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Supplementary Material

Variation in fur properties may explain differences in heat-related mortality among Australian flying-foxes

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S1. Additional information on flying-fox museum specimens

Below are the catalogue numbers and basic information for the flying-fox fur specimens examined.

Cat No	Collected Date	Location	Species	Sex	Age
M37480	01-03-04	NSW	BFF	M	A
M37478	01-09-03	Ballina, NSW	BFF	F	A
M8127	01-06-60	Wen, QLD	BFF	F	A
M7481	01-01-49	QLD	BFF	M	A
M1709	01-06-03	QLD	BFF	M	A
M1710	01-06-03	QLD	BFF	F	A
M1711	01-06-03	QLD	BFF		J
M5724	01-09-34	Mackay, QLD	BFF	M	A
M7189	01-02-46	Cairns, QLD	SFF	M	J
M8126	01-06-60	Coen, QLD	SFF	F	A
A1366	20-02-05	Cairns, QLD	SFF	M	A
A1363	20-02-05	Cairns, QLD	SFF	M	A
M7784	01-07-52	NE QLD	SFF	F	J
M22828	01-01-73	Galstone, NSW	GHFF	M	A
M22827	01-01-73	NSW	GHFF	F	A
M23628	01-10-86	NSW	GHFF	F	A

M23975	01-04-81	NSW	GHFF	F	A
M41351			GHFF		J
M41352			GHFF		J
M42882	01-07-10	Sydney	GHFF	M	A
M45923	01-02-10	Sydney	GHFF	F	A
M42685	01-06-10	Ashfield, NSW	GHFF	M	A
M2609	01-01-16	Sydney	GHFF		J
M2610	01-01-16	Sydney	GHFF		J
M5208	01-11-31	Sydney	GHFF		J
M1924	01-10-07	Sydney	GHFF		J
M8561	01-10-63	QLD	LRFF	M	A
M10367	01-10-75	NT	LRFF	F	A
M11508	01-11-80	NT	LRFF	M	A
M11719	01-03-80	NT	LRFF	F	A
M8563	01-10-63	QLD	LRFF	M	A
M8562	01-10-63	QLD	LRFF	M	A
M8559	01-10-63		LRFF	M	A
M8109	01-06-60	QLD	LRFF	F	A
C4836		Warrnambool, VIC	GHFF	F	A
C2309	01-11-51	Port Welsh Pool, VIC	GHFF	M	A
C2303	01-11-51	Port Welsh Pool, VIC	GHFF	M	A
C2177	01-11-51	Port Welsh Pool, VIC	GHFF	M	A

C2180	01-11-51	Port Welsh Pool, VIC	GHFF	M	A
C4834		Harcourt, VIC	GHFF	F	A
C9061	01-02-69	Buxton, VIC	GHFF	M	A
C2181	01-11-51	Port Welsh Pool, VIC	GHFF	F	A
C23295	01-03-76	Hume Reservoir, VIC	LRFF	F	A
DTC112	01-06-32	Barehill, North QLD	LRFF	F	A
DTC113	01-06-32	Barehill, North QLD	LRFF	M	A
DTC117	01-06-32	Barehill, North QLD	LRFF	F	A
DTC114	01-06-32	Barehill, North QLD	LRFF	M	A
C4330	01-08-62	NT	LRFF		J
C16245	01-01-76	Pianjil, VIC	LRFF	F	A
C22014	01-01-76	Glengary, VIC	LRFF	M	A
C16243	01-01-76	Melbourne, VIC	LRFF	F	A
C3581	01-09-62	Silverplains Station, QLD	LRFF	M	A
C23127	01-03-76	Hume Reservoir, VIC	LRFF	M	A
DTC115	01-06-32	Barehill, North QLD	LRFF	M	A
DTC126	01-06-33	Lr Archer River, QLD	LRFF	M	A
C2304	01-11-61	Port Welsh Pool, VIC	GHFF	M	A
C1658		Clarence River, NSW	GHFF		J
C1659		Clarence River, NSW	GHFF		J
C16660		Clarence River, NSW	GHFF		J
C3649	01-10-62	Silverplains Station, QLD	SFF	F	A

C3648	01-10-62	Silverplains Station, QLD	SFF	M	A
C28056	01-01-49	Edgehill, QLD	SFF	M	A
C1515	01-01-11	North QLD	SFF		A
C1509	01-01-11	North QLD	SFF		A
C1507	25-02-1871	NT	BFF		A
C36801	01-07-10	Hawthorn East, VIC	BFF	F	A
DTC128	01-06-32	Barehill, North QLD	BFF	M	A
C22014	01-01-76	Glengary, VIC	LRFF	M	A
C2586	09-05-05	Melbourne, VIC	GHFF	F	A
C2179	01-11-51	Port Welsh Pool, VIC	GHFF	M	A
C2175	01-11-51	Port Welsh Pool, VIC	GHFF	M	A
C2183	01-11-51	Port Welsh Pool, VIC	GHFF	M	A
DTC127	01-06-32	Barehill, North QLD	BFF	M	A

NSW, New South Wales; VIC, Victoria; QLD, Queensland

BFF, *P. alecto*; GHFF, *P. poliocephalus*; LRFF, *P. scapulatus;* SFF, *P. conspicillatus*

