Supplementary material for:

Relationship between capillaries, mitochondria and maximum power of the heart: a meta-study from shrew to elephant

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Statistical analyses: Source code for phylogenetic generalized least squares regression models implemented using the caper v1.0.1 package in R v3.6.1.

```
#Load packages:
library(caper)
library(nlme)
library(MCMCglmm)
#Import data:
data <- read.csv("Cardiac trait.csv")
#Import phylogenetic tree:
tree <- read.nexus("phylogenetic tree.nex")
#Take only the tree with best dates:
tree <- tree[[1]]
#See if tree is dichotomous, i.e. no polytomies:
is.binary.tree(tree)
#Plot the tree:
par(mfrow = c(1,1), mar = c(0,0,0,0) + 0.5)
plot(tree, show.tip.label = F)
#Plot the data:
par(mfrow = c(1,1), mar = c(4,4,0,0) + 0.5)
plot(Log_cardiactrait ~ Log_bodymass, data = data)
#Model the OLS:
model.ols <- lm(Log_cardiactrait ~ Log_bodymass, data = data)
summary(model.ols)
#Get list of residuals
res.ols <- resid(model.ols)
#Produce residual vs. fitted plot
plot(fitted(model.ols), res.ols)
```

```
#Add a horizontal line at 0

abline(0,0)

#Create Q-Q plot for residuals

qqnorm(res.ols)

#Add a straight diagonal line to the plot

qqline(res.ols)

#Create density plot of residuals

plot(density(res.ols))

#Before you run the PGLS, check for species in phylogeny but not in data:

setdiff(tree$tip.label, data$Binomial)

#Before you run the PGLS, check for species in data but not in phylogeny:

setdiff(data$Binomial, tree$tip.label)

#Run the PGLS:

Log_cardiactrait.cdat <- comparative.data(phy = tree,

    data = data,

    names.col = "Mesquite_name",

    vcv = TRUE)

#Take a look at the constructed matrix:

Log_cardiactrait.cdat$vcv

#Take a look at the pruned tree:

plot(Log_cardiactrait.cdat$phy)

#Plot the data (again):

par(mfrow = c(1,1), mar = c(4,4,0,0) + 0.5)

plot(Log_cardiactrait ~ Log_bodymass, data = data)

#Model the PGLS:

model.pgls <- pgls(Log_cardiactrait ~ Log_bodymass, data = Log_cardiactrait.cdat, lambda = "ML")

summary(model.pgls)

#Get list of residuals
```

```
res.pgls <- resid(model.pgls)

#Produce residual vs. fitted plot

plot(fitted(model.pgls), res.pgls)

#Add a horizontal line at 0

abline(0,0)

#Create Q-Q plot for residuals

qqnorm(res.pgls)

#Add a straight diagonal line to the plot

qqline(res.pgls)

#Create density plot of residuals

plot(density(res.pgls))

#Likelihood profiles for lambda:

lambda.profile <- pgls.profile(model.pgls, "lambda")

plot(lambda.profile)

pgls.confint(model.pgls, "lambda")$ci.val
```

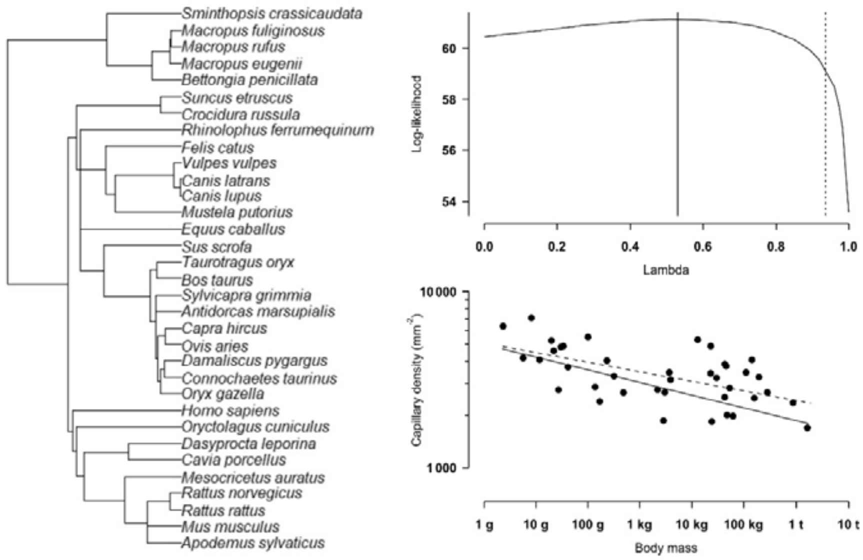

Figure S1: Evolutionary tree and phylogenetic signal (lambda) used to inform phylogenetic generalized least squares scaling (solid line) of cardiac capillary numerical density (profile counts per mm^2 of cardiomyocyte) against body mass in 39 species of mammal. Ordinary least squares scaling (dashed line) superimposed for comparison.

