

Supplementary Material

Supplementary Text

In our viral database we note the method of identification, such as isolation, serology (evidence of antibodies), or PCR. Fifteen and eleven viruses were identified in bats and rodents, respectively, solely by serological evidence. It is possible that some of these accounts could list the wrong virus due to antibody crossreactivity. For example, Mokola virus, a (rabies-related) lyssavirus, is one of the viruses listed in our database for which there is only serological evidence for its presence in bats. The virus has not yet been isolated from a bat, and the serological finding may be a result of antibodies to another lyssavirus, Lagos bat virus, which may cross-react with Mokola virus [1]. Therefore, some caution must be used in defining species based on serology alone. Other potential sources of bias may be a number of spillover hosts that are not important reservoirs, but are included in the analysis because infection has been detected in the species.

Supplementary Tables

Table S1. Loading values for principal components (PCs) summarizing life history traits of rodents.

	PC1	PC2	PC3	PC4
litter size	-0.374	0.774	-0.482	-0.168
litters per year	-0.428	-0.619	-0.659	-0.009
maximum longevity	0.591	-0.068	-0.310	-0.742
body mass	0.572	0.114	-0.488	0.649
proportion of variance	0.571	0.229	0.134	0.067

Table S2. Full set of generalized least squares rankings for rodents, including phylogenetic correction, considering species traits, with the number of zoonotic viruses identified in a species as the response variable.

Model	AICc	npar	Weight	p value	R	λ
~cit. + rodent sympatry + IUCN	356.4	5	0.213	9.80×10^{-8}	0.60	0.000
~cit. + rodent sympatry	356.4	4	0.213	6.26×10^{-8}	0.58	0.000
~cit. + rodent sympatry + torpor	357.6	6	0.114	2.24×10^{-7}	0.61	0.000
~cit. + rodent sympatry + PC2 _r	357.6	5	0.112	1.83×10^{-7}	0.59	0.000
~cit. + rodent sympatry + latitude	357.7	5	0.108	1.89×10^{-7}	0.59	0.000
~cit. + rodent sympatry + PC3 _r	358.6	5	0.070	2.90×10^{-7}	0.58	0.000
~cit. + IUCN	359.3	4	0.050	2.68×10^{-7}	0.56	0.000
~cit. + torpor	359.8	5	0.038	5.21×10^{-7}	0.57	0.000
~cit.	360.7	3	0.025	2.42×10^{-7}	0.53	0.000
~cit. + IUCN + PC3 _r	361.3	5	0.018	1.06×10^{-6}	0.56	0.000
~cit. + IUCN + PC1 _r	361.3	5	0.018	1.07×10^{-6}	0.56	0.000
~cit. + area	362.6	4	0.010	1.38×10^{-6}	0.53	0.000
~cit. + PC3 _r	362.8	4	0.008	1.60×10^{-6}	0.53	0.000
~cit. + area + latitude	364.5	5	0.004	4.98×10^{-6}	0.54	0.000
~rodent sympatry	379.0	3	0.000	3.99×10^{-3}	0.31	0.000
the null (intercept) model	385.2	2	0.000			0.017

Table S3. Loading values for principal components (PCs) summarizing life history traits of bats.

	PC1	PC2	PC3	PC4
litter size	-0.654	-0.104	-0.564	0.493
litters per year	0.295	0.721	0.070	0.624
maximum longevity	0.345	-0.681	0.246	0.597
body mass	0.605	-0.075	-0.785	-0.111
proportion of variance	0.378	0.328	0.176	0.119

Table S4. Full set of generalized least squares rankings for bats considering species traits, with the number of zoonotic viruses identified in a species as the response variable and λ showing the strength of the phylogenetic correction.

Model	AICc	npar	Weight	p value	R	λ
\sim cit. + bat sympatry + PC1 _b	290.5	5	0.787	1.06×10^{-8}	0.70	0.000
\sim cit. + bat sympatry + torpor	294.0	6	0.137	7.21×10^{-8}	0.69	0.000
\sim cit. + bat sympatry + latitude	297.3	5	0.026	2.96×10^{-7}	0.66	0.000
\sim cit. + bat sympatry	297.4	4	0.025	2.12×10^{-7}	0.64	0.000
\sim cit. + bat sympatry + IUCN	299.8	6	0.008	1.09×10^{-6}	0.66	0.000
\sim cit. + bat sympatry + PC2 _b	299.8	5	0.008	9.61×10^{-7}	0.64	0.000
\sim cit. + latitude + area	300.0	5	0.007	1.06×10^{-6}	0.64	0.000
\sim bat sympatry	301.7	3	0.003	8.55×10^{-7}	0.59	0.000
\sim cit. + PC1 _b	303.8	4	0.001	5.02×10^{-6}	0.58	0.188
\sim cit. + PC1 _b + migration	308.4	6	0.000	6.16×10^{-5}	0.58	0.178
\sim cit.	316.5	3	0.000	2.19×10^{-3}	0.36	0.254
\sim cit. + PC3 _b	318.7	4	0.000	8.87×10^{-3}	0.36	0.250
the null (intercept) model	323.7	2	0.000			0.295

Table S5. Loading values for principal components (PCs) summarizing life history traits of both rodents and bats.

	PC1	PC2	PC3	PC4
litter size	0.586	-0.235	0.413	0.657
litters per year	0.545	0.146	-0.822	0.083
maximum longevity	-0.598	-0.179	-0.358	0.694
body mass	0.052	-0.944	-0.162	-0.283
proportion of variance	0.511	0.267	0.137	0.085

Table S6. Generalized least squares rankings for rodents and bats together considering species traits, with response variable, number of zoonotic viruses identified in a species and λ showing the strength of the phylogenetic correction.

