)**				**0.40 (0.38 to 0.43)**
Large intest.	BM	387	257.8	357.1	a	**1.75 (1.71 to 1.78)**	0.97 (0.95 to 0.99)	-214.9	184.8	**1.57 (1.09 to 2.06)**
					b	**0.41 (0.39 to 0.434)**				**0.37 (0.34 to 0.41)**
Consistent data (species for which small intestine, caecum and colon/rectum length are available)										
Total intest.	BM	351	-82.5	4.0	a	**2.31 (2.29 to 2.33)**	0.94 (0.90 to 0.97)	-391.7	0.0	**2.19 (1.88 to 2.51)**
					b	**0.44 (0.42 to 0.46)**				**0.39 (0.36 to 0.41)**
Small intest.	BM	351	-86.4	0.0	a	**2.13 (2.11 to 2.15)**	0.96 (0.92 to 0.98)	-347.5	44.2	**2.04 (1.68 to 2.40)**
					b	**0.45 (0.44 to 0.47)**				**0.40 (0.37 to 0.43)**
Large intest.	BM	351	182.5	268.9	a	**1.77 (1.74 to 1.81)**	0.97 (0.94 to 0.98)	-223.4	168.4	**1.59 (1.13 to 2.05)**
					b	**0.41 (0.38 to 0.43)**				**0.36 (0.33 to 0.40)**
Caecum	BM	351	234.9	321.3	a	**0.98 (0.95 to 1.02)**	0.96 (0.94 to 0.98)	-169.0	222.7	**0.71 (0.23 to 1.20)**
					b	**0.21 (0.18 to 0.24)**				**0.29 (0.25 to 0.32)**
Colon/Rect.	BM	351	222.2	308.6	a	**1.67 (1.63 to 1.70)**	0.97 (0.95 to 0.99)	-132.0	259.7	**1.48 (0.95 to 2.02)**
					b	**0.45 (0.42 to 0.47)**				**0.38 (0.34 to 0.42)**

AIC_c: small sample corrected Akaike's information criterion (for analyses using the same species set, indicated by the same n, a lower AIC_c indicates a better model fit); ΔAIC_c: indicates the difference in AIC_c to the model with the lowest AIC_c (i.e., a value of 0.0 indicates the best-supported model amongst those using the same dataset). Note that AIC_c cannot be compared between GLS and PGLS models.

Table S3 Summary statistics for models assessing different diet proxies with mammalian total intestine length (n = 519 species) as dependent variable according to log(total intestine length) = a + b log(BM) + c (diet proxy); (significant parameters in **bold**)

	GLS				**PGLS**			
Diet proxy	**AICc**	**ΔAIC**		**parameter (95%CI)**	**lambda (95%CI)**	**AICc**	**ΔAIC**	**parameter (95%CI)**
(none)	-54.8	135.7	a	**2.26 (2.24 to 2.28)**	0.93 (0.88 to 0.96)	-479.3	3.1	**2.17 (1.85 to 2.49)**
			b	**0.48 (0.46 to 0.49)**				**0.40 (0.38 to 0.43)**
Trophic70	-181.9	8.5	a	**2.11 (2.08 to 2.15)**	0.92 (0.86 to 0.95)	-482.4	0.0	**2.15 (1.84 to 2.46)**
			b	**0.45 (0.44 to 0.47)**				**0.40 (0.38 to 0.42)**
			70Herbivore	**0.24 (0.20 to 0.28)**				**0.08 (0.01 to 0.14)**
			70Omnivore	0.02 (-0.05 to 0.10)				0.00 (-0.07 to 0.07)
Trophic90	-182.3	8.1	a	**2.09 (2.06 to 2.13)**	0.92 (0.87 to 0.95)	-479.1	3.3	**2.15 (1.83 to 2.46)**
			b	**0.45 (0.43 to 0.46)**				**0.40 (0.38 to 0.43)**
			90Herbivore	**0.27 (0.23 to 0.32)**				**0.07 (0.00 to 0.14)**
			90Omnivore	**0.15 (0.10 to 0.19)**				0.04 (-0.02 to 0.10)
%faunivory	-190.5	0.0	a	**2.37 (2.34 to 2.39)**	0.92 (0.87 to 0.95)	-482.2	0.2	**2.23 (1.92 to 2.54)**
			b	**0.45 (0.44 to 0.46)**				**0.40 (0.38 to 0.42)**
			c	**-0.28 (-0.32 to -0.23)**				**-0.09 (-0.16 to -0.01)**
%less digestible plants	-167.1	23.4	a	**2.15 (2.12 to 2.17)**	0.92 (0.87 to 0.95)	-478.6	3.8	**2.16 (1.84 to 2.48)**
			b	**0.44 (0.42 to 0.45)**				**0.40 (0.38 to 0.43)**
			c	**0.29 (0.24 to 0.34)**				0.04 (-0.03 to 0.11)
%digestible plants	-60.2	130.3	a	**2.24 (2.22 to 2.27)**	0.93 (0.88 to 0.96)	-478.1	4.4	**2.17 (1.85 to 2.49)**
			b	**0.48 (0.47 to 0.49)**				**0.41 (0.38 to 0.43)**
			c	**0.10 (0.03 to 0.16)**				0.03 (-0.04 to 0.11)

Trophic70 / 90: species classified as faunivores (>70 or 90% faunivory), omnivores, or herbivores (<30 or 10% faunivory); less digestible plant parts = leaves and stems; digestible plant parts = fruit, nectar, seeds

AIC_c: small sample corrected Akaike's information criterion (a lower AIC_c indicates a better model fit); ΔAIC_c: indicates the difference in AIC_c to the model with the lowest AIC_c (i.e., a value of 0.0 indicates the best-supported model amongst those using the same dataset). Note that AIC_c cannot be compared between GLS and PGLS models.

Table S4 Summary statistics for models assessing different mammalian intestinal sections only with body mass (BM) or additionally with a diet proxy according to log(length) = a + b log(BM) + c (diet proxy); (significant parameters in **bold**)

			GLS					PGLS				
Dependent	**Model**	**n**	**AICc**	**ΔAIC (trophic)**	**ΔAIC (all)**		**parameter (95%CI)**	**lambda (95%CI)**	**AICc**	**ΔAIC (trophic)**	**ΔAIC (all)**	**parameter (95% CI)**
All data												
Total intest.	BM	519	-54.8	135.7	-	a	**2.26 (2.24 to 2.28)**	0.93 (0.88 to 0.96)	-479.3	2.9	-	**2.17 (1.85 to 2.49)**
						b	**0.48 (0.46 to 0.49)**					**0.40 (0.38 to 0.43)**
Total intest.	BM + %faunivory	519	-190.5	0.0	-	a	**2.37 (2.34 to 2.39)**	0.92 (0.87 to 0.95)	-482.2	0.0	-	**2.23 (1.92 to 2.54)**
						b	**0.45 (0.44 to 0.46)**					**0.40 (0.38 to 0.42)**
						c	**-0.28 (-0.32 to -0.23)**					**-0.09 (-0.16 to -0.01)**
Small intest.	BM	397	-96.0	18.9	-	a	**2.13 (2.11 to 2.15)**	0.93 (0.87 to 0.96)	-339.9	0.0	-	**2.04 (1.69 to 2.39)**
						b	**0.46 (0.44 to 0.48)**					**0.40 (0.38 to 0.43)**
Small intest.	BM + %faunivory	397	-114.9	0.0	-	a	**2.17 (2.14 to 2.20)**	0.94 (0.89 to 0.97)	-338.2	1.7	-	**2.02 (1.67 to 2.38)**
						b	**0.46 (0.44 to 0.47)**					**0.40 (0.38 to 0.43)**
						c	**-0.13 (-0.19 to -0.08)**					0.03 (-0.07 to 0.13)
Large intest.	BM	387	257.8	316.1	-	a	**1.75 (1.71 to 1.78)**	0.97 (0.95 to 0.99)	-214.9	24.8	-	**1.57 (1.09 to 2.06)**
						b	**0.41 (0.39 to 0.44)**					**0.37 (0.34 to 0.41)**
Large intest.	BM + %faunivory	387	-58.3	0.0	-	a	**1.94 (1.91 to 1.97)**	0.95 (0.92 to 0.98)	-239.7	0.0	-	**1.77 (1.34 to 2.20)**
						b	**0.39 (0.38 to 0.41)**					**0.37 (0.33 to 0.40)**
						c	**-0.70 (-0.77 to -0.64)**					**-0.33 (-0.45 to -0.21)**
Caecum	BM	352	236.6	177.5	-	a	**0.98 (0.95 to 1.02)**	0.96 (0.94 to 0.98)	-168.5	15.2	-	**0.71 (0.23 to 1.20)**
						b	**0.21 (0.18 to 0.24)**					**0.28 (0.25 to 0.32)**
Caecum	BM + %faunivory	352	59.1	0.0	-	a	**1.14 (1.10 to 1.17)**	0.95 (0.92 to 0.97)	-183.7	0.0	-	**0.90 (0.45 to 1.36)**
						b	**0.19 (0.17 to 0.22)**					**0.27 (0.24 to 0.31)**
						c	**-0.63 (-0.71 to -0.55)**					**-0.32 (-0.46 to -0.17)**
Colon/Rect.	BM	370	264.1	254.9	-	a	**1.65 (1.61 to 1.68)**	0.97 (0.95 to 0.99)	-126.8	15.7	-	**1.47 (0.94 to 2.01)**
						b	**0.45 (0.42 to 0.48)**					**0.39 (0.35 to 0.43)**
Colon/Rect.	BM + %faunivory	370	9.3	0.0	-	a	**1.83 (1.80 to 1.86)**	0.96 (0.92 to 0.98)	-142.5	0.0	-	**1.66 (1.17 to 2.16)**
						b	**0.43 (0.41 to 0.45)**					**0.38 (0.34 to 0.41)**
						c	**-0.69 (-0.76 to -0.62)**					**-0.32 (-0.46 to -0.18)**

Table S4 ctd. Summary statistics for models assessing different mammalian intestinal sections only with body mass (BM) or additionally with a diet proxy according to log(length) = a + b log(BM) + c (diet proxy); (significant parameters in **bold**)

			GLS					**PGLS**				
Dependent	**Model**	**n**	**AICc**	**ΔAIC (trophic)**	**ΔAIC (all)**		**parameter (95%CI)**	**lambda (95%CI)**	**AICc**	**ΔAIC (trophic)**	**ΔAIC (all)**	**parameter (95% CI)**
Consistent data (species for which both small and large intestinal length are available)												
Total intest.	BM	387	-94.9	96.4	96.4	a	**2.31 (2.29 to 2.33)**	0.92 (0.86 to 0.96)	-399.8	1.9	1.9	**2.20 (1.89 to 2.50)**
						b	**0.44 (0.43 to 0.46)**					**0.40 (0.37 to 0.42)**
Total intest.	BM + %faunivory	387	-191.3	0.0	0.0	a	**2.38 (2.36 to 2.41)**	0.91 (0.84 to 0.95)	-401.7	0.0	0.0	**2.25 (1.96 to 2.55)**
						b	**0.44 (0.42 to 0.45)**					**0.39 (0.37 to 0.42)**
						c	**-0.28 (-0.33 to -0.23)**					**-0.09 (-0.18 to -0.00)**
Small intest.	BM	387	-99.2	21.8	92.1	a	**2.13 (2.11 to 2.16)**	0.94 (0.89 to 0.97)	-349.6	0.0	52.1	**2.04 (1.70 to 2.39)**
						b	**0.46 (0.44 to 0.47)**					**0.40 (0.38 to 0.43)**
Small intest.	BM + %faunivory	387	-121.0	0.0	70.3	a	**2.17 (2.15 to 2.20)**	0.94 (0.89 to 0.97)	-347.6	2.0	54.1	**2.04 (1.69 to 2.39)**
						b	**0.45 (0.44 to 0.47)**					**0.40 (0.38 to 0.43)**
						c	**-0.14 (-0.20 to -0.09)**					0.01 (-0.09 to 0.11)
Large intest.	BM	387	257.8	316.1	449.1	a	**1.75 (1.71 to 1.78)**	0.97 (0.95 to 0.99)	-214.9	24.8	186.7	**1.57 (1.09 to 2.06)**
						b	**0.41 (0.39 to 0.44)**					**0.37 (0.34 to 0.41)**
Large intest.	BM + %faunivory	387	-58.3	0.0	133.0	a	**1.94 (1.91 to 1.97)**	0.95 (0.92 to 0.98)	-239.7	0.0	162.0	**1.77 (1.34 to 2.20)**
						b	**0.39 (0.38 to 0.41)**					**0.37 (0.33 to 0.40)**
						c	**-0.70 (-0.77 to -0.64)**					**-0.33 (-0.45 to -0.21)**