M, Male; F, Female

A, Adult; J, Juvenile

S2. R script to calculate total solar reflectance

We used a custom R script based on the Fortran program created by Warren Porter and James Jaeger (2004) to convert the measured solar reflectance values to solar reflectivity. This was done by calculating the weighted average across 37 bandwidths between 260-2600nm. Below is the R code used:

```
### R Script for converting solar reflectance values into total solar
reflectivity
### Last script update by Himali Ratnayake 20-05-2020

# The following script is based on a Fortran program by James Jaeger and
Warren Porter [2004]
# This program computes the weighted mean of the reflectance for the entire
spectrum 290-2600 nm using 37 bandwidths.
# Summary output includes five regions within the spectrum: UV, 2 visible
regions and 2 IR regions.
# The data are the median of the reflectances i.e. the midpoint of each of
the 37 intervals.

#read in output file of the spectrophotometer
input<-read.csv("D:/Documents/furscans.csv")
tail(input)
nreadings<-ncol(input)-1 # first column is wavelengths

wavelengths<-c(305,335,375,425,475,525,575,625,675,725,775,825,875,

925,975,1025,1075,1125,1175,1225,1275,1325,1375,1425,1475,1525,
               1575,1650,1750,1850,1950,2050,2150,2250,2350,2450,2550) #
These are the mid-points of each band

wavlengths_St_End<-
c(300,320,355,400,450,500,550,600,650,700,750,800,850,900,950,1000,1050,1100,
1150,

1200,1250,1300,1350,1400,1450,1500,1550,1612.5,1700,1800,1900,2000,2100,2200,
2300,
                     2400,2500,2550) # Start/End values of each wavelength
section

row_st_End<-
c(1,41,118,217,329,443,557,674,792,912,1033,1157,1283,1411,1541,1674,1694,171
5,1735,1756,1777,

1797,1818,1839,1860,1881,1902,1928,1965,2007,2049,2091,2091,2091,2091,2091,20
91,2137)

check_rows<-cbind(wavlengths_St_End,input[c(row_st_End),1])
```

```r
plot(check_rows) # Note that these won't be exact becasue spec only measures
particular wavelengths


for(i in 1:nreadings){
  Refs<-input[,(i+1)] # read the data for that column
  names<-colnames(input)
  names<-names[-1]
  R<-list()

  R[1]<-mean(Refs[1:40])
  R[2]<-mean(Refs[41:117])
  R[3]<-mean(Refs[118:216])
  R[4]<-mean(Refs[217:328])
  R[5]<-mean(Refs[329:442])
  R[6]<-mean(Refs[443:556])
  R[7]<-mean(Refs[557:673])
  R[8]<-mean(Refs[674:791])
  R[9]<-mean(Refs[792:911])
  R[10]<-mean(Refs[912:1032])
  R[11]<-mean(Refs[1033:1156])
  R[12]<-mean(Refs[1157:1282])
  R[13]<-mean(Refs[1283:1410])
  R[14]<-mean(Refs[1411:1540])
  R[15]<-mean(Refs[1541:1673])
  R[16]<-mean(Refs[1674:1693],na.rm=TRUE)
  R[17]<-mean(Refs[1694:1714])
  R[18]<-mean(Refs[1715:1734])
  R[19]<-mean(Refs[1735:1755])
  R[20]<-mean(Refs[1756:1776])
  R[21]<-mean(Refs[1777:1796])
  R[22]<-mean(Refs[1797:1817])
  R[23]<-mean(Refs[1818:1838])
  R[24]<-mean(Refs[1839:1859])
  R[25]<-mean(Refs[1860:1880])
  R[26]<-mean(Refs[1881:1901])
  R[27]<-mean(Refs[1902:1927])
  R[28]<-mean(Refs[1928:1964])
  R[29]<-mean(Refs[1965:2006])
  R[30]<-mean(Refs[2007:2048])
  R[31]<-mean(Refs[2049:2090])
  R[32]<-mean(Refs[2091:2137])
  R[33]<-mean(Refs[2091:2137])
  R[34]<-mean(Refs[2091:2137])
  R[35]<-mean(Refs[2091:2137])
  R[36]<-mean(Refs[2091:2137])
  R[37]<-mean(Refs[2091:2137])


  R<-unlist(R)
  R[1]<-R[1] * 0.36
  R[2]<-R[2] * 1.92
  R[3]<-R[3] * 3.02
  R[4]<-R[4] * 5.23
  R[5]<-R[5] * 6.95
  R[6]<-R[6] * 6.86
  R[7]<-R[7] * 6.72
```

```
  R[8]<-R[8] * 6.45
  R[9]<-R[9] * 6.11
  R[10]<-R[10] * 5.68
  R[11]<-R[11] * 5.19
  R[12]<-R[12] * 4.67
  R[13]<-R[13] * 3.89
  R[14]<-R[14] * 3.24
  R[15]<-R[15] * 3.24
  R[16]<-R[16] * 3.14
  R[17]<-R[17] * 2.88
  R[18]<-R[18] * 2.10
  R[19]<-R[19] * 2.09
  R[20]<-R[20] * 1.99
  R[21]<-R[21] * 1.81
  R[22]<-R[22] * 1.41
  R[23]<-R[23] * 1.12
  R[24]<-R[24] * 1.31
  R[25]<-R[25] * 1.02
  R[26]<-R[26] * 1.18
  R[27]<-R[27] * 1.21
  R[28]<-R[28] * 2.20
  R[29]<-R[29] * 1.65
  R[30]<-R[30] * 0.66
  R[31]<-R[31] * 0.87
  R[32]<-R[32] * 0.77
  R[33]<-R[33] * 0.77
  R[34]<-R[34] * 0.72
  R[35]<-R[35] * 0.64
  R[36]<-R[36] * 0.49
  R[37]<-R[37] * 0.44

  T1<-R[1] + R[2] + R[3]
  T2<-R[4] + R[5]
  T3<-R[6] + R[7] + R[8] + R[9]
  T4<-sum(R[10:24])
  T5<-sum(R[25:37])
  Tot<-T1 + T2 + T3 + T4 + T5

  T1<-T1/5.3
  T2<-T2/12.18
  T3<-T3/26.14
  T4<-T4/43.76
  T5<-T5/12.62
  Tot<-Tot/100.0

  Out<-c(T1,T2,T3,T4,T5,Tot)

  if(i ==1){
    # first sample, create output file
    TSolarRef<-Out
  }else{
    TSolarRef<-rbind(TSolarRef,Out)
  }
}
colnames(TSolarRef)<-c("UV", "VIS1","VIS2","IR1","IR2","Total")
rownames(TSolarRef)<-names
```

```
write.csv(TSolarRef,"TotalSolarRef.csv") #output file containing mean solar
reflectances for each region in the spectrum extracted
```

S3. Model selection processes

We used the backward stepwise model selection method where we started with the full model containing all the predictor terms, and then excluded a predictor term one at a time and tested whether the reduced model was significantly different to the model that included the removed predictor term using the 'anova' function of the 'lmerTest' package on R. At each step, if the reduced model was significantly different to its counterpart that meant the removed term had a significant influence on the response and therefore was retained. However, if the reduced model was not significantly different that meant that the removed term did not significantly influence the response and thus was removed from the model. Once all the predictor terms were evaluated for their influence on the response, we included interactions of these chosen predictor terms and used the same method above to test for the significance of the influence of the interaction terms. The model with interactions was chosen as the final model if it was significantly different to the model that did not contain interactions, and if there was no significant difference between these two models the model without interactions was chosen as the final model.