Model	AICc	npar	Weight	p value	R	λ
~order * taxon sympatry + cit. + torpor	643.2	8	0.366	8.88×10^{-16}	0.66	0.000
~order * taxon sympatry + cit. + torpor + latitude	643.8	9	0.269	1.55×10^{-15}	0.66	0.000
~order * taxon sympatry + cit. + PC3 _{rb} + torpor	645.2	9	0.132	3.11×10^{-15}	0.66	0.000
~order * taxon sympatry + order * cit. + torpor	645.4	9	0.120	3.33×10^{-15}	0.66	0.000
~cit. + order * taxon sympatry + order * torpor	646.7	10	0.062	7.66×10^{-15}	0.66	0.000
~order * taxon sympatry + cit. + PC3 _{rb}	649.6	7	0.014	1.34×10^{-14}	0.63	0.000
~order * taxon sympatry + cit.	649.9	6	0.012	9.77×10^{-15}	0.62	0.000
~order + cit. + taxon sympatry + torpor	650.3	7	0.010	1.80×10^{-14}	0.63	0.000
~order * taxon sympatry + cit. + area	651.8	7	0.005	3.74×10^{-14}	0.62	0.000
~order * torpor + cit. + taxon sympatry	651.9	9	0.005	7.09×10^{-14}	0.64	0.000
~order * taxon sympatry + cit. + latitude	652.1	7	0.004	4.43×10^{-14}	0.62	0.000
~order + cit. + taxon sympatry + PC3 _{rb}	658.2	6	0.000	5.34×10^{-13}	0.59	0.000
~order + cit. + taxon sympatry	659.3	5	0.000	5.30×10^{-13}	0.58	0.000
~order + cit. + taxon sympatry + PC4 _{rb}	661.1	6	0.000	2.17×10^{-12}	0.58	0.000
~order + cit. + taxon sympatry + PC1 _{rb}	661.4	6	0.000	2.58×10^{-12}	0.58	0.000
~order + cit. + latitude * torpor	662.6	9	0.000	1.02×10^{-11}	0.60	0.000
~order + cit. + taxon sympatry + IUCN	663.5	7	0.000	1.04×10^{-11}	0.58	0.000
~cit. + taxon sympatry	672.6	4	0.000	1.93×10^{-10}	0.52	0.001
~order + cit.	680.5	4	0.000	9.80×10^{-9}	0.47	0.000
~order + taxon sympatry	686.9	4	0.000	2.39×10^{-7}	0.44	0.000
the null (intercept) model	713.2	2	0.000			0.037

* indicates the two variables and their interaction, "cit." indicates logged citations

Table S7. Details of the best GLS model for bats and rodents combined (number of zoonotic viruses \sim order * taxon sympatry + citations + torpor).

	coefficients	std. error	p value
(Intercept)	-1.650	0.741	0.028
order Rodentia	-0.432	0.678	0.525
sympatry	0.014	0.003	<0.001
citations	0.867	0.133	<0.001
some torpor use	-1.080	0.528	0.043
true hibernation	-1.395	0.4751	0.002
Rodentia:sympatry	-0.010	0.003	0.003

Table S8. Generalized least squares model rankings for rodents considering species traits, with the total number of viruses identified in a species as the response variable.

Model	AICc	npar	Weight	p value	R
~cit. + rodent sympatry + torpor	429.3	6	0.237	9.22×10^{-10}	0.68
~cit. + area + latitude	429.9	5	0.178	8.64×10^{-10}	0.66
~cit. + rodent sympatry	430.1	4	0.159	5.51×10^{-10}	0.65
~cit. + rodent sympatry + PC3 _r	431.0	5	0.101	1.50×10^{-09}	0.66
~cit. + torpor	431.7	5	0.074	2.03×10^{-09}	0.65
~cit. + rodent sympatry + PC2 _r	432.1	5	0.059	2.55×10^{-09}	0.65
~cit. + rodent sympatry + latitude	432.4	5	0.052	2.89×10^{-09}	0.65
~cit. + rodent sympatry + IUCN	432.4	5	0.051	2.93×10^{-09}	0.65
~cit. + rodent sympatry + IUCN + PC3 _r	433.3	6	0.033	6.09×10^{-09}	0.66
~cit. + PC3 _r	434.2	4	0.021	4.18×10^{-09}	0.62
~cit.	434.6	3	0.017	2.03×10^{-09}	0.61
~cit. + IUCN + PC3 _r	435.9	5	0.009	1.64×10^{-08}	0.63
~cit. + IUCN	436.6	4	0.006	1.40×10^{-08}	0.61
~cit. + IUCN + PC1 _r	438.1	5	0.003	4.80×10^{-08}	0.62
~rodent sympatry	462.7	3	0.000	5.15×10^{-03}	0.31
~1	468.4	2	0.000		

* indicates the two variables and their interaction, cit. indicates logged citations

For all models, λ (strength of the phylogenetic correction) was estimated to be < 0.01

Table S9. Generalized least squares model rankings for bats considering species traits, with the total number of viruses identified in a species as the response variable.