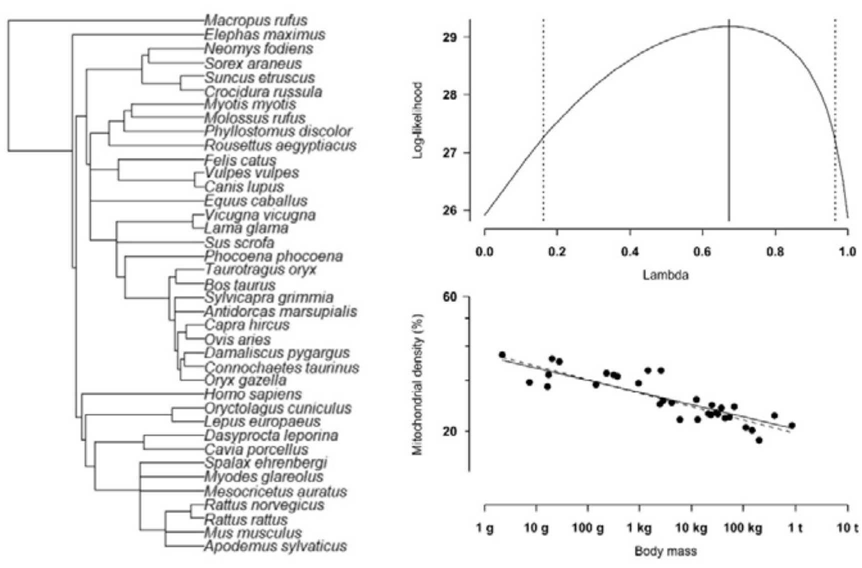

Figure S2: Evolutionary tree, phylogenetic signal (lambda) and phylogenetic generalized least squares scaling (solid line) of cardiac mitochondrial volume density (% volume of cardiomyocyte) against body mass in 33 species of mammal. Ordinary least squares scaling (dashed line) superimposed for comparison.