Table S4 ctd. Summary statistics for models assessing different mammalian intestinal sections only with body mass (BM) or additionally with a diet proxy according to log(length) = a + b log(BM) + c (diet proxy); (significant parameters in **bold**)

			GLS					PGLS				
Dependent	**Model**	**n**	**AICc**	**ΔAIC (trophic)**	**ΔAIC (all)**		**parameter (95%CI)**	**lambda (95%CI)**	**AICc**	**ΔAIC (trophic)**	**ΔAIC (all)**	**parameter (95% CI)**
Consistent data (species for which small intestine, caecum and colon/rectum length are available)												
Total intest.	BM	351	-82.5	92.2	92.2	a	**2.31 (2.29 to 2.33)**	0.94 (0.90 to 0.97)	-391.7	0.0	0.0	**2.19 (1.88 to 2.51)**
						b	**0.44 (0.42 to 0.46)**					**0.39 (0.36 to 0.41)**
Total intest.	BM + %faunivory	351	-174.7	0.0	0.0	a	**2.38 (2.36 to 2.41)**	0.93 (0.89 to 0.97)	-391.3	0.4	0.0	**2.23 (1.92 to 2.55)**
						b	**0.43 (0.42 to 0.45)**					**0.38 (0.36 to 0.41)**
						c	**-0.31 (-0.37 to -0.25)**					-0.07 (-0.17 to 0.04)
Small intest.	BM	351	-86.4	26.5	88.3	a	**2.13 (2.11 to 2.15)**	0.96 (0.93 to 0.98)	-347.5	0.0	44.2	**2.04 (1.68 to 2.40)**
						b	**0.45 (0.44 to 0.47)**					**0.40 (0.37 to 0.43)**
Small intest.	BM + %faunivory	351	-112.9	0.0	61.8	a	**2.17 (2.15 to 2.20)**	0.96 (0.92 to 0.98)	-345.8	1.8	45.5	**2.02 (1.65 to 2.39)**
						b	**0.45 (0.43 to 0.47)**					**0.40 (0.37 to 0.43)**
						c	**-0.18 (-0.24 to -0.11)**					0.03 (-0.08 to 0.15)
Large intest.	BM	351	182.5	270.6	357.2	a	**1.77 (1.74 to 1.81)**	0.97 (0.94 to 0.98)	-223.4	18.0	168.4	**1.59 (1.13 to 2.05)**
						b	**0.41 (0.38 to 0.43)**					**0.36 (0.33 to 0.40)**
Large intest.	BM + %faunivory	351	-88.1	0.0	86.6	a	**1.94 (1.91 to 1.97)**	0.95 (0.90 to 0.97)	-241.3	0.0	150.0	**1.78 (1.37 to 2.19)**
						b	**0.39 (0.37 to 0.41)**					**0.36 (0.32 to 0.39)**
						c	**-0.68 (-0.75 to -0.62)**					**-0.33 (-0.46 to -0.19)**
Caecum	BM	351	234.9	179.7	409.6	a	**0.98 (0.95 to 1.02)**	0.96 (0.94 to 0.98)	-169.0	16.9	222.7	**0.71 (0.23 to 1.20)**
						b	**0.21 (0.18 to 0.24)**					**0.29 (0.25 to 0.32)**
Caecum	BM + %faunivory	351	55.2	0.0	229.9	a	**1.14 (1.10 to 1.17)**	0.95 (0.92 to 0.97)	-185.8	0.0	205.5	**0.91 (0.46 to 1.37)**
						b	**0.19 (0.17 to 0.22)**					**0.27 (0.24 to 0.31)**
						c	**-0.64 (-0.72 to -0.55)**					**-0.33 (-0.48 to -0.19)**
Colon/Rect.	BM	351	222.2	242.3	396.9	a	**1.67 (1.63 to 1.70)**	0.97 (0.95 to 0.99)	-132.0	16.5	259.7	**1.48 (0.95 to 2.02)**
						b	**0.45 (0.42 to 0.47)**					**0.38 (0.34 to 0.42)**
Colon/Rect.	BM + %faunivory	351	-20.2	0.0	154.5	a	**1.84 (1.80 to 1.87)**	0.95 (0.90 to 0.98)	-148.5	0.0	242.8	**1.70 (1.22 to 2.18)**
						b	**0.43 (0.41 to 0.45)**					**0.37 (0.33 to 0.41)**
						c	**-0.70 (-0.77 to -0.62)**					**-0.36 (-0.51 to -0.21)**

AIC_c: small sample corrected Akaike's information criterion (for analyses using the same species set, indicated by the same n, a lower AIC_c indicates a better model fit); ΔAIC_c: indicates the difference in AIC_c to the model with the lowest AIC_c (i.e., a value of 0.0 indicates the best-supported model amongst those using the same dataset). Note that AIC_c cannot be compared between GLS and PGLS models. ΔAIC_c (trophic) compares a model with BM and the same model with the additional trophic signal; ΔAIC_c (all) compares all models using the same species set.

Table S5 Summary statistics for models assessing total or large intestinal length in different mammal subgroups with body mass (BM) or additionally with a diet proxy according to log(length) = a + b log(BM) + c (diet proxy); (significant parameters in **bold**)

Taxon	Dependent	Model		GLS				PGLS			
			n	AICc	ΔAIC		parameter (95% CI)	lambda (95%CI)	AICc	ΔAIC	parameter (95% CI)
Marsupials	Total intest.	BM	36	30.0	7.5	a	**2.15 (2.05 to 2.26)**	0.88 (0.16 to 0.99)	13.8	4.6	**2.17 (1.59 to 2.75)**
						b	**0.44 (0.34 to 0.55)**				**0.28 (0.16 to 0.40)**
		BM + %faunivory		22.5	0.0	a	**2.38 (2.23 to 2.53)**	0.46 (NA to 0.97)	9.1	0.0	**2.44 (2.09 to 2.80)**
						b	**0.32 (0.20 to 0.43)**				**0.29 (0.17 to 0.40)**
						c	**-0.50 (-0.76 to -0.23)**				**-0.46 (-0.78 to -0.15)**
	Large intest.	BM	33	48.8	12.7	a	**1.60 (1.45 to 1.75)**	0.97 (0.84 to 0.99)	16.6	2.8	**1.60 (0.79 to 2.42)**
						b	**0.50 (0.33 to 0.68)**				**0.24 (0.10 to 0.38)**
		BM + %faunivory		36.1	0.0	a	**1.95 (1.76 to 2.14)**	0.95 (0.70 to 0.99)	13.8	0.0	**2.02 (1.23 to 2.80)**
						b	**0.32 (0.17 to 0.48)**				**0.21 (0.07 to 0.34)**
						c	**-0.79 (-1.13 to -0.45)**				**-0.63 (-1.17 to -0.09)**
Eutheria	Total intest.	BM	483	-73.0	123.0	a	**2.27 (2.25 to 2.29)**	0.91 (0.87 to 0.95)	-523.9	1.3	**2.17 (1.82 to 2.53)**
						b	**0.48 (0.46 to 0.49)**				**0.42 (0.39 to 0.44)**
		BM + %faunivory		-196.0	0.0	a	**2.37 (2.35 to 2.39)**	0.91 (0.86 to 0.94)	-525.2	0.0	**2.22 (1.87 to 2.57)**
						b	**0.45 (0.44 to 0.46)**				**0.42 (0.39 to 0.44)**
						c	**-0.27 (-0.31 to -0.22)**				-0.07 (-0.14 to 0.00)
	Large intest.	BM	352	219.6	292.4	a	**1.76 (1.73 to 1.80)**	0.93 (0.88 to 0.97)	-243.4	22.8	**1.62 (1.42 to 1.81)**
						b	**0.41 (0.38 to 0.43)**				**0.39 (0.36 to 0.43)**
		BM + %faunivory		-72.8	0.0	a	**1.94 (1.91 to 1.97)**	0.89 (0.80 to 0.94)	-266.2	0.0	**1.76 (1.59 to 1.94)**
						b	**0.39 (0.38 to 0.41)**				**0.39 (0.35 to 0.42)**
						c	**-0.70 (-0.76 to -0.64)**				**-0.31 (-0.43 to -0.20)**
Afrotheria	Total intest.	BM	23	6.3	4.2	a	**2.11 (2.02 to 2.20)**	0.80 (0.34 to 0.97)	-16.6	2.6	**2.10 (1.92 to 2.29)**
						b	**0.41 (0.35 to 0.47)**				**0.36 (0.27 to 0.44)**
		BM + %faunivory		2.1	0.0	a	**2.35 (2.18 to 2.52)**	0.72 (0.13 to 0.96)	-19.2	0.0	**2.34 (2.08 to 2.61)**
						b	**0.31 (0.23 to 0.39)**				**0.31 (0.23 to 0.40)**
						c	**-0.43 (-0.69 to -0.16)**				**-0.40 (-0.77 to -0.04)**
	Large intest.	BM	12	12.4	7.2	a	**1.75 (1.61 to 1.89)**	0.97 (0.72 to NA)	-8.9	3.3	**1.78 (1.48 to 2.09)**
						b	**0.45 (0.37 to 0.53)**				**0.40 (0.28 to 0.52)**
		BM + %faunivory		5.2	0.0	a	**2.03 (1.88 to 2.18)**	0.93 (NA to NA)	-12.2	0.0	**2.10 (1.74 to 2.45)**
						b	**0.32 (0.25 to 0.40)**				**0.32 (0.20 to 0.43)**
						c	**-0.61 (-0.88 to -0.33)**				**-0.68 (-1.24 to -0.11)**
Boroeutheria	Total intest.	BM	453	-80.8	125.3	a	**2.28 (2.26 to 2.30)**	0.83 (0.75 to 0.89)	-515.1	0.9	**2.28 (2.17 to 2.39)**
						b	**0.48 (0.47 to 0.49)**				**0.42 (0.40 to 0.45)**
		BM + %faunivory		-206.2	0.0	a	**2.38 (2.35 to 2.40)**	0.82 (0.73 to 0.89)	-516.0	0.0	**2.31 (2.20 to 2.43)**
						b	**0.46 (0.45 to 0.47)**				**0.42 (0.40 to 0.44)**
						c	**-0.28 (-0.32 to -0.23)**				-0.07 (-0.14 to 0.01)
	Large intest.	BM	337	213.0	284.9	a	**1.77 (1.73 to 1.80)**	0.93 (0.87 to 0.97)	-237.6	19.8	**1.62 (1.43 to 1.82)**
						b	**0.40 (0.38 to 0.43)**				**0.39 (0.36 to 0.43)**
		BM + %faunivory		-71.9	0.0	a	**1.94 (1.91 to 1.97)**	0.89 (0.80 to 0.94)	-257.4	0.0	**1.74 (1.56 to 1.92)**
						b	**0.40 (0.38 to 0.42)**				**0.39 (0.35 to 0.42)**
						c	**-0.73 (-0.80 to -0.66)**				**-0.30 (-0.42 to -0.18)**