Model	AICc	npar	Weight	p value	R	λ
~cit. + bat sympatry + PC1 _b	335.8	5	0.857	9.89×10^9	0.69	0.000
~cit. + bat sympatry + torpor	340.9	6	0.065	1.47×10^7	0.68	0.000
~cit. + PC1 _b	342.4	4	0.032	1.64×10^7	0.62	0.165
~cit. + bat sympatry	343.6	4	0.017	3.09×10^7	0.63	0.000
~cit. + bat sympatry + lat	344.7	5	0.010	7.71×10^7	0.64	0.000
~cit. + bat sympatry + PC3 _b	345.5	5	0.007	1.11×10^6	0.63	0.000
~cit. + bat sympatry + PC2 _b	346.0	5	0.005	1.39×10^6	0.63	0.000
~cit. + PC1 _b + migration	346.8	6	0.004	2.32×10^6	0.63	0.157
~cit. + lat + area	347.2	5	0.003	2.59×10^6	0.62	0.000
~bat sympatry	354.0	3	0.000	3.14×10^5	0.51	0.000
~cit.	355.6	3	0.000	7.20×10^5	0.45	0.211
~1	369.1	2	0.000			0.244

Table S10. Generalized least squares model rankings for both bats and rodents considering species traits, with the total number of viruses identified in a species as the response variable.

Model	AICc	npar	Weight	p value	R
~order * taxon sympatry + cit. + torpor	762.5	8	0.334	0.00	0.68
~order * taxon sympatry + cit. + PC3 _{rb} + torpor	763.7	9	0.180	1.11×10 ⁻¹⁶	0.68
~order + cit. + taxon sympatry + torpor	764.2	7	0.147	0.00	0.67
~order * taxon sympatry + cit. + torpor + latitude	764.6	9	0.121	1.11×10 ⁻¹⁶	0.68
~order * taxon sympatry + order * cit. + torpor	764.6	9	0.117	1.11×10 ⁻¹⁶	0.68
~cit. + order * taxon sympatry + order * torpor	766.7	10	0.041	3.33×10 ⁻¹⁶	0.68
~order * torpor + cit. + taxon sympatry	767.7	9	0.025	3.33×10 ⁻¹⁶	0.67
~order * taxon sympatry + cit. + PC3 _{rb}	769.2	7	0.012	3.33×10 ⁻¹⁶	0.65
~order * taxon sympatry + cit.	770.4	6	0.007	4.44×10 ⁻¹⁶	0.64
~order + cit. + taxon sympatry + PC3 _{rb}	770.8	6	0.005	4.44×10 ⁻¹⁶	0.64
~order * taxon sympatry + cit. + latitude	772.0	7	0.003	1.44×10 ⁻¹⁵	0.64
~order * taxon sympatry + cit. + area	772.1	7	0.003	1.55×10 ⁻¹⁵	0.64
~order + cit. + taxon sympatry	772.6	5	0.002	6.66×10 ⁻¹⁶	0.63
~order + cit. + latitude * torpor	773.5	9	0.001	5.88×10 ⁻¹⁵	0.65
~order + cit. + taxon sympatry + PC1 _{rb}	773.9	6	0.001	2.33×10 ⁻¹⁵	0.63
~order + cit. + taxon sympatry + PC4 _{rb}	774.5	6	0.001	3.00×10 ⁻¹⁵	0.63
~order + cit. + taxon sympatry + IUCN	776.5	7	0.000	1.31×10 ⁻¹⁴	0.63
~cit. + taxon sympatry	783.4	4	0.000	5.78×10 ⁻¹⁴	0.58
~order + cit.	789.7	4	0.000	1.37×10 ⁻¹²	0.56
~order + taxon sympatry	820.0	4	0.000	5.23×10 ⁻⁶	0.39
~1	840.1	2	0.000		

* indicates the two variables and their interaction, cit. indicates logged citations

For all models, λ (strength of the phylogenetic correction) was estimated to be < 0.01

Table S11. χ^2 tests comparing traits of zoonotic and non-zoonotic viruses.

	nucleic acid				num. segments				replication site			
	RNA	DNA	χ^2	p	single	mult.	χ^2	p	nucl.	cyto.	χ^2	p
Zoonotic	107	2	42.7	<0.001	69	40	12.3	<0.001	2	107	41.8	<0.001
Non-zoonotic	141	77			178	40			76	142		

Table S12. χ^2 tests comparing traits of viruses in rodents and bats.

	nucleic acid				num. segments				replication site			
	RNA	DNA	χ^2	p	single	mult.	χ^2	p	nucl.	cyto.	χ^2	p
Rodents	148	51	2.45	0.118	139	60	6.89	0.008	47	152	0.69	0.407
Bats	123	27			124	26			29	121		

Table S13. Estimates for λ , indicating the strength of the effect of phylogeny on the given variables, in the null (intercept) model. If λ is near one, this indicates that the relationship between species traits was proportional to their shared branch lengths. If $\lambda = 0$, then species traits were not related to their shared branch lengths.

Model	Rodents	Bats	Both
zoonotic viruses	0.017	0.295	0.037
citations	0.620	0.000	0.000
area	0.000	0.135	0.297
sympatry	0.313	0.434	0.487
latitude	0.780	0.265	0.000
torpor	1.000	0.607	0.670
PC1	0.970	0.137	0.550
PC2	0.712	0.078	0.172
PC3	0.687	0.000	0.088

See separate supplemental file for Table S14: species traits used in the analysis.