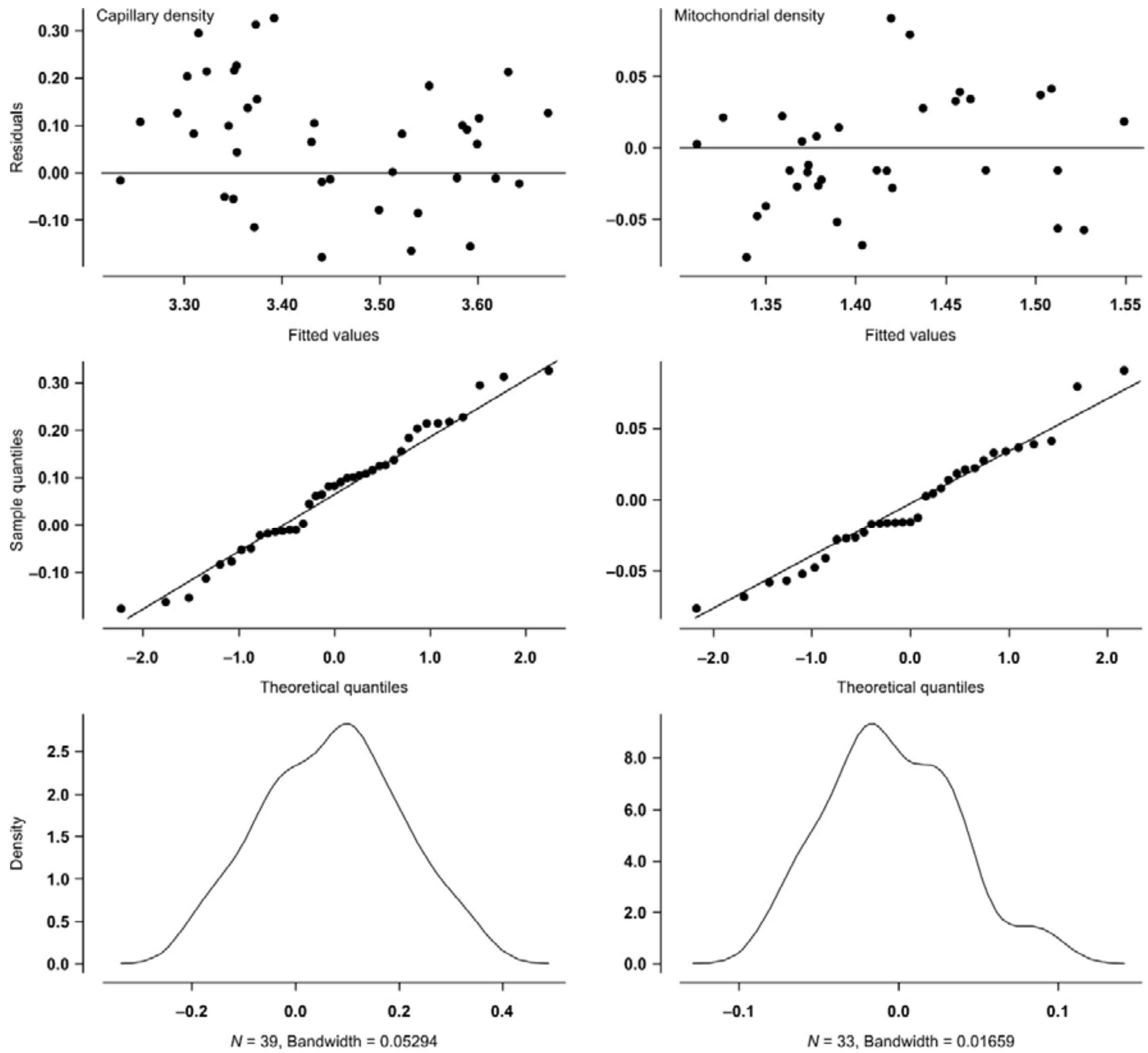

Figure S3: Analyses of the fitted phylogenetic generalized least squares scaling models, comprising the distribution of residuals, q-q plots and density plots for cardiac capillary numerical density (39 species of mammal; left-side panels) and cardiac mitochondrial volume density (33 species of mammal; right-side panels).

Data extraction: The literature was searched for studies on the numerical density of capillaries and volume density of mitochondria in the hearts of mammals, preferably obtained by unbiased stereological analysis of light and electron micrographs. Brevity of methodological detail often meant that we could not verify the absolute integrity of the presented values and so most studies were accepted under the assumption that appropriate unbiased stereological methods were followed. For example, estimates of capillary numerical density are affected by image orientation, and in many studies we had to assume that only cross-sectional images were assessed for this purpose because it was not explicitly stated in the text. We further assumed that capillary numerical density (in units of mm^{-2}) is approximately equivalent to its length density ($mm\ mm^{-3}$) because of the near-anisotropic geometry of capillary networks that service the tissue of the heart. It is standard practice to present both capillary numerical density and mitochondrial volume density with the cell (cardiomyocyte) as the reference space, although it was not always possible to confirm that all studies followed this convention. The literature search was not exhaustive with priority given to maximising species diversity and body mass range. A small proportion of identified studies were not included (prior to any analysis) over concerns primarily with either stereological methods, lack of suitable control group data, failure to use a cardiomyocyte reference space, or lack of extractable data.

Table S1: Mean values of cardiac capillary numerical density (profile counts per mm^2 of cardiomyocyte) and body mass in 39 species of mammal sourced from the literature.