Table S5 ctd. Summary statistics for models assessing total or large intestinal length in different mammal subgroups with body mass (BM) or additionally with a diet proxy according to log(length) = a + b log(BM) + c (diet proxy); (significant parameters in **bold**)

Taxon	**Dependent**	**Model**	**n**	**GLS AICc**	**ΔAIC**		**parameter (95% CI)**	**PGLS lambda (95%CI)**	**AICc**	**ΔAIC**	**parameter (95% CI)**
Euarchontoglires	Total intest.	BM	210	-162.8	2.7	a	**2.31 (2.29 to 2.33)**	0.80 (0.63 to 0.90)	-285.0	0.0	**2.33 (2.23 to 2.43)**
						b	**0.41 (0.39 to 0.43)**				**0.38 (0.34 to 0.41)**
		BM + %faunivory		-165.6	0.0	a	**2.33 (2.31 to 2.36)**	0.80 (0.63 to 0.90)	-284.1	0.9	**2.34 (2.24 to 2.44)**
						b	**0.40 (0.38 to 0.42)**				**0.37 (0.34 to 0.41)**
						c	**-0.15 (-0.25 to -0.05)**				-0.05 (-0.16 to 0.05)
	Large intest.	BM	204	-24.2	39.7	a	**1.81 (1.77 to 1.84)**	0.88 (0.73 to 0.96)	-140.7	14.8	**1.81 (1.64 to 1.97)**
						b	**0.39 (0.36 to 0.42)**				**0.37 (0.32 to 0.42)**
		BM + %faunivory		-63.9	0.0	a	**1.87 (1.84 to 1.91)**	0.82 (0.62 to 0.93)	-155.5	0.0	**1.88 (1.73 to 2.02)**
						b	**0.37 (0.34 to 0.39)**				**0.36 (0.31 to 0.41)**
						c	**-0.47 (-0.60 to -0.34)**				**-0.30 (-0.45 to -0.16)**
Primates	Total intest.	BM	62	-75.6	0.0	a	**2.24 (2.21 to 2.27)**	0.92 (0.73 to 0.99)	-110.9	0.0	**2.28 (2.09 to 2.46)**
						b	**0.39 (0.34 to 0.43)**				**0.37 (0.31 to 0.43)**
		BM + %faunivory		-70.6	5.0	a	**2.25 (2.19 to 2.31)**	0.93 (0.72 to 0.99)	-109.2	1.8	**2.29 (2.10 to 2.49)**
						b	**0.38 (0.33 to 0.43)**				**0.36 (0.30 to 0.43)**
						c	-0.03 (-0.20 to 0.13)				-0.04 (-0.23 to 0.14)
	Large intest.	BM	62	-15.3	0.0	a	**1.71 (1.66 to 1.76)**	0.98 (0.89 to NA)	-61.1	0.0	**1.76 (1.41 to 2.11)**
						b	**0.36 (0.29 to 0.43)**				**0.31 (0.21 to 0.40)**
		BM + %faunivory		-13.9	1.4	a	**1.78 (1.68 to 1.87)**	0.93 (0.72 to 0.99)	-59.9	1.3	**1.81 (1.41 to 2.21)**
						b	**0.32 (0.23 to 0.40)**				**0.25 (0.14 to 0.36)**
						c	-0.23 (-0.50 to 0.04)				-0.14 (-0.33 to 0.06)
Rodents	Total intest.	BM	140	-108.0	0.0	a	**2.38 (2.35 to 2.42)**	0.67 (0.42 to 0.84)	-165.6	0.0	**2.35 (2.25 to 2.44)**
						b	**0.46 (0.43 to 0.50)**				**0.39 (0.34 to 0.43)**
		BM + %faunivory		-105.6	2.3	a	**2.39 (2.36 to 2.43)**	0.66 (0.42 to 0.84)	-164.2	1.4	**2.35 (2.25 to 2.45)**
						b	**0.46 (0.42 to 0.49)**				**0.39 (0.34 to 0.43)**
						c	-0.12 (-0.25 to 0.01)				-0.05 (-0.19 to 0.08)
	Large intest.	BM	135	-34.2	28.2	a	**1.90 (1.86 to 1.95)**	0.67 (0.42 to 0.84)	-81.2	18.7	**1.87 (1.74 to 2.00)**
						b	**0.46 (0.42 to 0.50)**				**0.39 (0.33 to 0.45)**
		BM + %faunivory		-62.4	0.0	a	**1.94 (1.90 to 1.99)**	0.56 (0.26 to 0.81)	-99.9	0.0	**1.93 (1.81 to 2.04)**
						b	**0.43 (0.39 to 0.46)**				**0.39 (0.34 to 0.45)**
						c	**-0.48 (-0.64 to -0.33)**				**-0.40 (-0.56 to -0.23)**

Table S5 ctd. Summary statistics for models assessing total or large intestinal length in different mammal subgroups with body mass (BM) or additionally with a diet proxy according to log(length) = a + b log(BM) + c (diet proxy); (significant parameters in **bold**)

Taxon	Dependent	Model	n	GLS AICc	GLS ΔAIC		GLS parameter (95% CI)	PGLS lambda (95%CI)	PGLS AICc	PGLS ΔAIC	PGLS parameter (95% CI)
Laurasiatheria	Total intest.	BM	243	-10.4	55.8	a	**2.21 (2.18 to 2.24)**	0.86 (0.76 to 0.93)	-247.1	0.0	**2.24 (2.09 to 2.39)**
						b	**0.52 (0.50 to 0.53)**				**0.45 (0.42 to 0.48)**
		BM + %faunivory		-66.3	0.0	a	**2.36 (2.32 to 2.41)**	0.85 (0.73 to 0.92)	-246.8	0.3	**2.29 (2.12 to 2.46)**
						b	**0.48 (0.46 to 0.50)**				**0.45 (0.41 to 0.48)**
						c	**-0.27 (-0.33 to -0.21)**				-0.07 (-0.18 to 0.04)
	Large intest.	BM	133	148.0	169.7	a	**1.46 (1.34 to 1.58)**	0.94 (0.85 to 0.98)	-102.8	3.2	**1.37 (1.11 to 1.64)**
						b	**0.57 (0.50 to 0.64)**				**0.41 (0.37 to 0.46)**
		BM + %faunivory		-21.7	0.0	a	**1.94 (1.86 to 2.02)**	0.92 (0.79 to 0.98)	-106.0	0.0	**1.52 (1.25 to 1.78)**
						b	**0.43 (0.39 to 0.47)**				**0.41 (0.36 to 0.46)**
						c	**-0.82 (-0.90 to -0.73)**				**-0.27 (-0.49 to -0.05)**
Eulipotyphla	Total intest.	BM	18	7.6	0.0	a	**2.33 (2.07 to 2.58)**	0.67 (0.10 to NA)	-7.3	0.0	**2.35 (2.04 to 2.67)**
						b	**0.46 (0.32 to 0.61)**				**0.45 (0.26 to 0.63)**
		BM + %faunivory		8.5	0.9	a	**2.02 (1.03 to 3.00)**	0.75 (0.15 to NA)	-6.5	0.8	**1.92 (1.05 to 2.79)**
						b	**0.48 (0.32 to 0.64)**				**0.46 (0.26 to 0.65)**
						c	0.36 (-0.75 to 1.46)				0.48 (-0.40 to 1.36)
Chiroptera	Total intest.	BM	73	-23.4	19.9	a	**2.27 (2.12 to 2.43)**	0.92 (0.73 to NA)	-79.5	5.0	**1.93 (1.73 to 2.12)**
						b	**0.58 (0.49 to 0.67)**				**0.38 (0.30 to 0.46)**
		BM + %faunivory		-43.4	0.0	a	**2.25 (2.12 to 2.39)**	0.86 (0.57 to 0.99)	-84.5	0.0	**2.14 (1.92 to 2.36)**
						b	**0.45 (0.36 to 0.54)**				**0.39 (0.31 to 0.47)**
						c	**-0.28 (-0.37 to -0.18)**				**-0.23 (-0.39 to -0.07)**
Carnivora	Total intest.	BM	60	-9.1	0.0	a	**2.09 (2.01 to 2.16)**	0.71 (0.43 to 0.91)	-68.3	0.0	**2.08 (1.93 to 2.23)**
						b	**0.48 (0.43 to 0.54)**				**0.47 (0.41 to 0.52)**
		BM + %faunivory		-4.1	5.0	a	**2.09 (1.93 to 2.25)**	0.69 (0.41 to 0.90)	-67.0	1.3	**2.03 (1.84 to 2.22)**
						b	**0.48 (0.43 to 0.54)**				**0.47 (0.41 to 0.52)**
						c	0.00 (-0.18 to 0.17)				0.07 (-0.10 to 0.24)
	Large intest.	BM	40	-34.6	0.0	a	**1.25 (1.18 to 1.32)**	0.22 (na to 0.75)	-50.6	0.0	**1.26 (1.17 to 1.35)**
						b	**0.35 (0.30 to 0.40)**				**0.35 (0.29 to 0.40)**
		BM + %faunivory		-30.1	4.5	a	**1.24 (1.03 to 1.45)**	0.69 (0.41 to 0.90)	-48.8	1.8	**1.22 (1.00 to 1.43)**
						b	**0.35 (0.30 to 0.40)**				**0.35 (0.29 to 0.41)**
						c	0.01 (-0.22 to 0.23)				0.05 (-0.17 to 0.27)
Artiodactyla	Total intest.	BM	81	-80.4	0.0	a	**2.50 (2.41 to 2.59)**	0.39 (NA to NA)	-96.0	0.0	**2.40 (2.26 to 2.55)**
						b	**0.43 (0.38 to 0.49)**				**0.44 (0.39 to 0.50)**
		BM + %faunivory		-79.0	1.4	a	**2.51 (2.42 to 2.60)**	0.38 (NA to NA)	-94.0	2.0	**2.41 (2.25 to 2.56)**
						b	**0.43 (0.38 to 0.48)**				**0.44 (0.39 to 0.50)**
						c	-0.32 (-0.86 to 0.23)				-0.03 (-0.73 to 0.67)
	Large intest.	BM	79	-58.3	0.0	a	**1.94 (1.83 to 2.04)**	0.82 (0.31 to 0.97)	-78.9	0.0	**1.79 (1.53 to 2.04)**
						b	**0.45 (0.39 to 0.51)**				**0.47 (0.40 to 0.54)**
		BM + %faunivory		-56.8	1.5	a	**1.95 (1.84 to 2.06)**	0.82 (0.31 to 0.97)	-76.9	2.0	**1.78 (1.52 to 2.05)**
						b	**0.45 (0.39 to 0.51)**				**0.47 (0.40 to 0.54)**
						c	-0.31 (-0.94 to 0.31)				0.02 (-0.85 to 0.89)

AIC_c: small sample corrected Akaike's information criterion (for analyses using the same species, indicated by the same n, a lower AIC_c indicates a better model fit); ΔAIC_c: indicates the difference in AIC_c to the model with the lowest AIC_c (i.e., a value of 0.0 indicates the best-supported model amongst those using the same dataset). Note that AIC_c cannot be compared between GLS and PGLS models.