Supplemental Figures

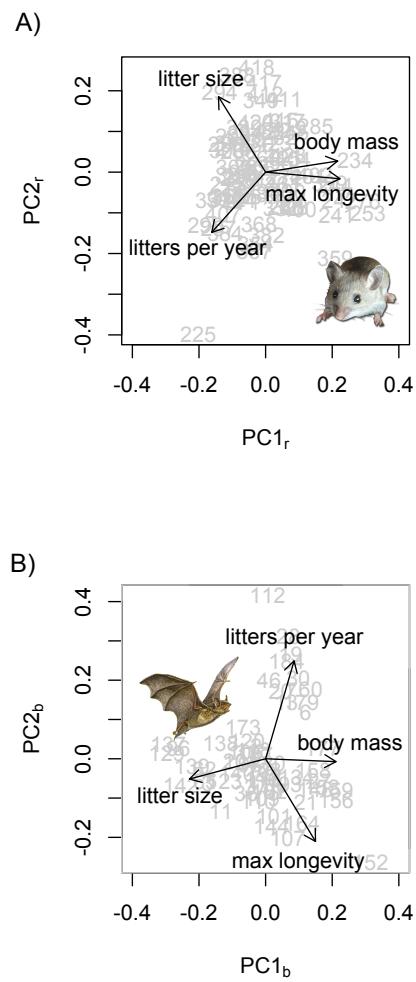


Fig. S1. Principal components analysis (PC) of (a) rodent (r) life history data showing $PC1_r$ and $PC2_r$ and (b) bat (b) life history data showing $PC1_b$ and $PC2_b$.

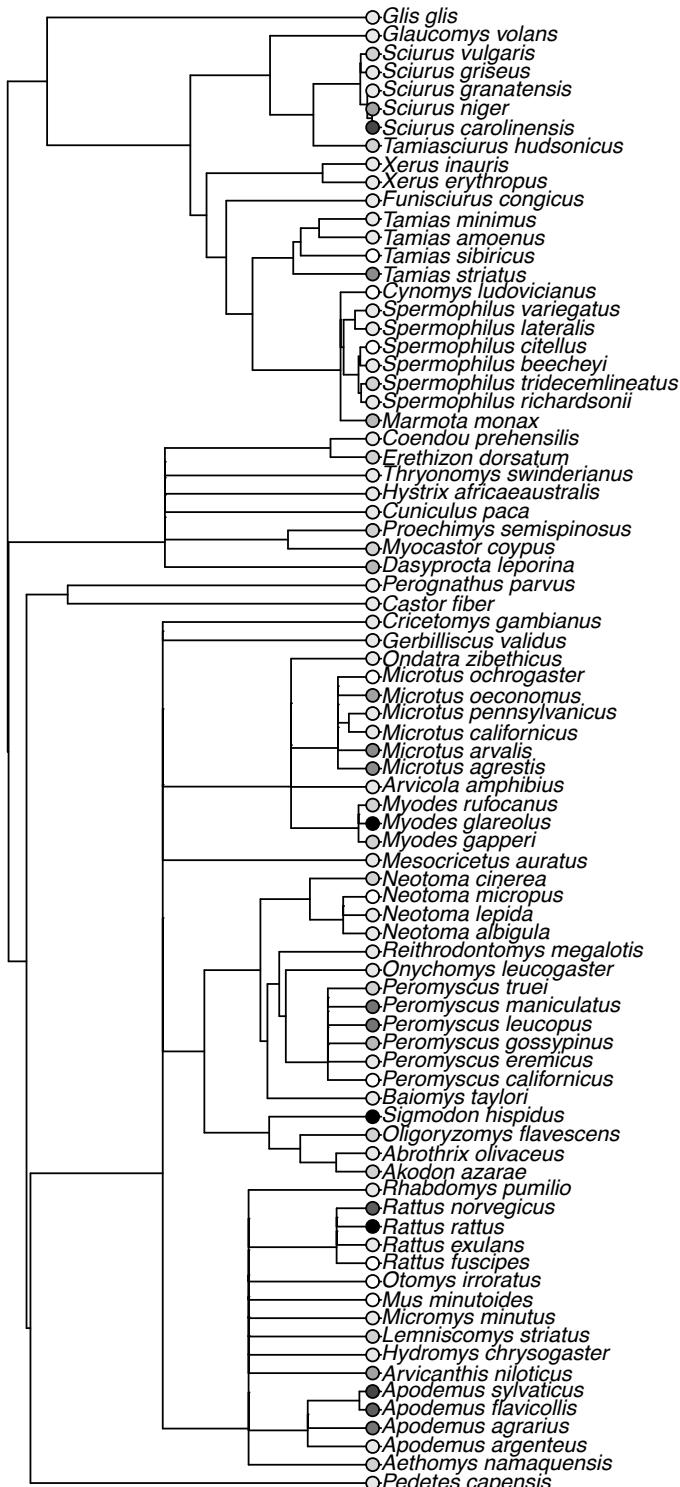


Fig. S2. The rodent species in our traits analysis in the mammalian supertree [2], with darker shades of gray indicating more zoonotic viruses.