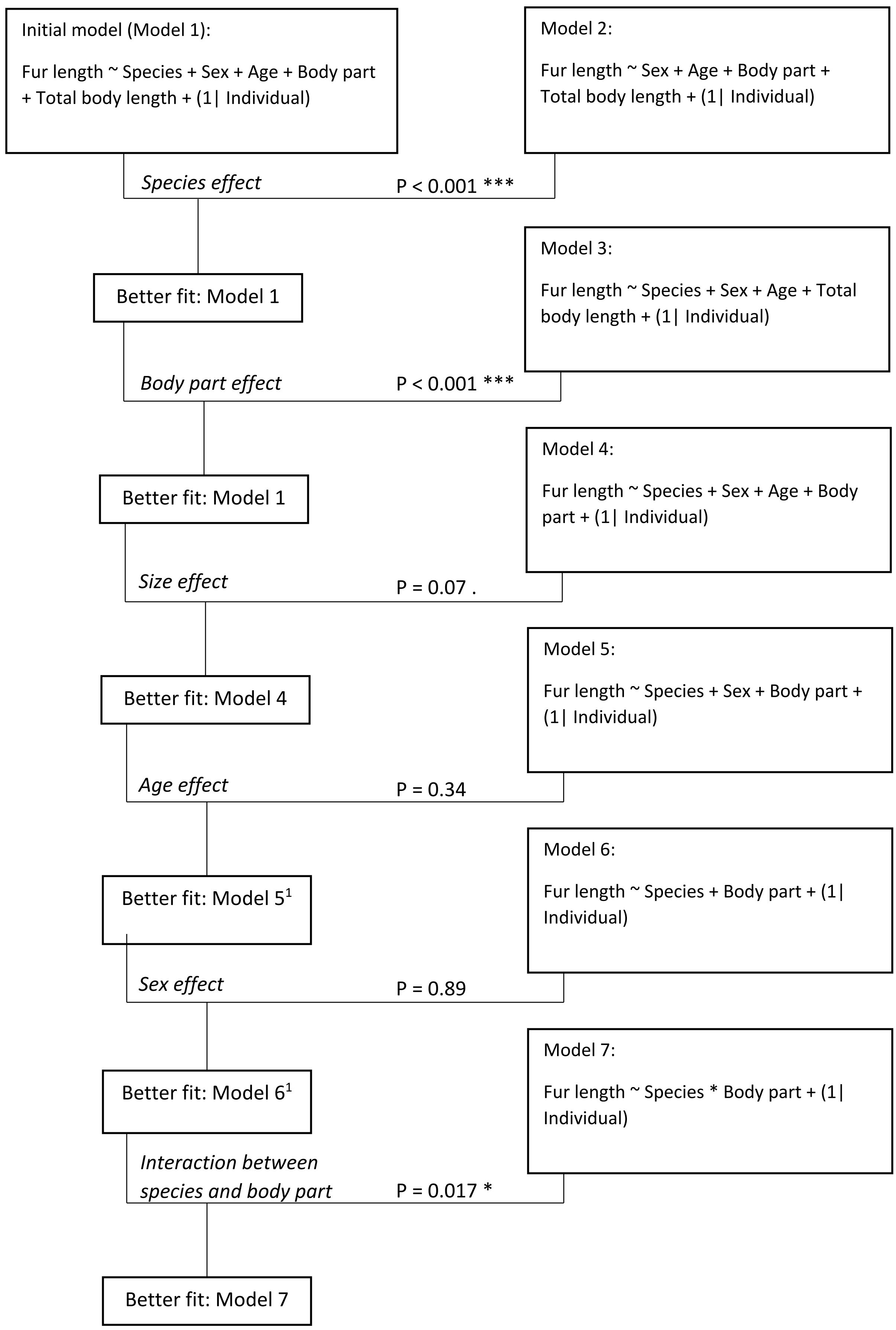
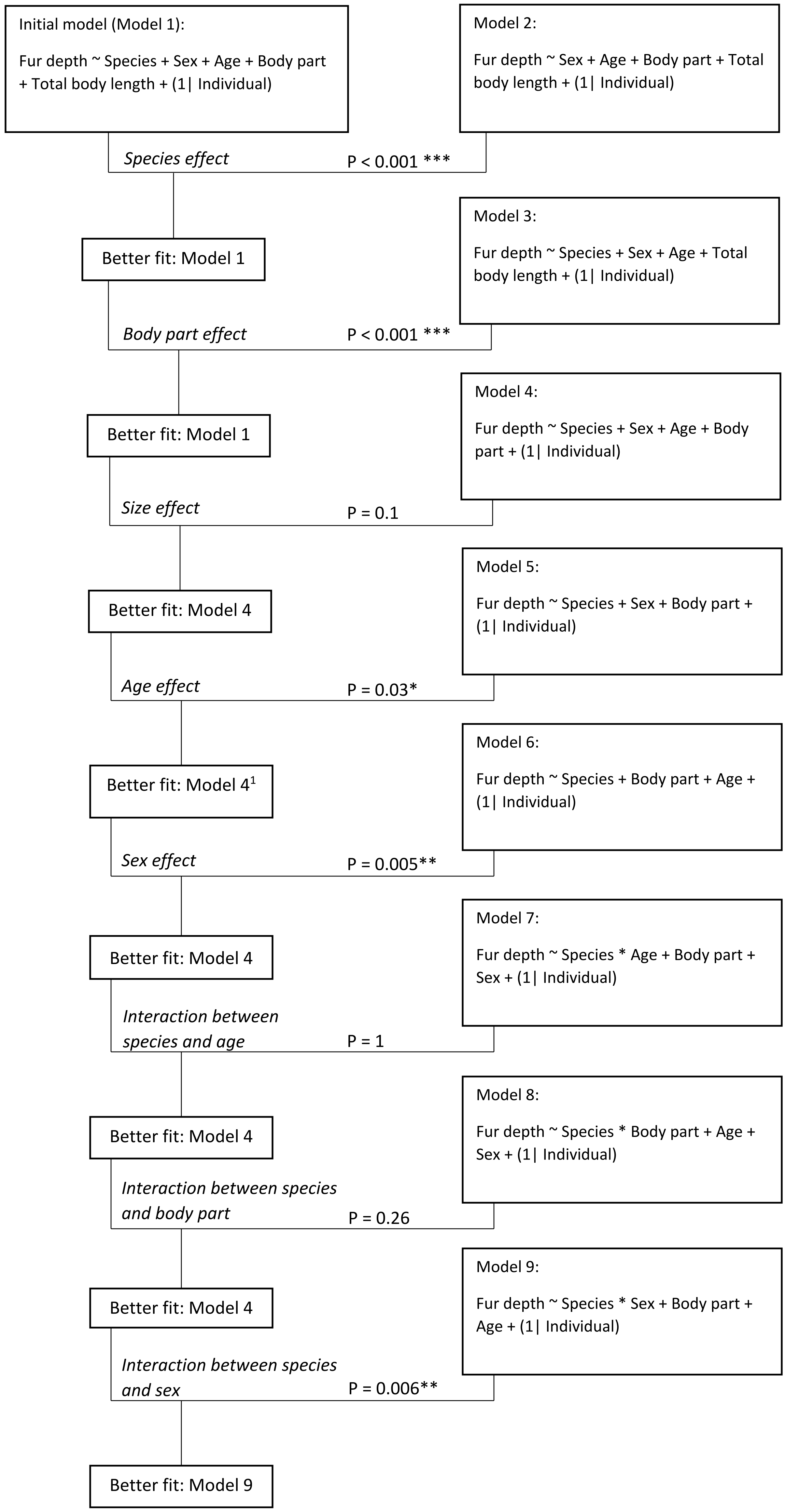