Animal	Species	Body mass (kg)	Capillary numerical density (mm^{-2})
Etruscan shrew	*Suncus etruscus*	0.00245	6268
Musk shrew	*Crocidura russula*	0.00850	7018
Common shrew	*Sorex araneus*	0.00607	4173
Water shrew	*Neomys fodiens*	0.0126	4059
Greater mouse-eared bat	*Myotis myotis*	0.0213	5233
Black mastiff bat	*Molossus rufus*	0.0357	4861
Pale spear-nosed bat	*Phyllostomus discolor*	0.0433	3708
Egyptian fruit bat	*Rousettus aegyptiacus*	0.147	2853
House mouse	*Mus musculus*	0.0280	2739
Wood mouse	*Apodemus sylvaticus*	0.0228	4577
Black rat	*Rattus rattus*	0.245	4025
Brown rat	*Rattus norvegicus*	0.329	3273 (± 678)
Guinea pig	*Cavia porcellus*	0.494	2648
Hamster	*Mesocricetus auratus*	0.103	5445
Bank vole	*Myodes glareolus*	0.0311	4796
Mole rat	*Spalax ehrenbergi*	0.182	2340
Agouti*	*Dasyprocta leporina*	3.00	1834
Rabbit	*Oryctolagus cuniculus*	3.07	2643 (± 652)
European hare	*Lepus europaeus*	3.89	3456
Cat	*Felis catus*	2.32	2739
Red fox	*Vulpes vulpes*	4.16	3133
Dog	*Canis lupus*	23.78	3386 (± 124)
Goat	*Capra hircus*	30.41	3196 (± 286)
Sheep	*Ovis aries*	44.20	3818
Common duiker	*Sylvicapra grimmia*	13.33	5255
Springbok	*Antidorcas marsupialis*	24.33	4864
Blesbok	*Damaliscus pygargus*	56.00	2792
Gemsbok	*Oryx gazella*	114.3	3451
Blue wildebeest	*Connochaetes taurinus*	149.3	4081
Common eland	*Taurotragus oryx*	206.3	3226
Vicuna	*Vicugna vicugna*	46.50	3713
Llama	*Lama glama*	167.5	2470
Pig	*Sus scrofa*	44.48	2504 (± 302)
Horse/pony	*Equus caballus*	290.0	2631 (± 264)
Cattle/steer	*Bos taurus*	920.0	2311
Human	*Homo sapiens*	65.10	1955 (± 489)
Harbour porpoise	*Phocoena phocoena*	50.00	1975
Elephant^	*Elephas maximus*	1700	1660
Red kangaroo	*Macropus rufus*	25.60	1808

Data were taken from adult, normal, healthy, control, sham, non-exercised and disease-free groups only. Values were accepted from either, or both, the left and right ventricular chambers (myocardium, endocardium, epicardium or papillary). In many instances, the mean values presented above are averages across multiple studies. Where mean values were derived from at least three studies, the standard deviation is provided in parentheses. In some studies, body masses were estimated based on adult averages for that species (or strain), and species were deduced for some common domestic or laboratory animals. *Agouti data assumed to belong to *Dasyprocta leporine*. ^Elephant data assumed to belong to *Elephas maximus*.

Table S2: Mean values of cardiac mitochondrial volume density (% volume of cardiomyocyte) and body mass in 33 species of mammal sourced from the literature.

Animal	Species	Body mass (kg)	Mitochondrial volume density (%)
Etruscan shrew	*Suncus etruscus*	0.00233	36.96 (± 3.08)
White-toothed shrew	*Crocidura russula*	0.00790	29.40
Greater horseshoe bat	*Rhinolophus ferrumequinum*	0.0170	28.54
House mouse	*Mus musculus*	0.0287	34.62 (± 3.21)
Wood mouse	*Apodemus sylvaticus*	0.0207	35.50
Black rat	*Rattus rattus*	0.237	31.47 (± 5.07)
Brown rat	*Rattus norvegicus*	0.326	31.42 (± 4.33)
Guinea pig	*Cavia porcellus*	0.374	30.80 (± 4.75)
Hamster	*Mesocricetus auratus*	0.150	28.60
Ferret	*Mustela putorius*	1.50	32.31
Agouti*	*Dasyprocta leporina*	3.00	25.15
Rabbit	*Oryctolagus cuniculus*	2.62	32.41 (± 5.34)
Cat	*Felis catus*	2.57	24.65 (± 4.41)
Red fox	*Vulpes vulpes*	4.16	24.85
Coyote	*Canis latrans*	12.60	25.40
Dog/wolf	*Canis lupus*	21.87	22.78 (± 2.65)
Goat	*Capra hircus*	31.96	22.96 (± 1.65)
Sheep	*Ovis aries*	44.20	21.89
Common duiker	*Sylvicapra grimmia*	13.33	21.75
Springbok	*Antidorcas marsupialis*	24.33	22.49
Blesbok	*Damaliscus pygargus*	56.00	22.24
Gemsbok	*Oryx gazella*	114.3	20.37
Blue wildebeest	*Connochaetes taurinus*	149.3	19.82
Common eland	*Taurotragus oryx*	206.3	18.30
Pig	*Sus scrofa*	37.71	23.71
Horse/pony	*Equus caballus*	405.0	22.29 (± 3.26)
Cattle/steer	*Bos taurus*	920.0	20.63
Human	*Homo sapiens*	70.00	24.07
Fat-tailed dunnart	*Sminthopsis crassicaudata*	0.0179	31.30
Brush-tailed bettong	*Bettongia penicillata*	0.990	29.20
Tammar wallaby	*Macropus eugenii*	6.20	21.65
Western grey kangaroo	*Macropus fuliginosus*	32.59	22.72
Red kangaroo	*Macropus rufus*	25.60	24.30

See footnote to Table S1 for further explanation.

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