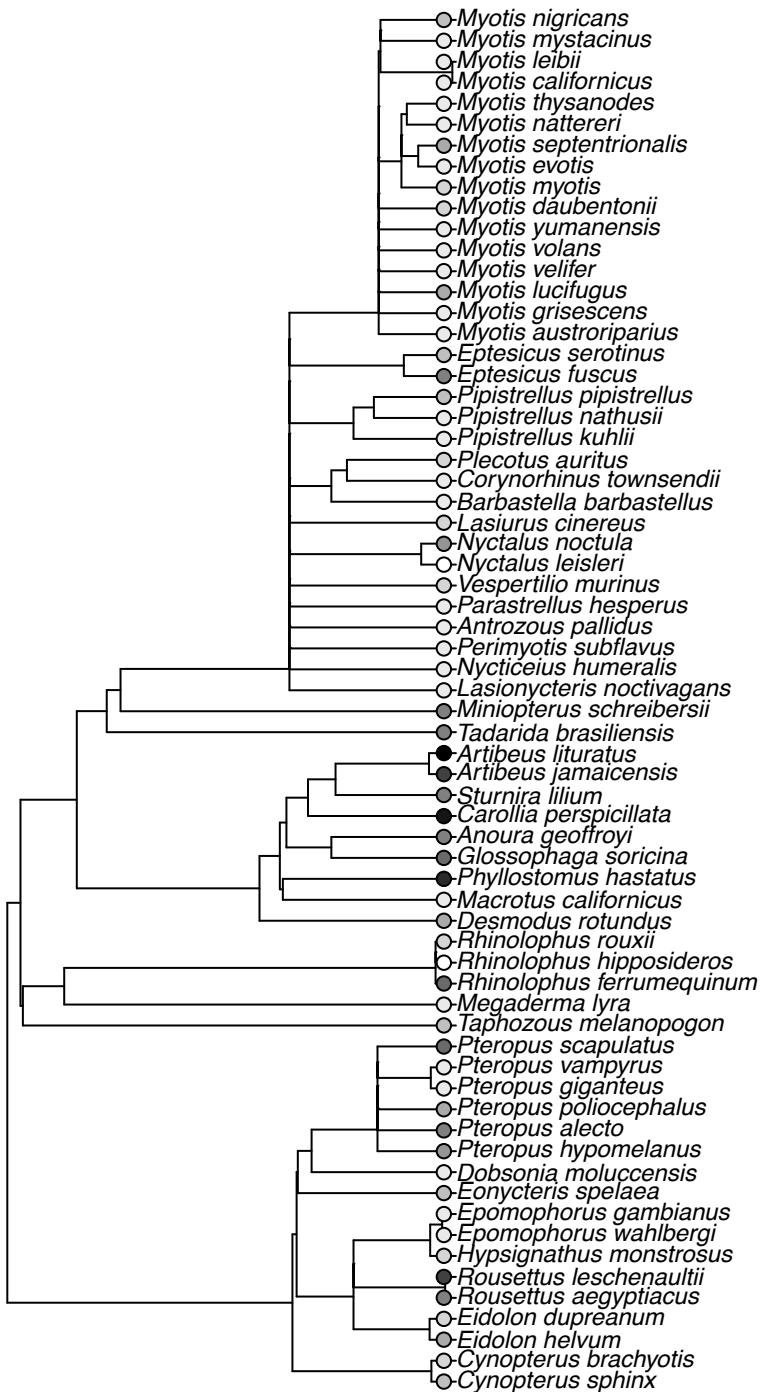


Fig. S3. The bat species in our traits analysis in the mammalian supertree [2], with darker shades of gray indicating more zoonotic viruses.