Fig. S1. Fur length model selection process. The sample sizes of Model 5[1] and Model 6 are smaller than Model 5 and Model 6[1], respectively, because the sex of all individuals were not reported. The P value denotes the significance of the difference between the two models compared using an ANOVA test.


Initial model (Model 1):
Fur depth ~ Species + Sex + Age + Body part + Total body length + (1| Individual)
Model 2:
Fur depth ~ Sex + Age + Body part + Total body length + (1| Individual)
Species effect
P < 0.001 ***
Better fit: Model 1
Model 3:
Fur depth ~ Species + Sex + Age + Total body length + (1| Individual)
Body part effect
P < 0.001 ***
Better fit: Model 1
Model 4:
Fur depth ~ Species + Sex + Age + Body part + (1| Individual)
Size effect
P = 0.1
Better fit: Model 4
Model 5:
Fur depth ~ Species + Sex + Body part + (1| Individual)
Age effect
P = 0.03*
Better fit: Model 4[1]
Model 6:
Fur depth ~ Species + Body part + Age + (1| Individual)
Sex effect
P = 0.005**
Better fit: Model 4
Model 7:
Fur depth ~ Species * Age + Body part + Sex + (1| Individual)
Interaction between species and age
P = 1
Better fit: Model 4
Model 8:
Fur depth ~ Species * Body part + Age + Sex + (1| Individual)
Interaction between species and body part
P = 0.26
Better fit: Model 4
Model 9:
Fur depth ~ Species * Sex + Body part + Age + (1| Individual)
Interaction between species and sex
P = 0.006**
Better fit: Model 9

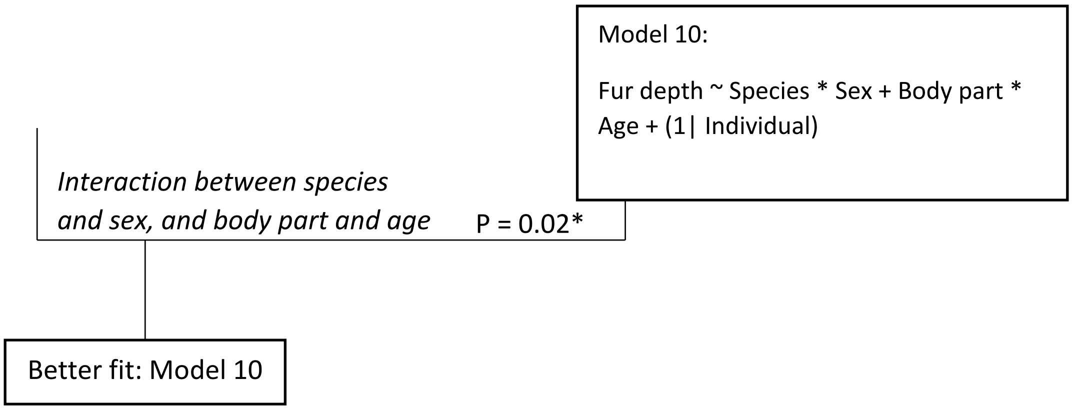


Fig. S2. Fur depth model selection process. The sample size of Model 4[1] is smaller than Model 4 because the sex of all individuals were not reported. The P value denotes the significance of the difference between the two models compared using an ANOVA test.