Table S6 Summary statistics for models assessing the total mammalian intestinal length (n = 519 species) with body mass (BM), or additionally with a diet proxy and other biological factors (being volant Vol, being marine Mar, having a forestomach FStom) according to log(length) = a + b log(BM) + c (diet proxy) + d ... (factors); (significant parameters in **bold**)

	GLS				PGLS			
Model	**AICc**	**ΔAIC**		**parameter (95%CI)**	**lambda (95%CI)**	**AICc**	**ΔAIC**	**parameter (95%CI)**
BM	-54.8	197.1	a	**2.26 (2.24 to 2.28)**	0.93 (0.88 to 0.96)	-479.3	5.9	**2.17 (1.85 to 2.49)**
			b	**0.48 (0.46 to 0.49)**				**0.40 (0.38 to 0.43)**
BM + %faunivory	-190.5	61.4	a	**2.37 (2.34 to 2.39)**	0.92 (0.87 to 0.95)	-482.2	2.9	**2.23 (1.92 to 2.54)**
			b	**0.45 (0.44 to 0.46)**				**0.40 (0.38 to 0.42)**
			c	**-0.28 (-0.32 to -0.23)**				**-0.09 (-0.16 to -0.01)**
BM + Vol	-110.2	141.6	a	**2.29 (2.27 to 2.31)**	0.92 (0.87 to 0.95)	-481.9	3.2	**2.18 (1.87 to 2.49)**
			b	**0.45 (0.43 to 0.46)**				**0.40 (0.38 to 0.42)**
			c	**-0.24 (-0.30 to -0.18)**				**-0.32 (-0.60 to -0.03)**
BM + Mar	-53.3	198.6	a	**2.26 (2.24 to 2.28)**	0.93 (0.88 to 0.96)	-478.0	7.1	**2.17 (1.85 to 2.49)**
			b	**0.48 (0.46 to 0.49)**				**0.40 (0.38 to 0.43)**
			c	-0.04 (-0.15 to 0.07)				0.06 (-0.07 to 0.18)
BM + Fstom	-121.3	130.6	a	**2.20 (2.18 to 2.23)**	0.93 (0.88 to 0.96)	-478.0	7.1	**2.17 (1.85 to 2.49)**
			b	**0.46 (0.45 to 0.48)**				**0.40 (0.38 to 0.43)**
			c	**0.17 (0.13 to 0.21)**				0.05 (-0.06 to 0.15)
BM + %faunivory + Vol	-227.3	24.6	a	**2.38 (2.36 to 2.40)**	0.91 (0.85 to 0.95)	-484.6	0.6	**2.24 (1.93 to 2.54)**
			b	**0.43 (0.42 to 0.44)**				**0.40 (0.37 to 0.42)**
			c	**-0.25 (-0.29 to -0.21)**				**-0.08 (-0.16 to -0.01)**
			d	**-0.18 (-0.23 to -0.12)**				**-0.30 (-0.57 to -0.02)**
BM + %faunivory + Mar	-206.3	45.6	a	**2.37 (2.35 to 2.39)**	0.91 (0.85 to 0.95)	-482.7	2.5	**2.24 (1.93 to 2.55)**
			b	**0.44 (0.42 to 0.45)**				**0.40 (0.37 to 0.42)**
			c	**-0.31 (-0.36 to -0.27)**				**-0.11 (-0.18 to -0.03)**
			d	**0.22 (0.12 to 0.33)**				0.10 (-0.02 to 0.23)
BM + %faunivory + FStom	-206.7	45.1	a	**2.32 (2.29 to 2.35)**	0.92 (0.86 to 0.95)	-480.6	4.6	**2.22 (1.91 to 2.54)**
			b	**0.45 (0.43 to 0.46)**				**0.40 (0.38 to 0.42)**
			c	**-0.23 (-0.28 to -0.19)**				**-0.09 (-0.16 to -0.01)**
			d	**0.09 (0.05 to 0.12)**				0.03 (-0.07 to 0.13)
BM + %faunivory + Vol + Mar	-243.2	8.6	a	**2.38 (2.36 to 2.41)**	0.90 (0.84 to 0.94)	-485.2	0.0	**2.25 (1.95 to 2.54)**
			b	**0.42 (0.41 to 0.43)**				**0.39 (0.37 to 0.42)**
			c	**-0.29 (-0.33 to -0.24)**				**-0.10 (-0.18 to -0.03)**
			d	**-0.17 (-0.23 to -0.12)**				**-0.29 (-0.56 to -0.03)**
			e	**0.22 (0.12 to 0.32)**				0.10 (-0.02 to 0.23)
BM + %faunivory + Vol + FStom	-236.4	15.4	a	**2.34 (2.31 to 2.37)**	0.91 (0.85 to 0.95)	-482.7	2.4	**2.23 (1.92 to 2.54)**
			b	**0.43 (0.42 to 0.45)**				**0.40 (0.37 to 0.42)**
			c	**-0.22 (-0.27 to -0.17)**				**-0.08 (-0.16 to -0.01)**
			d	**-0.16 (-0.22 to -0.10)**				**-0.29 (-0.57 to -0.01)**
			e	**0.07 (0.03 to 0.11)**				0.02 (-0.08 to 0.12)

BM + %faunivory + Mar + FStom	-221.9	30.0	a	**2.33 (2.29 to 2.36)**	0.91 (0.85 to 0.95)	-480.8	4.3	**2.23 (1.93 to 2.54)**
			b	**0.44 (0.42 to 0.45)**				**0.40 (0.37 to 0.42)**
			c	**-0.27 (-0.32 to -0.22)**				**-0.10 (-0.18 to -0.02)**
			d	**0.22 (0.11 to 0.32)**				0.10 (-0.03 to 0.23)
			e	**0.08 (0.05 to 0.12)**				0.02 (-0.08 to 0.12)
BM + %faunivory + Vol + Mar + FStom	-251.8	0.0	a	**2.35 (2.32 to 2.38)**	0.90 (0.84 to 0.94)	-483.2	2.0	**2.24 (1.94 to 2.54)**
			b	**0.42 (0.41 to 0.44)**				**0.39 (0.37 to 0.42)**
			c	**-0.26 (-0.30 to -0.21)**				**-0.10 (-0.18 to -0.02)**
			d	**-0.16 (-0.21 to -0.10)**				**-0.29 (-0.56 to -0.02)**
			e	**0.21 (0.11 to 0.31)**				0.10 (-0.02 to 0.23)
			f	**0.06 (0.03 to 0.10)**				0.01 (-0.08 to 0.11)

AIC_c: small sample corrected Akaike's information criterion (a lower AIC_c indicates a better model fit); ΔAIC_c: indicates the difference in AIC_c to the model with the lowest AIC_c (i.e., a value of 0.0 indicates the best-supported model amongst those using the same dataset). Note that AIC_c cannot be compared between GLS and PGLS models.

Table S7 Summary statistics for models assessing mammalian small intestinal length (n = 397 species) with body mass (BM), or additionally with a diet proxy and other biological factors (being volant Vol, being marine Mar, having a forestomach FStom) according to log(length) = a + b log(BM) + c (diet proxy) + d ... (factors); (significant parameters in **bold**)

	GLS				PGLS			
Model	**AICc**	**ΔAIC**		**parameter (95%CI)**	**lambda (95%CI)**	**AICc**	**ΔAIC**	**parameter (95%CI)**
BM	-96.0	49.6	a	**2.13 (2.11 to 2.15)**	0.93 (0.89 to 0.96)	-339.9	2.9	**2.04 (1.69 to 2.39)**
			b	**0.46 (0.44 to 0.47)**				**0.40 (0.38 to 0.43)**
BM + %faunivory	-114.9	30.7	a	**2.17 (2.14 to 2.20)**	0.94 (0.89 to 0.97)	-338.2	4.6	**2.02 (1.67 to 2.38)**
			b	**0.46 (0.44 to 0.47)**				**0.40 (0.38 to 0.43)**
			c	**-0.13 (-0.19 to -0.08)**				0.03 (-0.07 to 0.13)
BM + Vol	-94.0	51.6	a	**2.13 (2.11 to 2.15)**	0.93 (0.89 to 0.96)	-338.2	4.7	**2.05 (1.70 to 2.39)**
			b	**0.46 (0.44 to 0.47)**				**0.40 (0.37 to 0.43)**
			c	0.00 (-0.21 to 0.22)				-0.10 (-0.48 to 0.27)
BM + Mar	-100.6	44.9	a	**2.13 (2.11 to 2.15)**	0.93 (0.88 to 0.96)	-342.8	0.0	**2.04 (1.70 to 2.38)**
			b	**0.45 (0.44 to 0.47)**				**0.40 (0.37 to 0.43)**
			c	**0.16 (0.04 to 0.27)**				**0.20 (0.02 to 0.38)**
BM + Fstom	-117.2	28.4	a	**2.09 (2.06 to 2.11)**	0.93 (0.89 to 0.96)	-338.6	4.2	**2.03 (1.69 to 2.38)**
			b	**0.46 (0.44 to 0.47)**				**0.40 (0.38 to 0.43)**
			c	**0.10 (0.06 to 0.14)**				0.05 (-0.06 to 0.16)
BM + %faunivory + Vol	-113.2	32.4	a	**2.17 (2.14 to 2.20)**	0.94 (0.89 to 0.97)	-336.5	6.4	**2.03 (1.67 to 2.38)**
			b	**0.46 (0.44 to 0.47)**				**0.40 (0.37 to 0.43)**
			c	**-0.14 (-0.19 to -0.08)**				0.03 (-0.07 to 0.13)
			d	0.07 (-0.14 to 0.28)				-0.11 (-0.49 to 0.27)
BM + %faunivory + Mar	-137.1	8.5	a	**2.18 (2.15 to 2.20)**	0.93 (0.88 to 0.96)	-340.8	2.0	**2.04 (1.67 to 2.38)**
			b	**0.44 (0.43 to 0.46)**				**0.40 (0.37 to 0.43)**
			c	**-0.20 (-0.26 to -0.13)**				0.00 (-0.10 to 0.10)
			d	**0.31 (0.19 to 0.43)**				**0.20 (0.02 to 0.38)**
BM + %faunivory + FStom	-124.7	20.9	a	**2.12 (2.09 to 2.16)**	0.94 (0.89 to 0.96)	-337.0	5.8	**2.01 (1.66 to 2.37)**
			b	**0.46 (0.44 to 0.47)**				**0.40 (0.38 to 0.43)**
			c	**-0.10 (-0.16 to -0.04)**				0.03 (-0.07 to 0.14)
			d	**0.08 (0.03 to 0.12)**				0.05 (-0.06 to 0.17)
BM + %faunivory + Vol + Mar	-135.6	9.9	a	**2.18 (2.15 to 2.20)**	0.93 (0.88 to 0.96)	-339.0	3.8	**2.04 (1.69 to 2.38)**
			b	**0.44 (0.43 to 0.46)**				**0.40 (0.37 to 0.43)**
			c	**-0.20 (-0.26 to -0.14)**				0.00 (-0.10 to 0.11)
			d	0.08 (-0.12 to 0.28)				-0.10 (-0.47 to 0.27)
			e	**0.31 (0.19 to 0.43)**				**0.20 (0.02 to 0.38)**
BM + %faunivory + Vol + FStom	-123.3	22.3	a	**2.12 (2.09 to 2.16)**	0.94 (0.89 to 0.96)	-335.2	7.6	**2.02 (1.66 to 2.37)**
			b	**0.46 (0.44 to 0.47)**				**0.40 (0.37 to 0.43)**
			c	**-0.10 (-0.16 to -0.04)**				0.04 (-0.07 to 0.14)
			d	0.09 (-0.12 to 0.29)				-0.09 (-0.47 to 0.28)
			e	**0.08 (0.03 to 0.12)**				0.05 (-0.06 to 0.17)