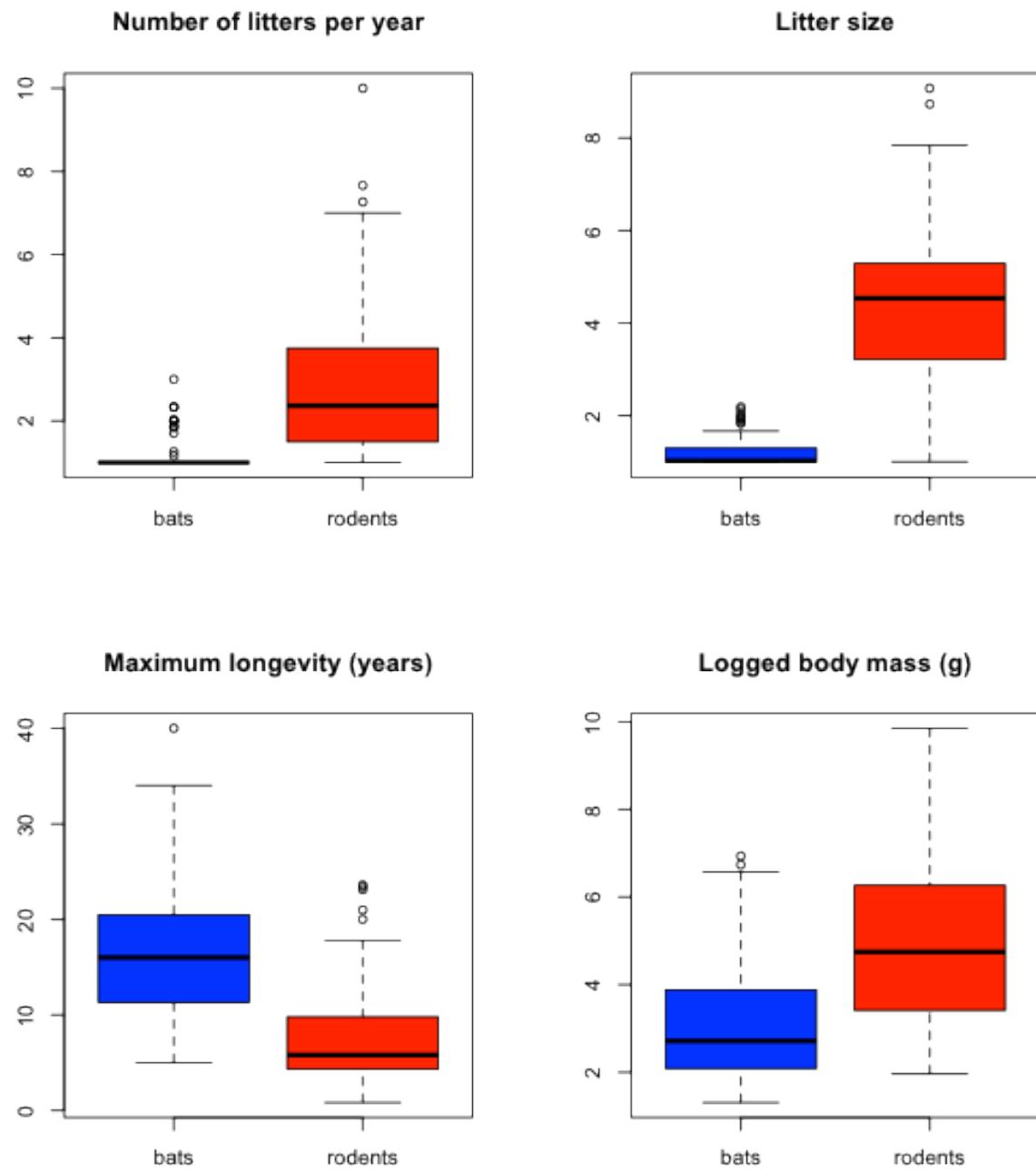
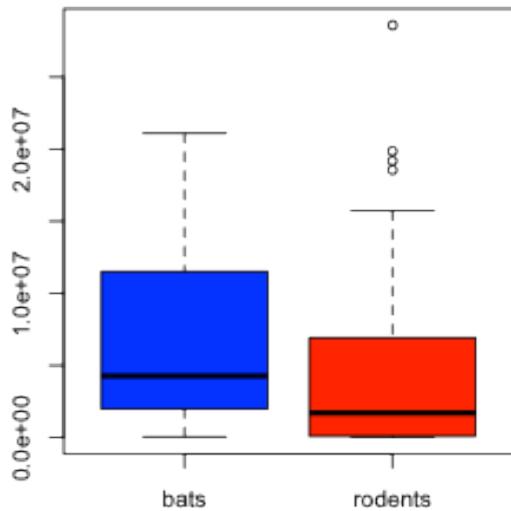
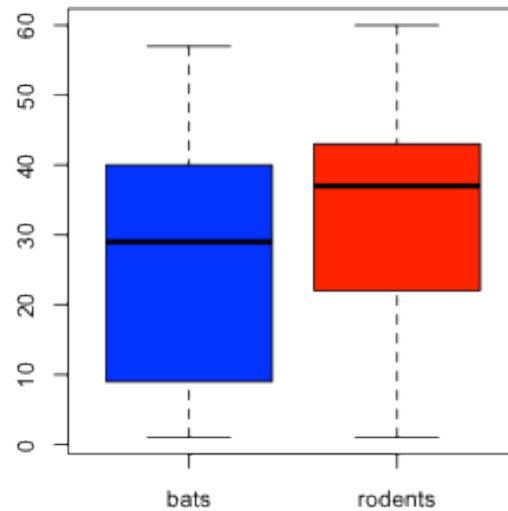


Fig. S4. Raw data for life history traits in rodents and bats.

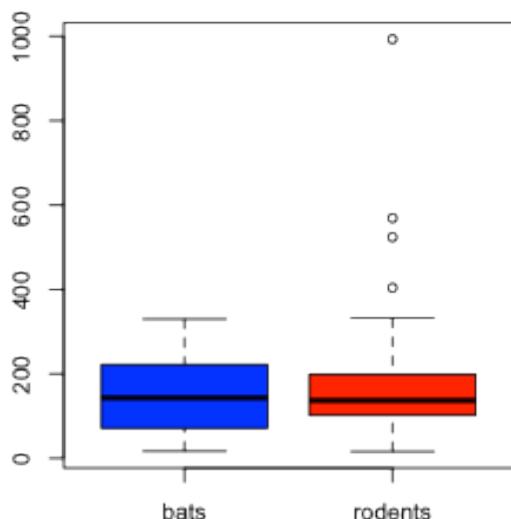
Species distribution area (km²)



Latitude



Num. sympatric species within order



Logged citations

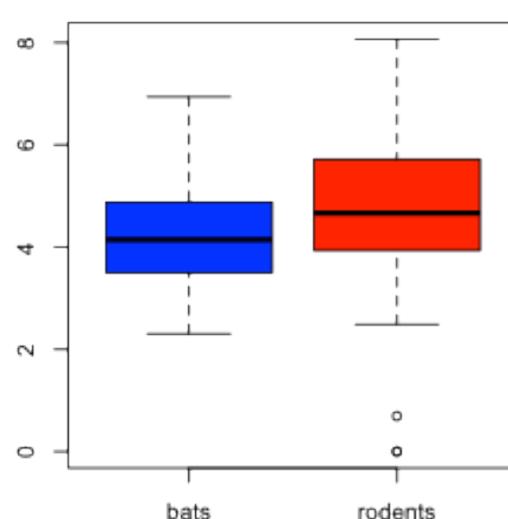


Fig. S5. Raw data for life history traits in rodents and bats (cont).