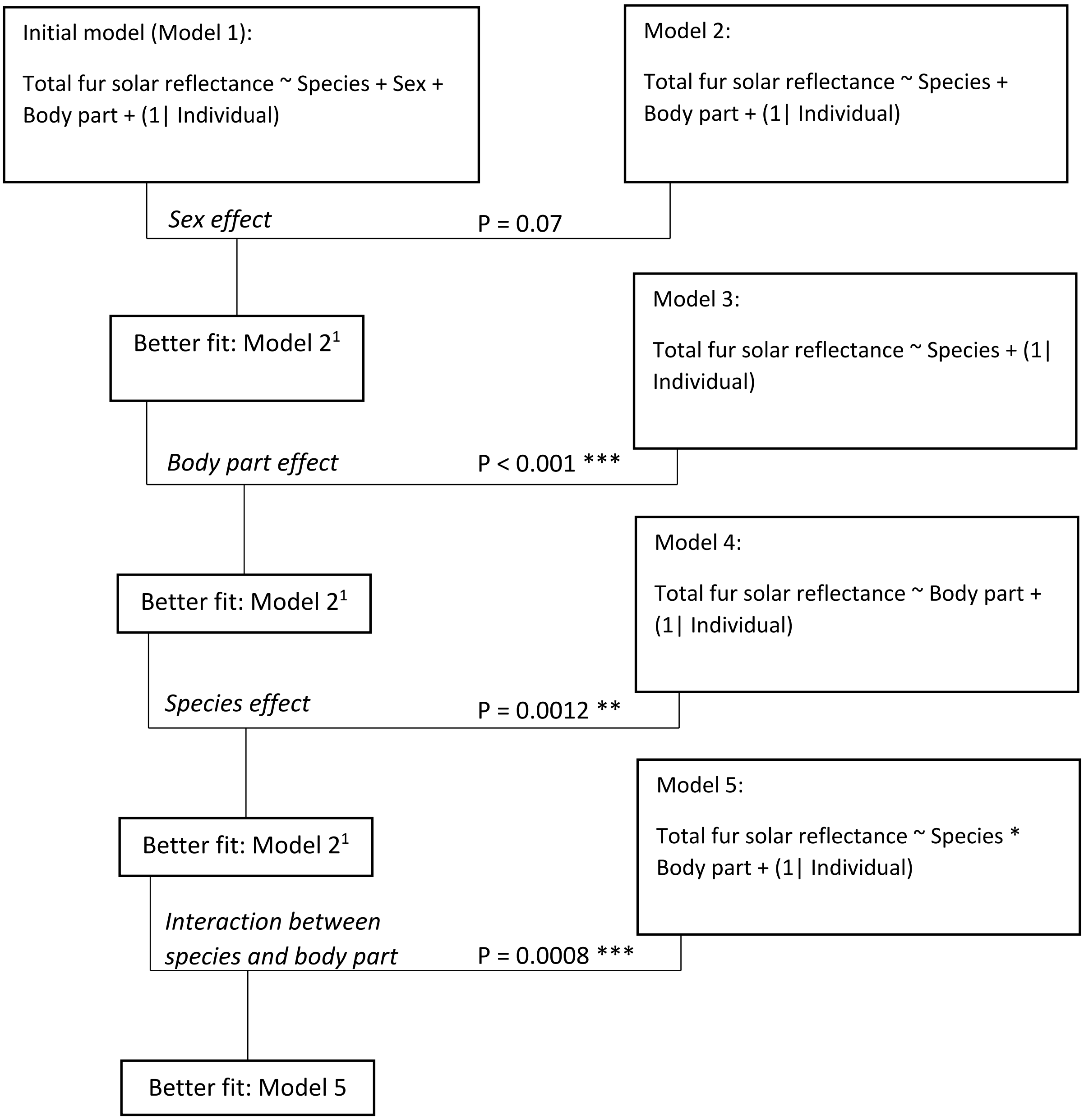


Fig. S3. Fur solar reflectivity model selection process. The sample size of Model 2[1] is smaller than Model 2 because the sex of all individuals was not reported. The P value denotes the significance of the difference between the two models compared using an ANOVA test.

S4. Model linearity using residual plots for the generalized mixed models of fur length, fur depth, and fur solar reflectance

Visual inspection of residual plots did not reveal any obvious deviations from homoscedasticity or normality.

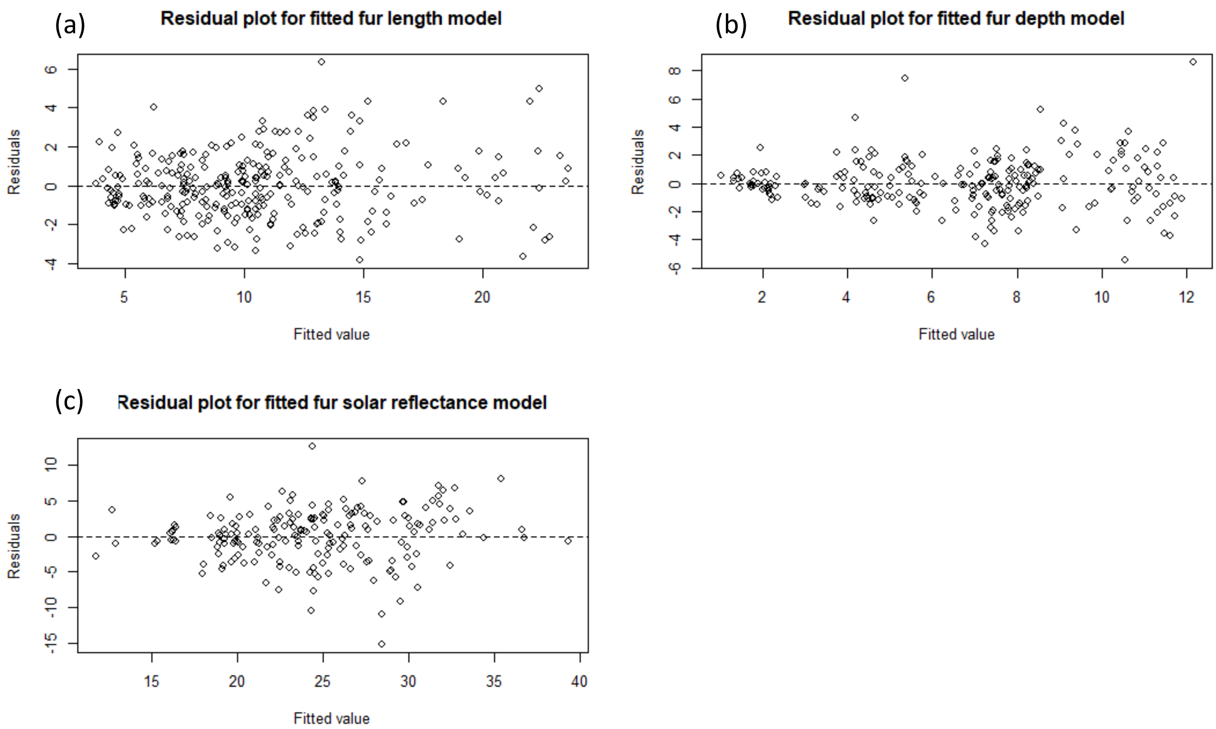


Fig. S4. Residual plots of (a) fur length generalized linear mixed model (GLMM), (b) fur depth GLMM, and (c) fur solar reflectivity GLMM

S5. Post hoc analyses of the generalized linear mixed effects models for fur length, fur depth, and fur solar reflectivity

Table S5. Detailed results of the post hoc analyses of the three generalized linear mixed effects models for fur length, fur depth, and fur solar reflectivity.