BM + %faunivory + Mar + FStom	-145.6	0.0	a	**2.14 (2.10 to 2.17)**	0.93 (0.88 to 0.96)	-339.3	3.6	**2.03 (1.68 to 2.38)**
			b	**0.44 (0.43 to 0.46)**				**0.40 (0.37 to 0.43)**
			c	**-0.16 (-0.22 to -0.09)**				0.01 (-0.10 to 0.11)
			d	**0.30 (0.18 to 0.42)**				**0.19 (0.01 to 0.37)**
			e	**0.07 (0.03 to 0.11)**				0.04 (-0.07 to 0.15)
BM + %faunivory + Vol + Mar + FStom	-144.4	1.2	a	**2.14 (2.10 to 2.17)**	0.93 (0.88 to 0.96)	-337.4	5.4	**2.03 (1.68 to 2.38)**
			b	**0.44 (0.43 to 0.46)**				**0.40 (0.37 to 0.43)**
			c	**-0.16 (-0.22 to -0.10)**				0.01 (-0.10 to 0.11)
			d	0.10 (-0.10 to 0.30)				-0.09 (-0.46 to 0.28)
			e	**0.30 (0.18 to 0.42)**				**0.19 (0.01 to 0.37)**
			f	**0.07 (0.029 to 0.11)**				0.04 (-0.07 to 0.15)

AIC_c: small sample corrected Akaike's information criterion (a lower AIC_c indicates a better model fit); ΔAIC_c: indicates the difference in AIC_c to the model with the lowest AIC_c (i.e., a value of 0.0 indicates the best-supported model amongst those using the same dataset). Note that AIC_c cannot be compared between GLS and PGLS models.

Table S8 Summary statistics for models assessing mammalian total intestinal length (n = 466 species) with body mass (BM), or additionally with a diet proxy and environmental factors (latitude LAT, precipitation Prec, temperature Temp, actual evapotranspiration AET) according to log(length) = a + b log(BM) + c (diet proxy) + d ... (factor); (significant parameters in **bold**)

	GLS				PGLS			
Model	**AICc**	**ΔAIC**		**parameter (95%CI)**	**lambda (95%CI)**	**AICc**	**ΔAIC**	**parameter (95%CI)**
BM	-27.8	186.4	a	**2.26 (2.24 to 2.28)**	0.94 (0.89 to 0.97)	-437.0	24.8	**2.17 (1.83 to 2.50)**
			b	**0.47 (0.46 to 0.49)**				**0.39 (0.36 to 0.41)**
BM + %faunivory	-175.7	38.5	a	**2.37 (2.35 to 2.40)**	0.93 (0.87 to 0.96)	-441.8	20.0	**2.24 (1.92 to 2.56)**
			b	**0.44 (0.42 to 0.45)**				**0.38 (0.36 to 0.41)**
			c	**-0.32 (-0.37 to -0.27)**				**-0.11 (-0.19 to -0.03)**
BM + %faunivory + Lat	-214.2	0.0	a	**2.29 (2.25 to 2.32)**	0.92 (0.87 to 0.96)	-455.3	6.6	**2.19 (1.88 to 2.5)**
			b	**0.44 (0.43 to 0.46)**				**0.39 (0.36 to 0.41)**
			c	**-0.31 (-0.35 to -0.26)**				**-0.11 (-0.19 to -0.03)**
			d	**0.0035 (0.0025 to 0.0046)**				**0.0021 (0.0011 to 0.0032)**
BM + %faunivory + Prec	-191.2	23.0	a	**2.43 (2.40 to 2.47)**	0.93 (0.87 to 0.96)	-441.2	20.6	**2.25 (1.93 to 2.573)**
			b	**0.44 (0.43 to 0.46)**				**0.38 (0.36 to 0.4102)**
			c	**-0.31 (-0.36 to -0.27)**				**-0.11 (-0.19 to -0.0292)**
			d	**-0.0007 (-0.0011 to -0.0004)**				-0.0002 (-0.0005 to 0.0001)
BM + %faunivory + Temp	-210.2	4.0	a	**2.48 (2.44 to 2.52)**	0.93 (0.87 to 0.96)	-461.8	0.0	**2.33 (2.01 to 2.64)**
			b	**0.44 (0.43 to 0.46)**				**0.38 (0.36 to 0.41)**
			c	**-0.31 (-0.36 to -0.27)**				**-0.11 (-0.19 to -0.03)**
			d	**-0.0063 (-0.0083 to -0.0043)**				**-0.0046 (-0.0066 to -0.0027)**
BM + %faunivory + AET	-197.1	17.1	a	**2.46 (2.42 to 2.50)**	0.93 (0.87 to 0.96)	-443.3	18.5	**2.27 (1.95 to 2.59)**
			b	**0.44 (0.43 to 0.46)**				**0.39 (0.36 to 0.41)**
			c	**-0.31 (-0.36 to -0.27)**				**-0.11 (-0.19 to -0.03)**
			d	**-0.0001 (-0.0002 to -0.0001)**				0.0000 (-0.0001 to 0.0000)

AIC_c: small sample corrected Akaike's information criterion (a lower AIC_c indicates a better model fit); ΔAIC_c: indicates the difference in AIC_c to the model with the lowest AIC_c (i.e., a value of 0.0 indicates the best-supported model amongst those using the same dataset). Note that AIC_c cannot be compared between GLS and PGLS models.

Table S9 Summary statistics for models assessing mammalian small intestinal length (n = 351 species) with body mass (BM), or additionally with a diet proxy and environmental factors (latitude LAT, precipitation Prec, temperature Temp, actual evapotranspiration AET) according to log(length) = a + b log(BM) + c (diet proxy) + d ... (factor); (significant parameters in **bold**)

	GLS				PGLS			
Model	**AICc**	**ΔAIC**		**parameter (95%CI)**	**lambda (95%CI)**	**AICc**	**ΔAIC**	**parameter (95%CI)**
BM	-87.1	46.1	a	**2.13 (2.10 to 2.15)**	0.94 (0.88 to 0.97)	-316.6	7.5	**2.04 (1.70 to 2.38)**
			b	**0.45 (0.43 to 0.47)**				**0.39 (0.36 to 0.42)**
BM + %faunivory	-124.9	8.4	a	**2.18 (2.15 to 2.20)**	0.94 (0.88 to 0.97)	-314.8	9.3	**2.03 (1.68 to 2.38)**
			b	**0.44 (0.42 to 0.46)**				**0.39 (0.36 to 0.42)**
			c	**-0.21 (-0.27 to -0.14)**				0.03 (-0.08 to 0.1317)
BM + %faunivory + Lat	-131.5	1.7	a	**2.12 (2.08 to 2.17)**	0.94 (0.89 to 0.97)	-321.4	2.7	**1.98 (1.63 to 2.33)**
			b	**0.45 (0.43 to 0.47)**				**0.39 (0.36 to 0.42)**
			c	**-0.19 (-0.25 to -0.13)**				0.03 (-0.07 to 0.13)
			d	**0.0021 (0.0001 to 0.0035)**				**0.0019 (0.0006 to 0.0032)**
BM + %faunivory + Prec	-125.1	8.2	a	**2.20 (2.16 to 2.24)**	0.94 (0.88 to 0.97)	-312.8	11.4	**2.03 (1.67 to 2.38)**
			b	**0.44 (0.43 to 0.46)**				**0.39 (0.36 to 0.42)**
			c	**-0.20 (-0.26 to -0.15)**				0.03 (-0.08 to 0.13)
			d	-0.0003 (-0.0007 to 0.0001)				0.0000 (-0.0004 to 0.0004)
BM + %faunivory + Temp	-133.2	0.0	a	**2.24 (2.19 to 2.29)**	0.94 (0.89 to 0.97)	-324.1	0.0	**2.10 (1.75 to 2.45)**
			b	**0.45 (0.43 to 0.47)**				**0.39 (0.36 to 0.42)**
			c	**-0.19 (-0.26 to -0.13)**				0.03 (-0.08 to 0.13)
			d	**-0.0040 (-0.0065 to -0.0016)**				**-0.0039 (-0.0061 to -0.0016)**
BM + %faunivory + AET	-126.0	7.2	a	**2.21 (2.17 to 2.26)**	0.94 (0.89 to 0.97)	-313.1	11.0	**2.04 (1.68 to 2.39)**
			b	**0.45 (0.43 to 0.46)**				**0.39 (0.36 to 0.42)**
			c	**-0.20 (-0.26 to -0.13)**				0.03 (-0.08 to 0.13)
			d	0.0000 (-0.0001 to 0.0000)				0.0000 (-0.0001 to 0.0000)

AIC_c: small sample corrected Akaike's information criterion (a lower AIC_c indicates a better model fit); ΔAIC_c: indicates the difference in AIC_c to the model with the lowest AIC_c (i.e., a value of 0.0 indicates the best-supported model amongst those using the same dataset). Note that AIC_c cannot be compared between GLS and PGLS models.

Table S10 Summary statistics for models assessing mammalian large intestinal length (n = 343 species) with body mass (BM), or additionally with a diet proxy and environmental factors (latitude LAT, precipitation Prec, temperature Temp, actual evapotranspiration AET) according to log(length) = a + b log(BM) + c (diet proxy) + d ... (factor); (significant parameters in **bold**)

	GLS				PGLS			
Model	**AICc**	**ΔAIC**		**parameter (95%CI)**	**lambda (95%CI)**	**AICc**	**ΔAIC**	**parameter (95%CI)**
BM	208.4	260.7	a	**1.77 (1.73 to 1.80)**	0.97 (0.95 to 0.99)	-181.3	29.8	**1.57 (1.08 to 2.05)**
			b	**0.43 (0.40 to 0.46)**				**0.37 (0.33 to 0.41)**
BM + %faunivory	-40.1	12.2	a	**1.94 (1.91 to 1.97)**	0.95 (0.91 to 0.98)	-205.2	5.9	**1.78 (1.34 to 2.21)**
			b	**0.39 (0.37 to 0.41)**				**0.36 (0.32 to 0.39)**
			c	**-0.69 (-0.76 to -0.6201)**				**-0.35 (-0.47 to -0.22)**
BM + %faunivory + Lat	-46.5	5.8	a	**1.88 (1.83 to 1.93)**	0.95 (0.91 to 0.98)	-207.1	4.0	**1.74 (1.31 to 2.17)**
			b	**0.40 (0.38 to 0.42)**				**0.36 (0.32 to 0.39)**
			c	**-0.67 (-0.74 to -0.60)**				**-0.34 (-0.47 to -0.22)**
			d	**0.0023 (0.0008 to 0.0039)**				**0.0015 (0.0000 to 0.0030)**
BM + %faunivory + Prec	-51.7	0.6	a	**2.00 (1.96 to 2.05)**	0.95 (0.91 to 0.98)	-208.8	2.3	**1.81 (1.39 to 2.2)**
			b	**0.40 (0.38 to 0.42)**				**0.36 (0.33 to 0.40)**
			c	**-0.67 (-0.74 to -0.60)**				**-0.34 (-0.47 to -0.22)**
			d	**-0.0009 (-0.0013 to -0.0004)**				**-0.0005 (-0.0009 to -0.0001)**
BM + %faunivory + Temp	-47.3	5.0	a	**2.01 (1.95 to 2.06)**	0.95 (0.91 to 0.98)	-209.8	1.2	**1.84 (1.41 to 2.27)**
			b	**0.40 (0.38 to 0.42)**				**0.36 (0.32 to 0.39)**
			c	**-0.68 (-0.75 to -0.61)**				**-0.35 (-0.47 to -0.22)**
			d	**-0.0043 (-0.0070 to -0.0015)**				**-0.0035 (-0.0061 to -0.0008)**
BM + %faunivory + AET	-52.3	0.0	a	**2.02 (1.97 to 2.08)**	0.95 (0.91 to 0.98)	-211.1	0.0	**1.84 (1.41 to 2.27)**
			b	**0.40 (0.38 to 0.42)**				**0.36 (0.32 to 0.39)**
			c	**-0.67 (-0.74 to -0.60)**				**-0.34 (-0.46 to -0.21)**
			d	**-0.0001 (-0.0002 to -0.0001)**				**-0.0001 (-0.0001 to 0.0000)**

AIC_c: small sample corrected Akaike's information criterion (a lower AIC_c indicates a better model fit); ΔAIC_c: indicates the difference in AIC_c to the model with the lowest AIC_c (i.e., a value of 0.0 indicates the best-supported model amongst those using the same dataset). Note that AIC_c cannot be compared between GLS and PGLS models.