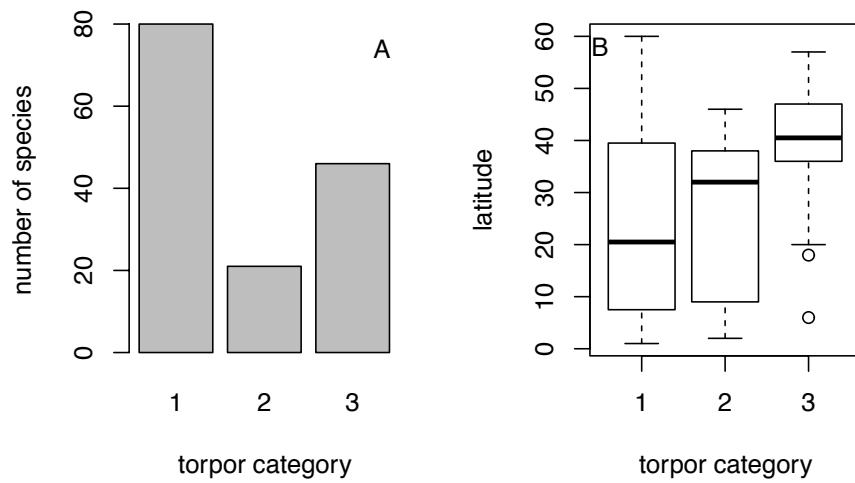


Fig. S6. a) Number of bat and rodent species using each of the 3 torpor categories, (1) no torpor use reported, (2) some torpor use but not true hibernation, and (3) hibernation. b) Latitude of midpoint of species distribution for the 3 torpor categories.

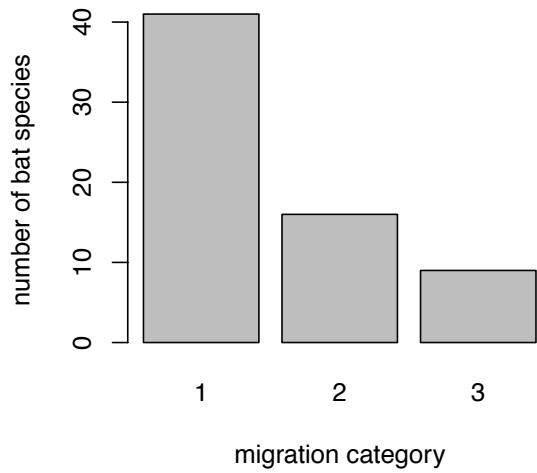


Fig. S7. Number of bats using each of the 3 migration categories, (1) sedentary or only local (< about 100km) migrations, (2) regional migrants (about 100-500 km), and (3) long-distance migrants (>500 km).