	Estimate	Standard error	Lower confidence interval	Upper confidence interval	P-value	Significant codes
Species						
Fur length						
P. alecto - P. poliocephalus	-3.2	0.9	-5.1	-1.3	<0.001	***
P. alecto - P. scapulatus	2.3	1.0	0.4	4.3	0.020	*
P. alecto - P. conspicillatus	-0.3	1.2	-2.6	2.0	0.770	
P. poliocephalus - P. scapulatus	5.5	0.8	4.0	7.1	<0.001	***
P. poliocephalus - P. conspicillatus	2.9	1.0	0.9	4.8	0.005	**
P. scapulatus - P. conspicillatus	-2.7	1.0	-4.7	-0.6	0.010	*
Fur depth						
P. alecto - P. poliocephalus	-2.6	0.3	-3.2	-1.9	<0.001	***
P. alecto - P. scapulatus	0.9	0.3	0.2	1.6	0.010	*
P. alecto - P. conspicillatus	0.5	0.5	-0.4	1.5	0.250	
P. poliocephalus - P. scapulatus	3.4	0.3	2.9	4.0	<0.001	***
P. poliocephalus - P. conspicillatus	3.1	0.4	2.3	4.0	<0.001	***
P. scapulatus - P. conspicillatus	-0.3	0.4	-1.2	0.5	0.440	

	Estimate	Standard error	Lower confidence interval	Upper confidence interval	P-value	Significant codes
Fur solar reflectivity						
P. alecto - P. poliocephalus	-7	1.9	-10.7	-3.2	<0.001	***
P. alecto - P. scapulatus	-8.3	1.9	-12.1	-4.4	<0.001	***
P. alecto - P. conspicillatus	-6.8	2.5	-11.8	-1.8	0.009	**
P. poliocephalus - P. scapulatus	-1.3	1.0	-3.3	0.7	0.190	
P. poliocephalus - P. conspicillatus	0.2	1.9	-3.6	3.9	0.920	
P. scapulatus - P. conspicillatus	1.5	1.9	-2.3	5.3	0.440	
Body parts						
Fur length						
Dorsal collar - Dorsal abdomen	4.5	0.4	3.8	5.2	<0.001	***
Dorsal collar - Ventral collar	2.6	0.4	1.9	3.3	<0.001	***
Dorsal collar - Ventral abdomen	4.6	0.4	3.9	5.2	<0.001	***
Dorsal abdomen - Ventral collar	-1.9	0.4	-2.6	-1.2	<0.001	***
Dorsal abdomen - Ventral abdomen	0.1	0.4	-0.6	0.8	0.800	
Ventral collar - Ventral abdomen	2.0	0.4	1.3	2.7	<0.001	***
Fur depth						
Dorsal collar - Dorsal abdomen	5.6	0.9	3.8	7.3	<0.001	***
Dorsal collar - Ventral collar	2.6	0.9	0.9	4.4	0.003	**
Dorsal collar - Ventral abdomen	8.6	0.9	6.9	10.4	<0.001	***
Dorsal abdomen - Ventral collar	-3.0	0.9	-4.7	-1.2	0.001	***

	Estimate	Standard error	Lower confidence interval	Upper confidence interval	P-value	Significant codes
Dorsal abdomen - Ventral abdomen	3.0	0.9	1.3	4.8	<0.001	***
Ventral collar - Ventral abdomen	6.0	0.9	4.2	7.7	<0.001	***
Fur solar reflectivity						
Dorsal abdomen – Dorsal collar	-12.2	1.3	-14.6	-9.7	<0.001	***
Dorsal abdomen – Ventral abdomen	-0.8	1.3	-3.3	1.6	0.500	
Dorsal abdomen – Ventral collar	-3.2	1.3	-5.7	-0.7	0.010	*
Dorsal collar – Ventral abdomen	11.3	1.3	8.8	13.8	<0.001	***
Dorsal collar – Ventral collar	9.0	1.3	6.5	11.5	<0.001	***
Ventral abdomen – Ventral collar	-2.3	1.3	-4.8	0.2	0.070	.
Sex						
Fur depth						
Female – Male	1.1	0.2	0.5	1.6	<0.001	***
Age						
Fur depth						
Adult – juvenile	-1.7	0.7	-3.1	-0.2	0.020	*

Significant codes – “***” denotes P < 0.001; “**” denotes P < 0.01; “*” denotes P < 0.05; “.” denotes P < 0.1; and no code denotes P > 0.1

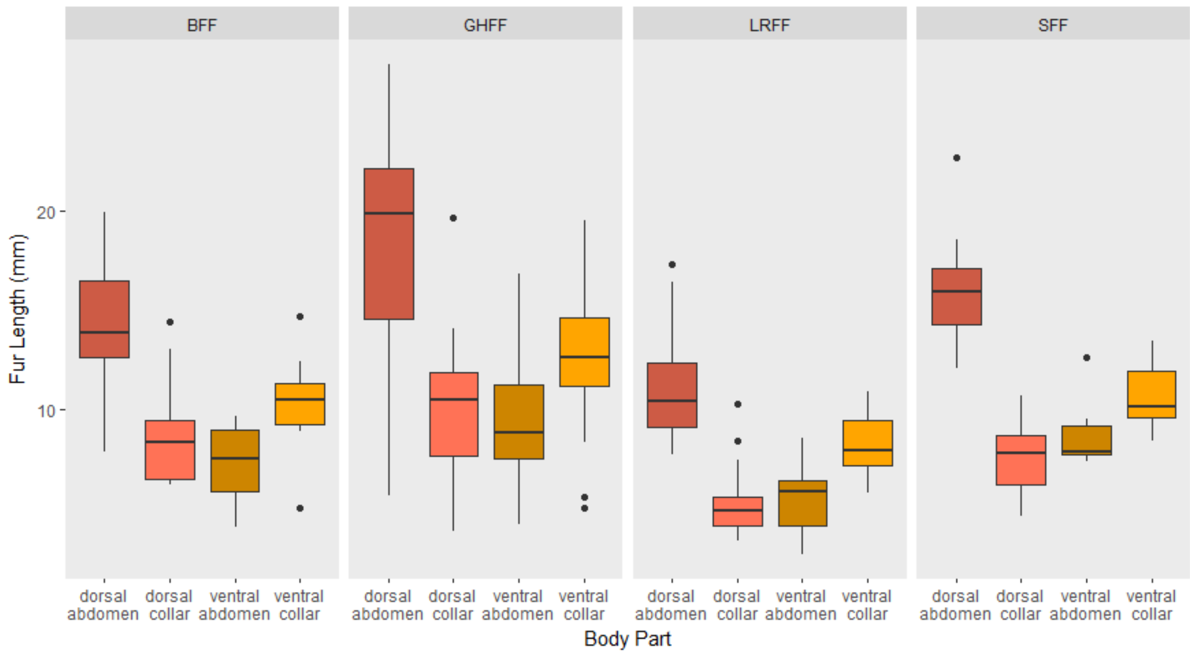


Figure S5. Detailed boxplots depicting fur lengths of the four mainland Australian flying-foxes in the separate body parts. The values in the boxplots represent the median and interquartile range of the distributions of the data. The black dots represent the outliers. BFF, *P. alecto*; GHFF, *P. poliocephalus*; LRFF, *P. scapulatus;* SFF, *P. conspicillatus*