Table S11 Summary statistics for models assessing mammalian colon/rectum length (n = 330 species) with body mass (BM), or additionally with a diet proxy and environmental factors (latitude LAT, precipitation Prec, temperature Temp, actual evapotranspiration AET) according to log(length) = a + b log(BM) + c (diet proxy) + d ... (factor); (significant parameters in **bold**)

	GLS				PGLS			
Model	**AICc**	**ΔAIC**		**parameter (95%CI)**	**lambda (95%CI)**	**AICc**	**ΔAIC**	**parameter (95%CI)**
BM	230.0	216.1	a	**1.66 (1.62 to 1.70)**	0.97 (0.94 to 0.99)	-95.2	21.7	**1.47 (0.94 to 2.00)**
			b	**0.46 (0.43 to 0.49)**				**0.39 (0.35 to 0.43)**
BM + %faunivory	22.2	8.3	a	**1.83 (1.80 to 1.87)**	0.95 (0.90 to 0.98)	-111.4	5.4	**1.69 (1.20 to 2.17)**
			b	**0.43 (0.41 to 0.45)**				**0.37 (0.33 to 0.41)**
			c	**-0.69 (-0.76 to -0.61)**				**-0.35 (-0.50 to -0.20)**
BM + %faunivory + Lat	19.4	5.5	a	**1.78 (1.73 to 1.84)**	0.95 (0.90 to 0.98)	-113.5	3.3	**1.64 (1.16 to 2.13)**
			b	**0.44 (0.42 to 0.46)**				**0.37 (0.33 to 0.41)**
			c	**-0.67 (-0.75 to -0.59)**				**-0.35 (-0.50 to -0.19)**
			d	**0.0020 (0.0002 to 0.0038)**				**0.0018 (0.0001 to 0.0036)**
BM + %faunivory + Prec	15.8	1.9	a	**1.89 (1.84 to 1.94)**	0.95 (0.90 to 0.98)	-113.3	3.6	**1.7 (1.24 to 2.21)**
			b	**0.44 (0.42 to 0.46)**				**0.37 (0.33 to 0.42)**
			c	**-0.67 (-0.75 to -0.59)**				**-0.35 (-0.50 to -0.19)**
			d	**-0.0008 (-0.0013 to -0.0002)**				**-0.0005 (-0.0010 to 0.0000)**
BM + %faunivory + Temp	18.6	4.7	a	**1.90 (1.83 to 1.96)**	0.95 (0.90 to 0.98)	-114.7	2.2	**1.76 (1.27 to 2.24)**
			b	**0.44 (0.41 to 0.46)**				**0.37 (0.33 to 0.41)**
			c	**-0.68 (-0.76 to -0.60)**				**-0.35 (-0.50 to -0.20)**
			d	**-0.0039 (-0.0070 to -0.0007)**				**-0.0037 (-0.0069 to -0.0006)**
BM + %faunivory + AET	13.9	0.0	a	**1.91 (1.85 to 1.97)**	0.95 (0.90 to 0.98)	-116.8	0.0	**1.76 (1.28 to 2.24)**
			b	**0.44 (0.42 to 0.46)**				**0.37 (0.33 to 0.41)**
			c	**-0.67 (-0.75 to -0.59)**				**-0.35 (-0.50 to -0.19)**
			d	**-0.0001 (-0.0002 to 0.000)**				**-0.0001 (-0.0002 to 0.0000)**

AIC_c: small sample corrected Akaike's information criterion (a lower AIC_c indicates a better model fit); ΔAIC_c: indicates the difference in AIC_c to the model with the lowest AIC_c (i.e., a value of 0.0 indicates the best-supported model amongst those using the same dataset). Note that AIC_c cannot be compared between GLS and PGLS models.

Table S12 Summary statistics for models assessing mammalian caecum length (n = 316 species) with body mass (BM), or additionally with a diet proxy and environmental factors (latitude LAT, precipitation Prec, temperature Temp, actual evapotranspiration AET) according to log(length) = a + b log(BM) + c (diet proxy) + d ... (factor); (significant parameters in **bold**)

	GLS				PGLS			
Model	**AICc**	**ΔAIC**		**parameter (95%CI)**	**lambda (95%CI)**	**AICc**	**ΔAIC**	**parameter (95%CI)**
BM	191.3	165.5	a	**0.99 (0.96 to 1.03)**	0.96 (0.93 to 0.97)	-168.4	13.3	**0.72 (0.27 to 1.17)**
			b	**0.21 (0.18 to 0.24)**				**0.30 (0.26 to 0.33)**
BM + %faunivory	36.0	10.2	a	**1.14 (1.10 to 1.17)**	0.94 (0.91 to 0.97)	-180.7	1.0	**0.90 (0.47 to 1.32)**
			b	**0.19 (0.16 to 0.21)**				**0.28 (0.24 to 0.32)**
			c	**-0.63 (-0.71 to -0.54)**				**-0.30 (-0.44 to -0.15)**
BM + %faunivory + Lat	25.8	0.0	a	**1.05 (0.99 to 1.11)**	0.94 (0.91 to 0.97)	-178.7	3.0	**0.90 (0.47 to 1.33)**
			b	**0.20 (0.18 to 0.22)**				**0.28 (0.24 to 0.32)**
			c	**-0.60 (-0.69 to -0.52)**				**-0.30 (-0.45 to -0.15)**
			d	**0.0033 (0.0015 to 0.0052)**				-0.0002 (-0.0018 to 0.0014)
BM + %faunivory + Prec	36.1	10.3	a	**1.17 (1.11 to 1.22)**	0.94 (0.91 to 0.97)	-181.0	0.7	**0.87 (0.44 to 1.30)**
			b	**0.19 (0.17 to 0.21)**				**0.28 (0.24 to 0.32)**
			c	**-0.62 (-0.71 to -0.53)**				**-0.30 (-0.45 to -0.15)**
			d	-0.0004 (-0.0009 to 0.0002)				0.0004 (-0.0001 to 0.0008)
BM + %faunivory + Temp	28.0	2.2	a	**1.2 (1.16 to 1.29)**	0.94 (0.91 to 0.97)	-178.9	2.8	**0.91 (0.48 to 1.34)**
			b	**0.19 (0.17 to 0.22)**				**0.28 (0.24 to 0.32)**
			c	**-0.61 (-0.70 to -0.53)**				**-0.30 (-0.45 to -0.15)**
			d	**-0.0054 (-0.0087 to -0.0021)**				-0.0008 (-0.0037 to 0.0021)
BM + %faunivory + AET	36.2	10.4	a	**1.17 (1.11 to 1.24)**	0.94 (0.91 to 0.97)	-181.7	0.0	**0.85 (0.43 to 1.28)**
			b	**0.19 (0.17 to 0.21)**				**0.28 (0.24 to 0.32)**
			c	**-0.62 (-0.70 to -0.53)**				**-0.30 (-0.45 to -0.15)**
			d	0.0000 (-0.0001 to 0.0000)				0.0001 (0.0000 to 0.0001)

AIC_c: small sample corrected Akaike's information criterion (a lower AIC_c indicates a better model fit); ΔAIC_c: indicates the difference in AIC_c to the model with the lowest AIC_c (i.e., a value of 0.0 indicates the best-supported model amongst those using the same dataset). Note that AIC_c cannot be compared between GLS and PGLS models.

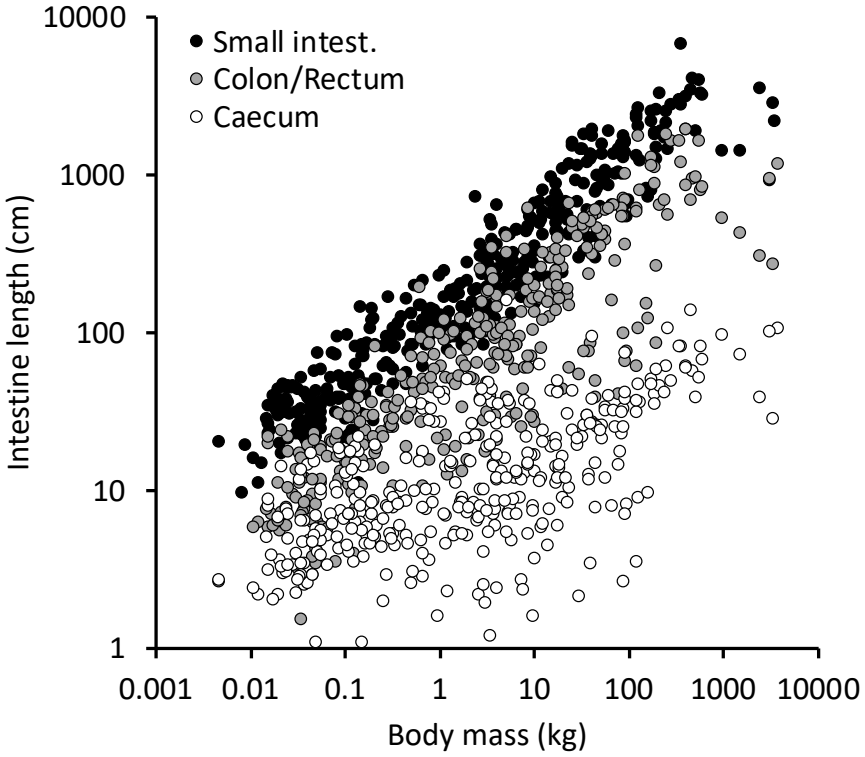

Figure S1 Magnitude comparison of the length of the small intestine, the colon/rectum, and the caecum in mammals. Note that while the relationship between the small and the large intestine stays similar, the caecum becomes relatively shorter at increasing body mass.