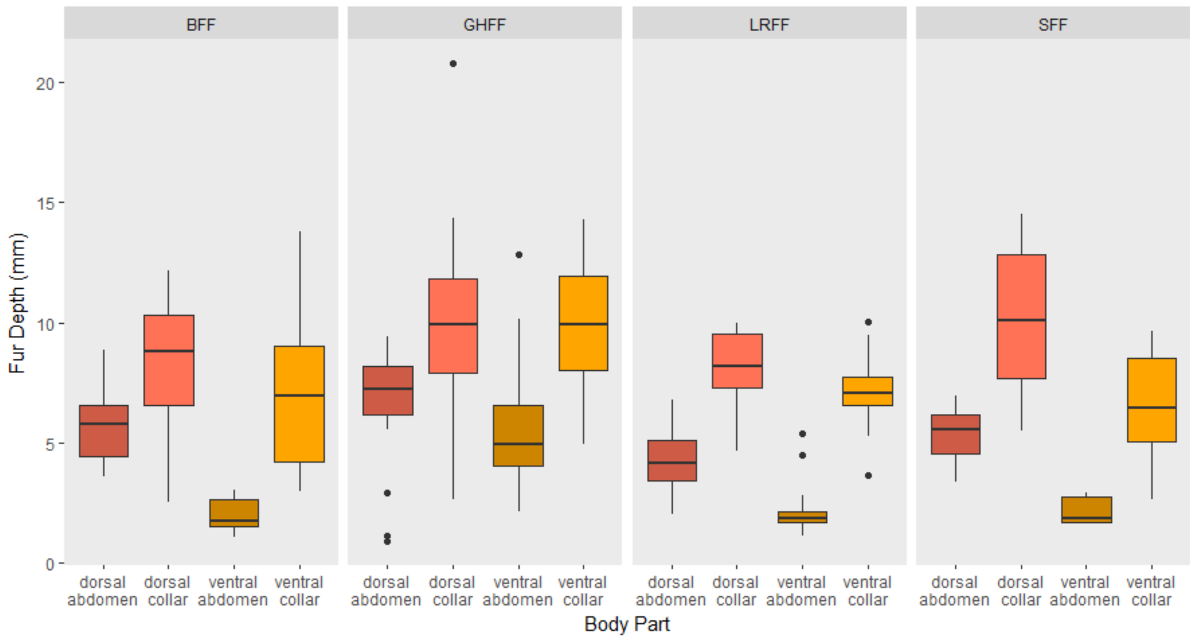


Figure S6. Detailed boxplots depicting fur depths of the four mainland Australian flying-foxes in the separate body parts. The values in the boxplots represent the median and interquartile range of the distributions of the data. The black dots represent the outliers. BFF, *P. alecto*; GHFF, *P. poliocephalus*; LRFF, *P. scapulatus;* SFF, *P. conspicillatus*

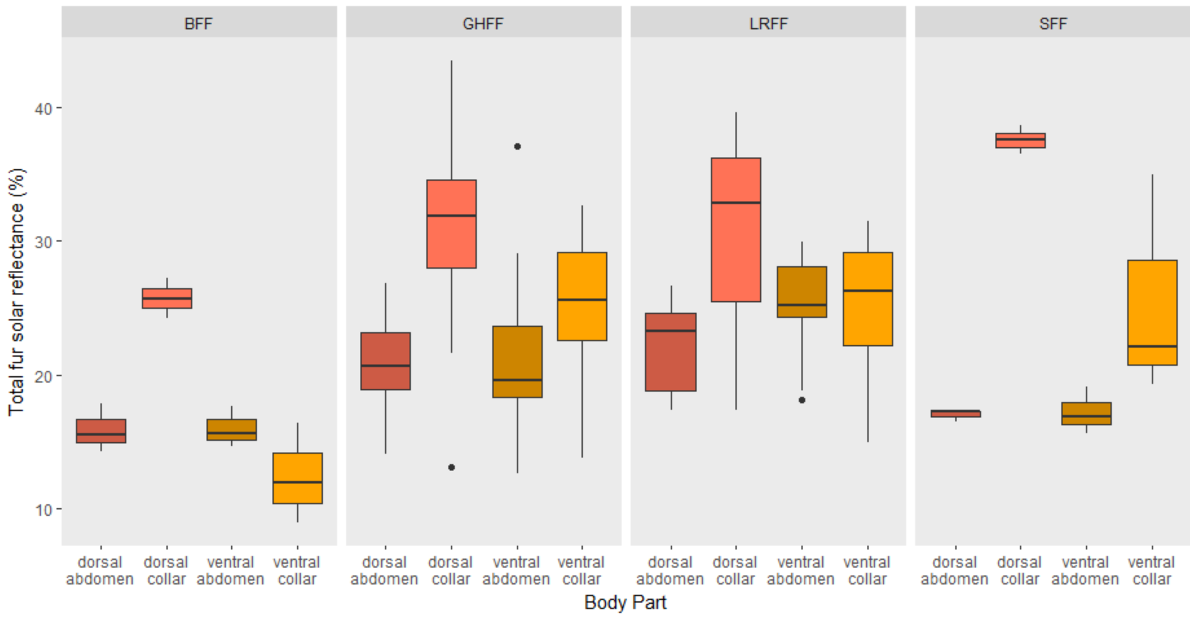


Figure S7. Detailed boxplots depicting total fur solar reflectances of the four mainland Australian flying-foxes in the separate body parts. The values in the boxplots represent the median and interquartile range of the distributions of the data. The black dots represent the outliers. BFF, *P. alecto*; GHFF, *P. poliocephalus*; LRFF, *P. scapulatus;* SFF, *P. conspicillatus*

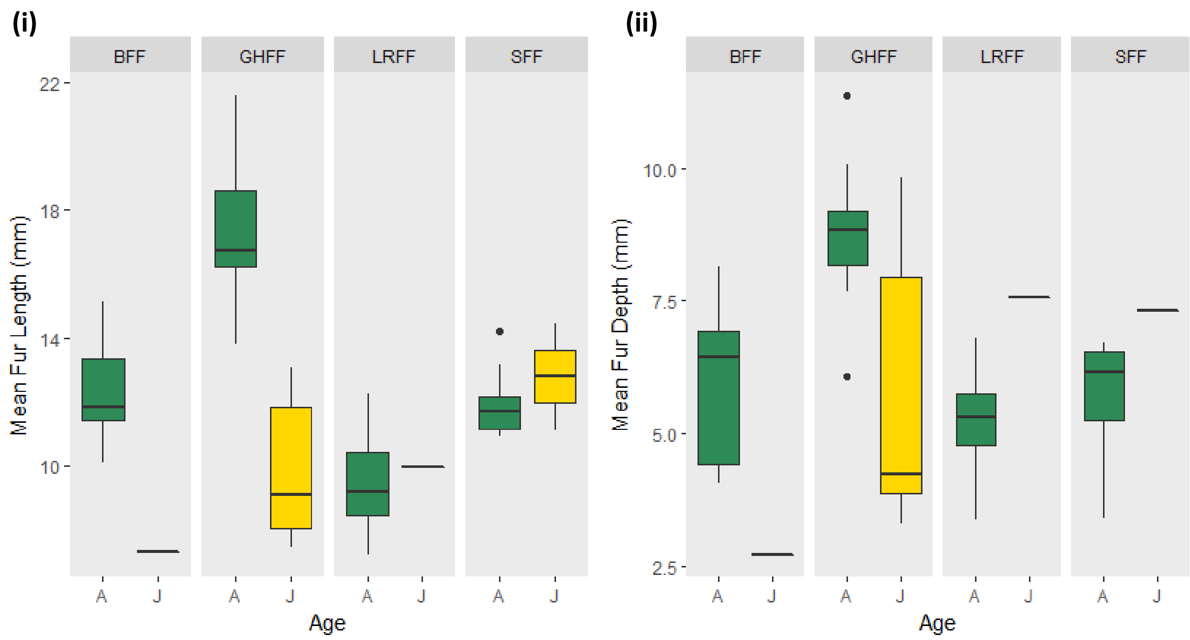


Figure S8. Detailed boxplots depicting (i) fur lengths and (ii) fur depths of the four mainland Australian flying-foxes for adults (A) and juveniles (J). The values in the boxplots represent the median and interquartile range of the distributions of the data. The black dots represent the outliers. BFF, *P. alecto*; GHFF, *P. poliocephalus*; LRFF, *P. scapulatus;* SFF, *P. conspicillatus*

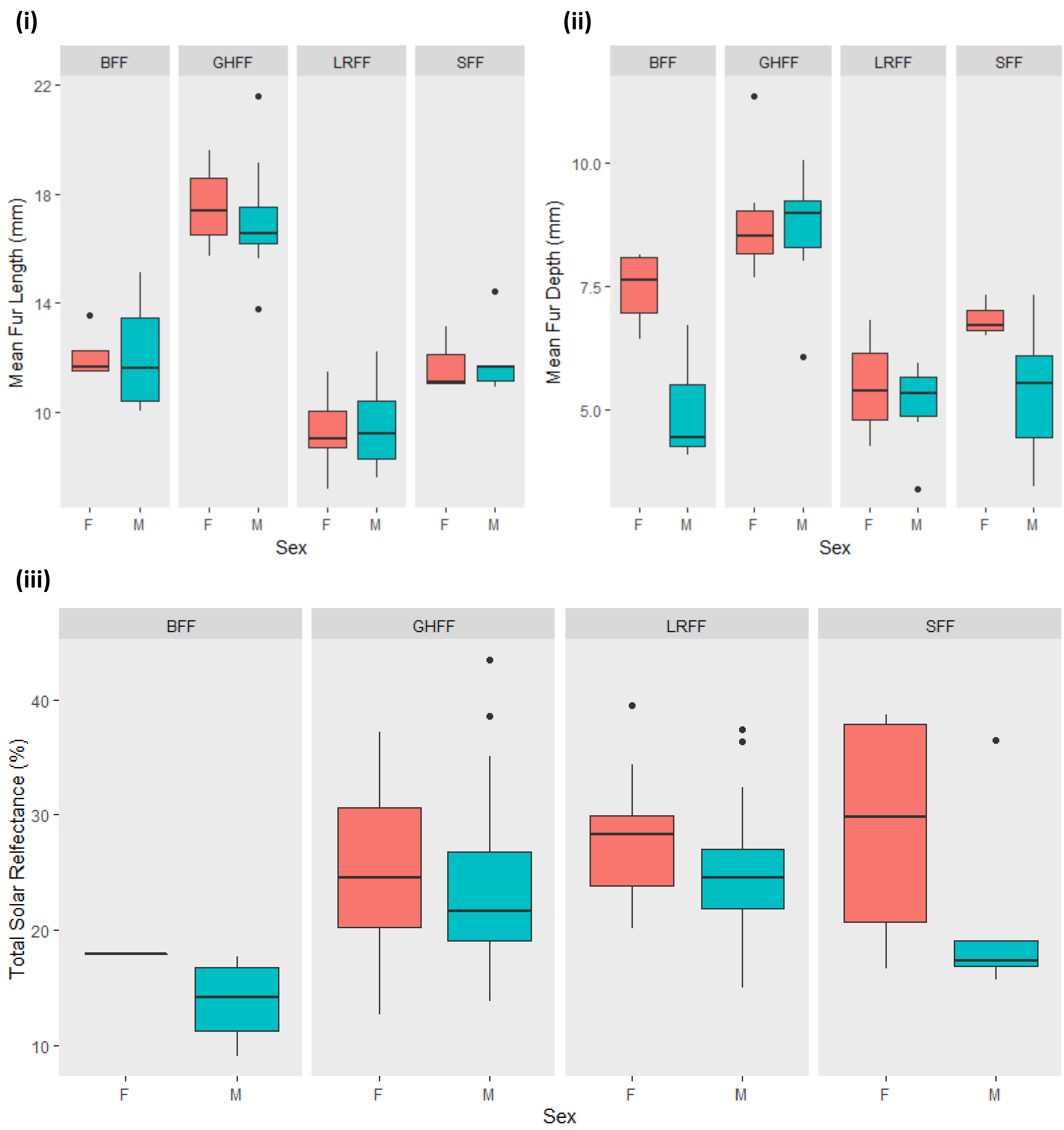


Figure S9. Detailed boxplots depicting (i) fur lengths, (ii) fur depths, and (iii) total fur solar reflectance of the four mainland Australian flying-foxes for males (M) and females (F). The values in the boxplots represent the median and interquartile range of the distributions of the data. BFF, *P. alecto*; GHFF, *P. poliocephalus*; LRFF, *P. scapulatus;* SFF, *P. conspicillatus*