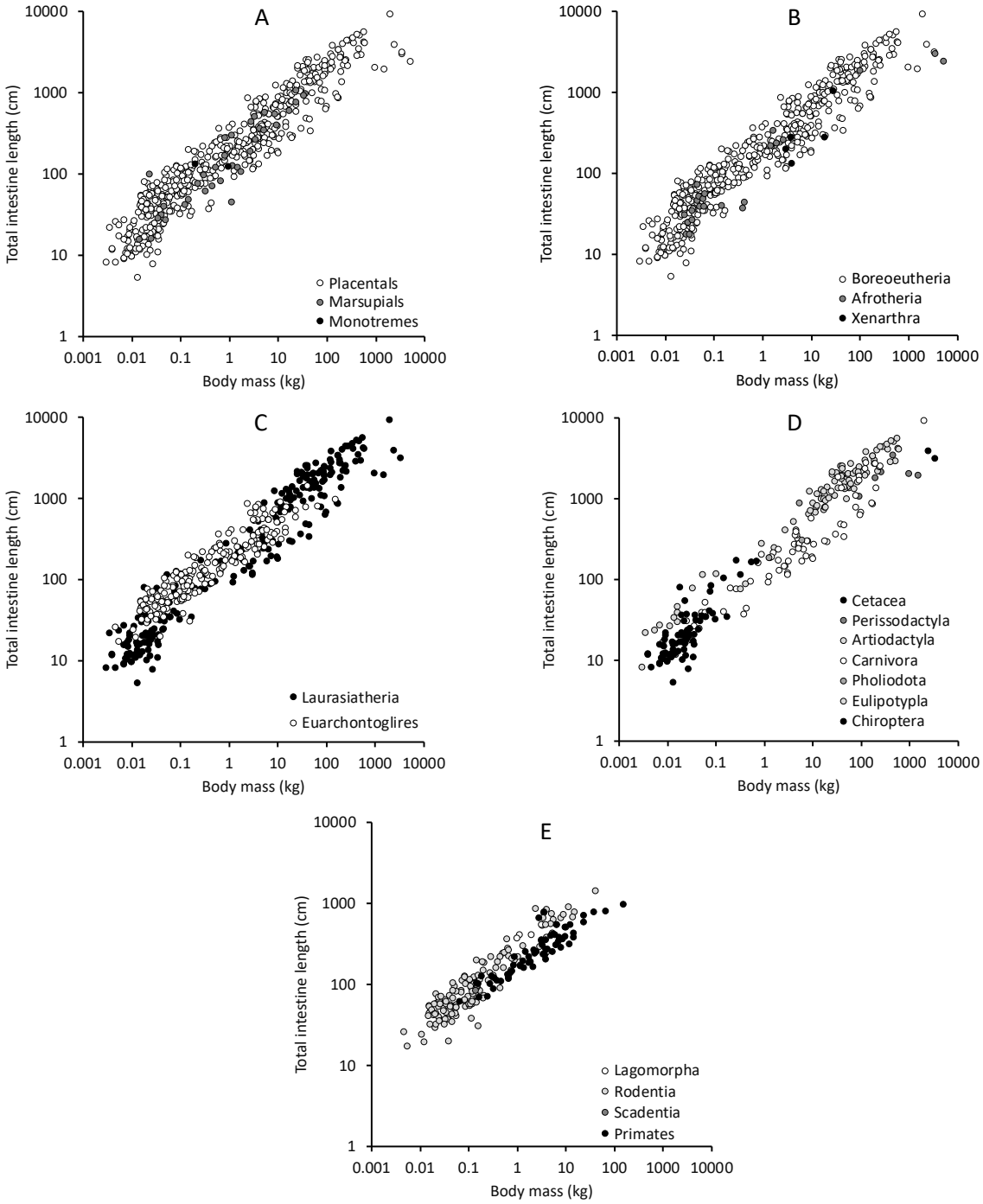

Figure S2 Relationships between mammalian intestinal length and body mass for taxonomic groups (A) Mammalian infraclasses, (B) The major Eutherian groups, (note that Laurasiatheria and Euarchontoglires are grouped as Boroeutheria), (C) two bigger Eutherian groups Laurasiatheria and Euarchontoglires, (D) Laurasiatheria, (E) Euarchontoglires.

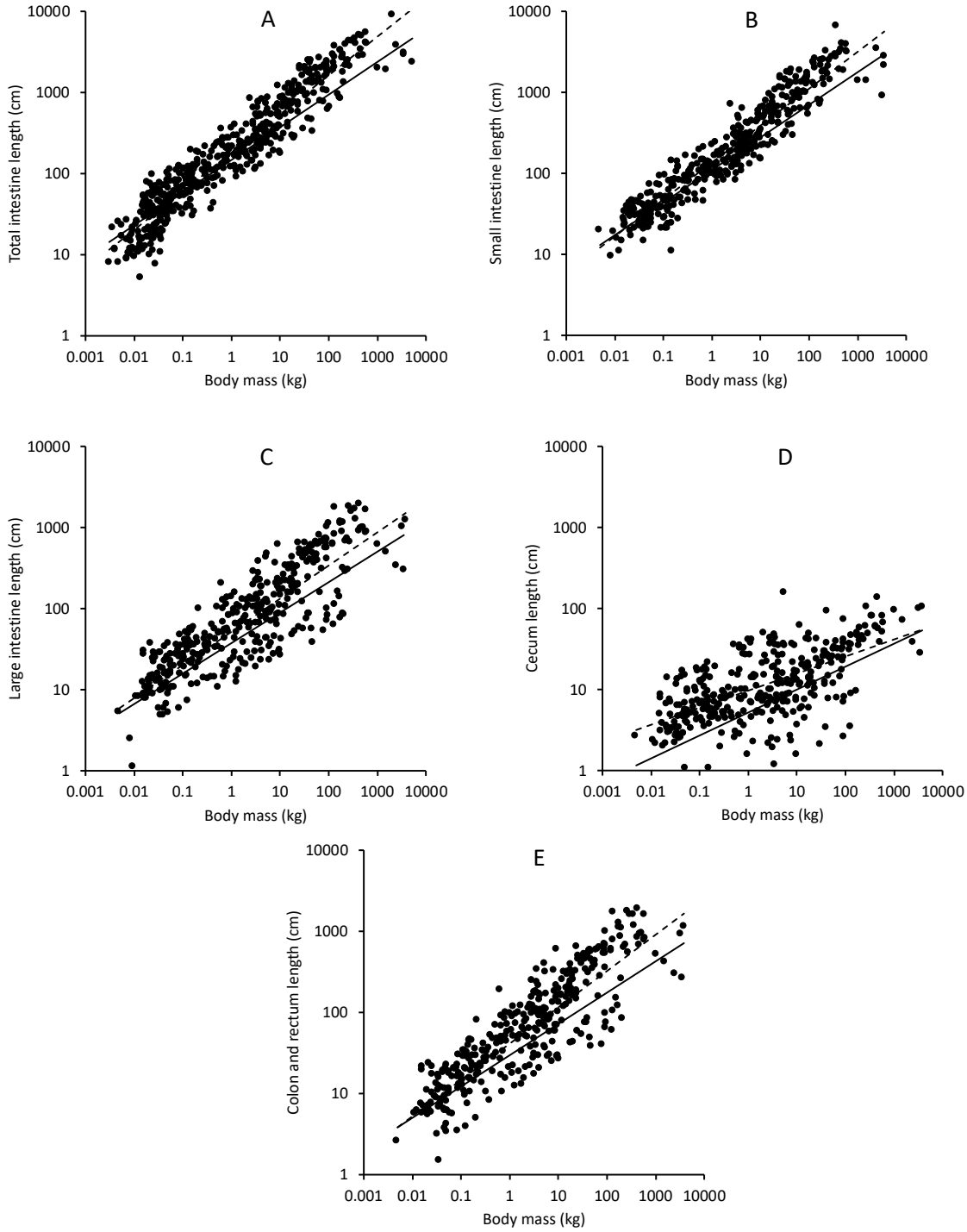

Figure S3 Relationships between mammalian intestinal length and body mass for (A) Total intestine (n=519 species), (B) Small intestine (n=397), (C) Large intestine (Caecum, colon and rectum) (n=387), (D) caecum (n=352), (E) colon and rectum (n=370). Dotted regression line in GLS using raw data; black regression line from PGLS accounting for phylogeny. For statistics, see Table S1.

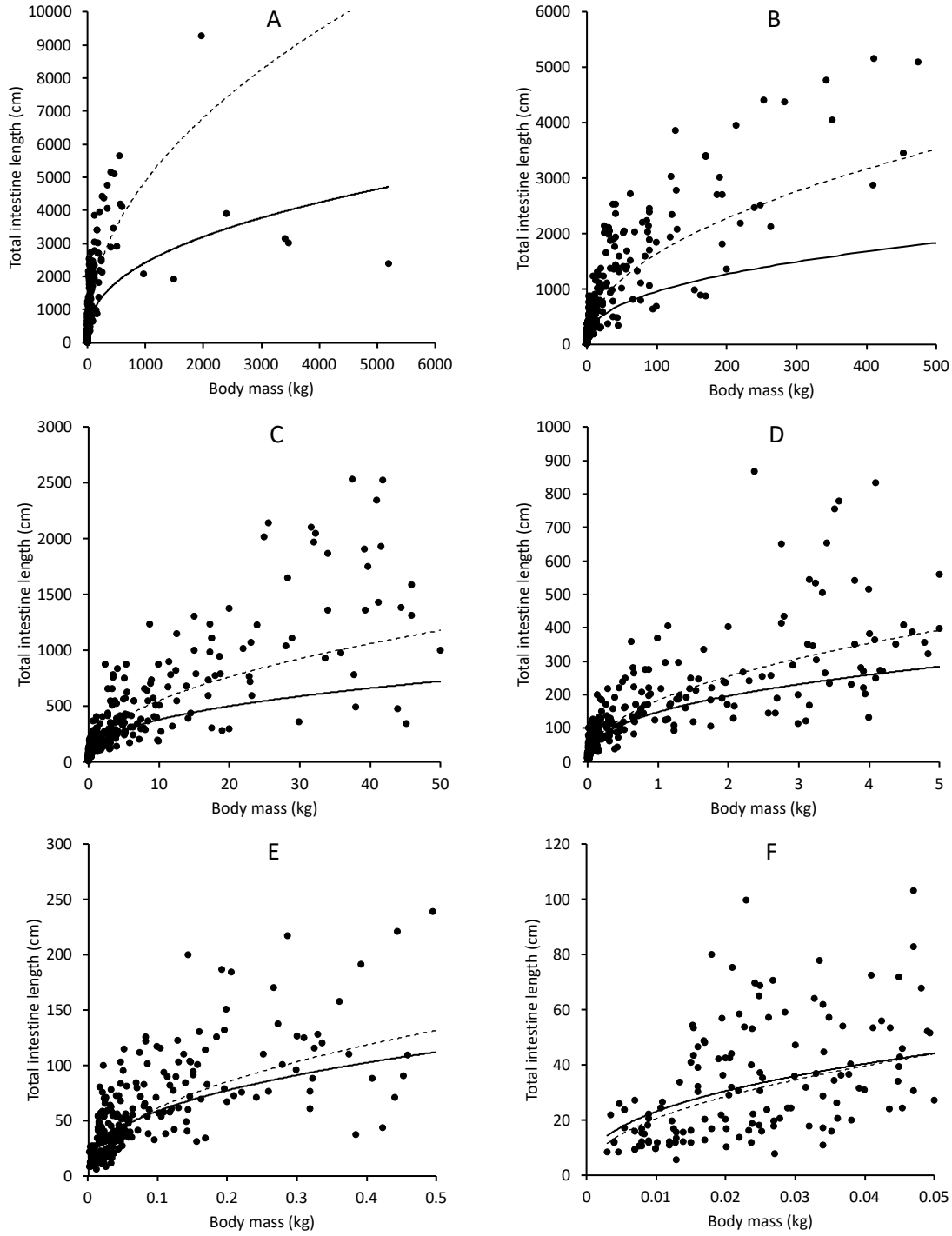

Figure S4 The same data and GLS and PGLS regression equations as in Fig. S3A, displayed (A) as the complete dataset, non-transformed, (B-F) data subset in the lower body mass range, non-transformed. Dotted regression line in GLS using raw data after log-transformation; black regression line from PGLS accounting for phylogeny after log-transformation.

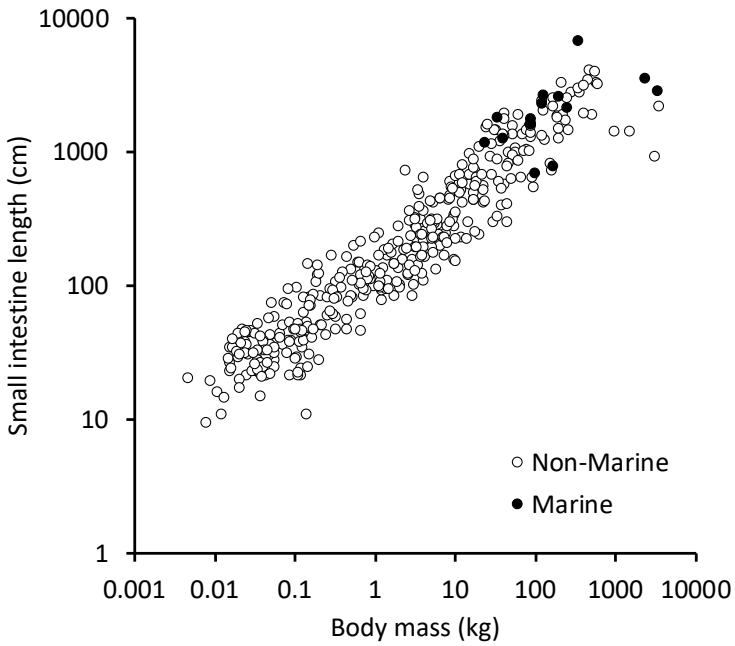

Figure S5 Relationship between small intestinal length and body mass for marine and non-marine mammals. Most data points refer to Carnivora, where one phocid had a surprisingly short small intestine; another short small intestine is from the afrotherian dugong (*Dugong dugon*); the two largest species are baleen whales, which have, compared to other Cetartiodactyla, rather short small intestines.

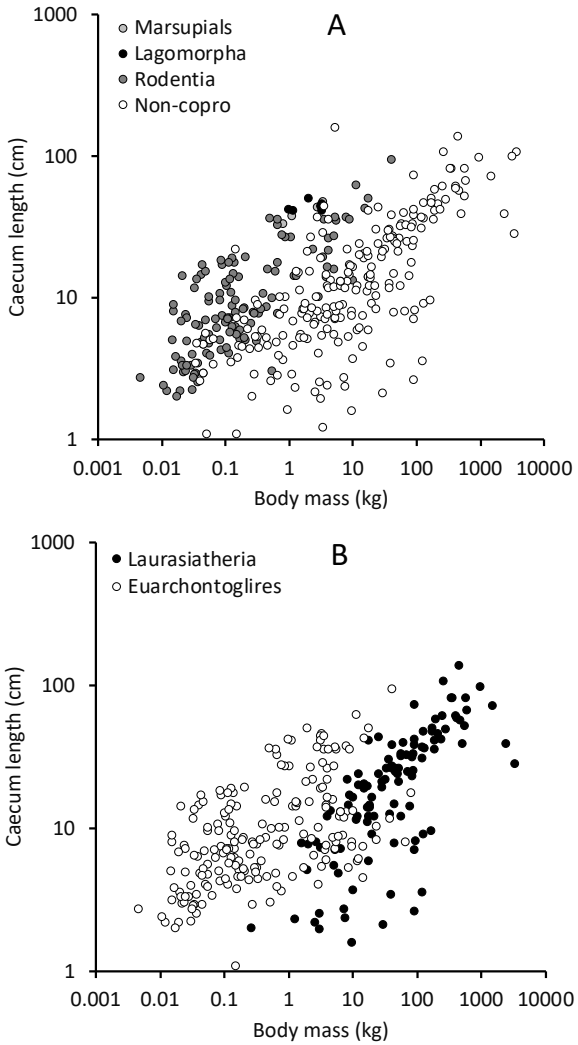

Figure S6 Relationship between caecum length and body mass (A) across mammals separated into orders in which coprophagy is a frequent digestive strategy (Lagomorpha, Rodentia) plus individual coprophageous marsupial species, and other groups in which it is not reported. The species with the very long caecum among the non-coprophageous mammals, is the koala (*Phascolarctos cinereus)*, a species that is known to use caecum contents for feeding its young [3]. Using GLS, the scaling between the two functional mammal groups had different confidence intervals for both the factor and the exponent, and geometric scaling was included in the confidence interval for non-coprophageous species (non-coprophageous: caecum length = 6.4 [5.6 to 7.3] $BM^{0.29\ [0.25\ to\ 0.33]}$; coprophageous: caecum length = 10.0 [9.1 to 10.9] $BM^{0.20\ [0.17\ to\ 0.23]}$); using PGLS, geometric scaling was included in the confidence interval for both groups, there were no differences in the scaling exponent, and the numerical difference in the factor was not maintained by the confidence intervals (non-coprophageous: caecum length = 4.5 [1.3 to 15.5] $BM^{0.29\ [0.24\ to\ 0.33]}$; coprophageous: caecum length = 7.8 [2.5 to 24.1] $BM^{0.29\ [0.25\ to\ 0.33]}$); (B) across Laurasiatheria and Euarchontoglires (because more evolutionary changes in the caecal appendix occurred in the latter compared to the former [4]). Euarchontoglires have longer caeca, and a shallower scaling, but confidence intervals overlap in PGLS (GLS: Lauras. caecum length = 4.1 [3.0 to 5.7] $BM^{0.40\ [0.32\ to\ 0.49]}$, Euarch. caecum length = 10.7 [9.7 to 11.9] $BM^{0.20\ [0.16\ to\ 0.25]}$; PGLS: Lauras. caecum length = 5.6 [2.8 to 11.1] $BM^{0.30\ [0.24\ to\ 0.36]}$, Euarch. caecum length = 11.6 [7.7 to 17.6] $BM^{0.29\ [0.24\ to\ 0.35]}$).

R Code
Generic descriptors in CAPITAL letters

GLS and PGLS analyses

R packages ‘caper’ [5] and ‘nlme’ [6]
Data tables are prepared in Excel from the original data file, including log-transformation; note that in R, commands that read like ‘log-transform’ may perform a ln-tranformation; tables saved as txt files

Loading the data
Data <- read.table("TABLE.txt", header=T)

ensuring variables (NAME) that are coded by numbers (such as 0,1 for dichotomous variables or 0,1,2 for three possible states) are used as factors and not as continuous variables
NAMEfactor <- as.factor("NAME")
Data$NAMEfactor <- as.factor(Data$NAME)

Loading the phylogenetic tree; Linking the data and the phylogenetic tree; both the data file and the tree file contain the descriptor ‘Species’, and the corresponding species names are identical in these two files
Tree <- read.tree("TREE.txt")
matrix <- comparative.data(Tree, Data, Species)

Checking the link; this command will indicate the number of species in tree not used (in example: 10), the number of species that occurred both in the tree and the data file (in example: 519), and the number of species that occurred in the datafile but not in the tree (in example: 0); example: tree { 10 (519 } 0) Data; the latter number must be zero
matrix

GLS models using various dependent (e.g., a log-transformed intestine length measure) and independent variables (e.g., log-transformed body mass, or additionally %faunivory) or factors
model1 <- gls(DEPENDENT ~ INDEPENDENT, data=Data)
or
model1 <- gls(DEPENDENT ~ INDEPENDENT1 + INDEPENDENT2, data=Data)
or
model1 <- gls(DEPENDENT ~ INDEPENDENT1 + NAMEfactor, data=Data)
etc.

calling the GLS model results, which are then copied into e.g. an Excel file
summary(model1)
the standard error SE from the model summary is then used to calculate the 95% confidence interval (as the estimate ‘value’ minus/plus 1.96 * SE); note that depending on results display, the ‘intercept’ estimate (a) might require de-logging as =10^a, e.g. when displaying the scaling result as an allometric equation $y = a\ x^b$; the information given includes the AIC, which is subsequently used to calculate differences in AIC between appropriate models in Excel

PGLS models using various dependent (e.g., a log-transformed intestine length measure) and independent variables (e.g., log-transformed body mass, or additionally %faunivory) or factors
model2 <- pgls(DEPENDENT ~ INDEPENDENT, data=matrix, lambda="ML")
or
model2 <- pgls(DEPENDENT ~ INDEPENDENT1 + INDEPENDENT2, data=matrix, lambda="ML")
or
model2 <- pgls(DEPENDENT ~ INDEPENDENT1 + NAMEfactor, data=matrix, lambda="ML")
etc.

sometimes, a PGLS model does not work; in this case, it needs to be repeated with excluding 0 as a solution for lambda, but with very small lambdas possible:
model2 <- pgls(DEPENDENT ~ INDEPENDENT, data=matrix, lambda="ML", bounds=list(lambda=c(0.000001,1))
this step might have to be repeated with different zero-decimals for the lower bound (e.g., 0.000001, 0.00001, 0.0001)

calling the PGLS model results, which are then copied into e.g. an excel file; this includes output for lambda; as the normal summary call does not yield AIC values, these have to be called individually; calculate 95% confidence interval and AIC differences as above; note that you must not compare AIC between GLS and PGLS models but only within the respective model group
summary(model2)
AIC(model2)

Analyses for Phylogenetic Signal

R package ‘phytools’ [2]
prepare the datasets with species and the variables that shall be submitted to analysis (e.g., log-transformed body mass and log-transformed intestinal section length), but ensure that the first column with the species names does not have a column heading (the other ones with the variables should have their heading); tables saved as txt files

Loading the data and the phylogenetic tree
Data <- read.table("TABLE.txt")
Tree <- read.tree("TREE.txt")

link the data rows to the species names
row.names(Data) <- Data[,1]
Data <- Data[,-1]

select the trait you want to analyse; if it is in the first column after the species names, use “1”, if it is in the second column after the species names, use “2”, etc., and link them to the species names
trait <- Data[,1]
names(trait) <- rownames(Data)

calculate the phylogenetic signal (either K or lambda) with the number of simulations you want (here, 9999); the result is displayed automatically, as is the number of species in the tree that is not used in the specific calculation
phylosig(Tree, trait, method="K", test=TRUE, nsim=999)
or
phylosig(Tree, trait, method="lambda", test=TRUE, nsim=999)

Supplement References

1. Chivers D.J., Hladik C.M. 1980 Morphology of the gastrointestinal tract in primates: comparisons with other mammals in relation to diet. *J Morphol* **166**, 337-386.
2. Revell L.J. 2012 phytools: an R package for phylogenetic comparative biology (and other things). *Methods Ecol Evol* **3**, 217-223.
3. Osawa R., Blanshard W.H., Ocallaghan P.G. 1993 Microbiological studies of the intestinal microflora of the koala, Phascolarctos-cinereus. 2. Pap, a special maternal feces consumed by juvenile koalas. *Aust J Zool* **41**, 611-620.
4. Smith H.F., Parker W., Kotzé S.H., Laurin M. 2017 Morphological evolution of the mammalian cecum and cecal appendix. *Comptes Rendus Palevol* **16**, 39-57.
5. Orme D. 2013 The caper package: comparative analysis of phylogenetics and evolution in R. *R package version* **0.5.2, http://CRAN.R-project.org/package=caper**.
6. Pinheiro J., Bates D., DebRoy S., Sarkar D., Core Team R. 2016 nlme: linear and nonlinear mixed effects models. R package version 3.1-128, http://CRAN.R-project.org/package=nlme.