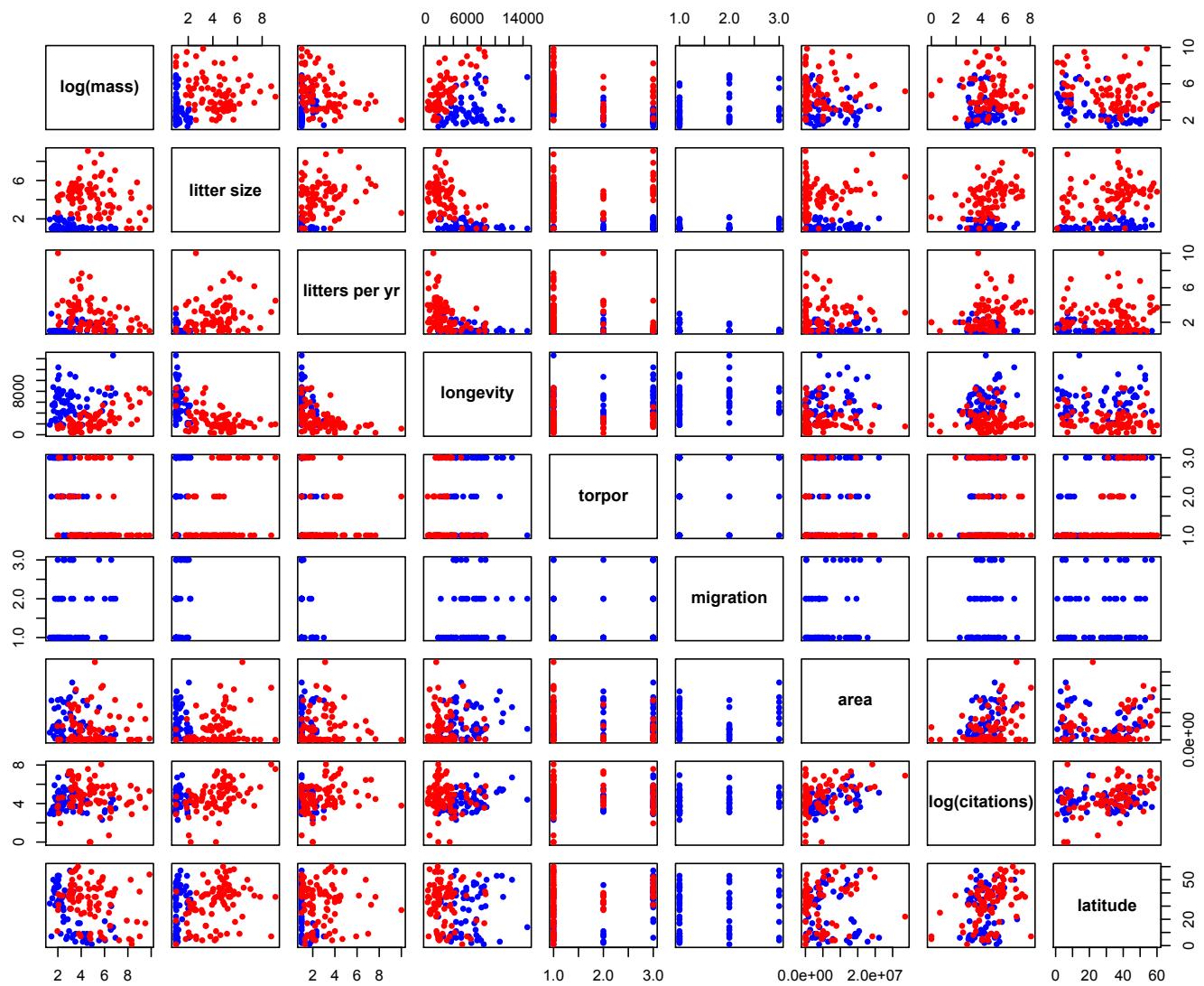


Fig. S8. Pairwise plots of all the variables examined. The bat data points are in blue, and the rodents in red.

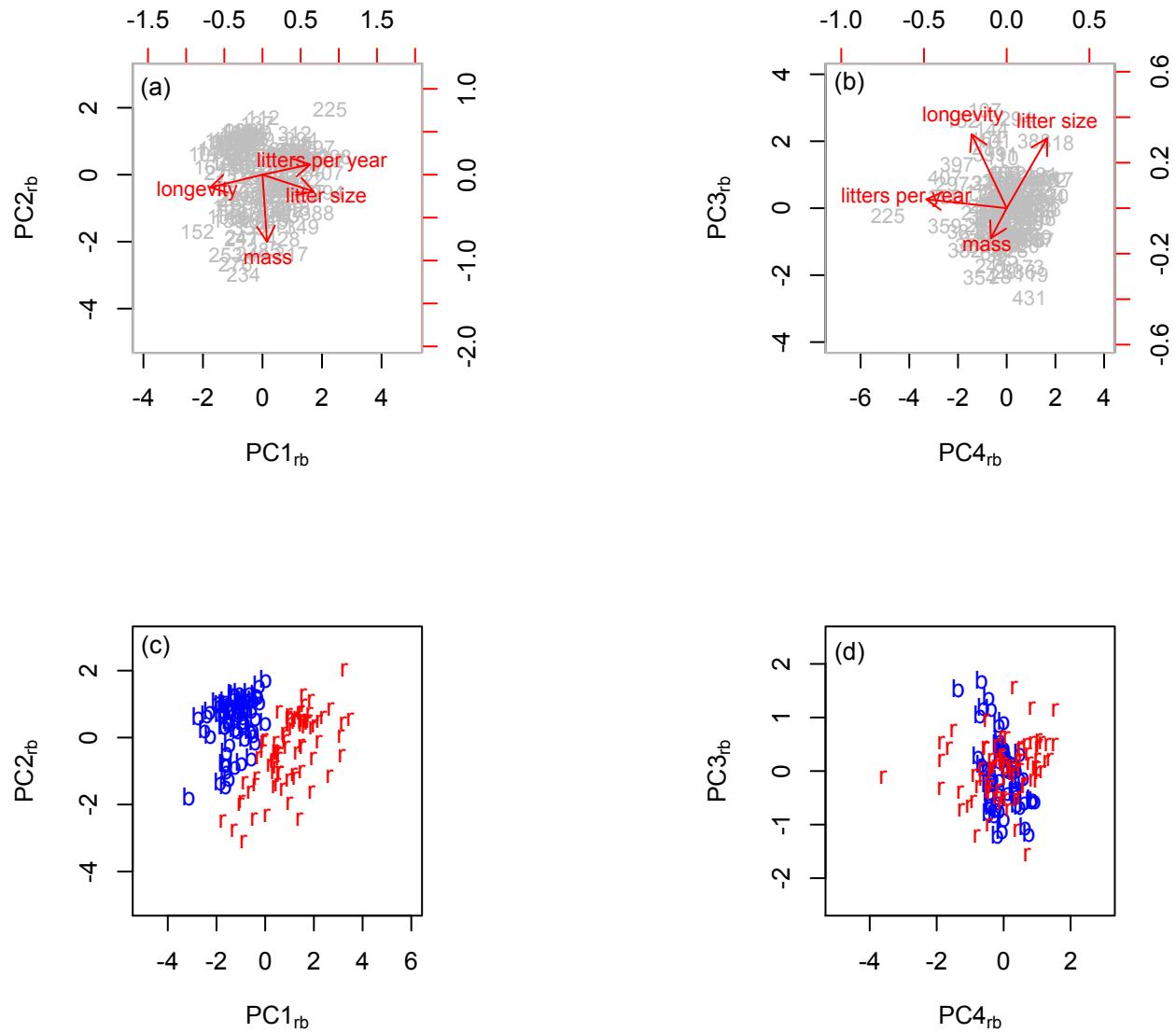


Fig. S9. Principal components analysis (PCA) for bats and rodents combined. Panel (a) shows PC1 and PC2, and panel (b) shows PC3 and 4. Panels (c) and (d) are the same principal components with bat data points as blue b's, and rodents as red r's.

References

- [1] Wright, E., Hayman, D., Vaughan, A., Temperton, N., Wood, J., Cunningham, A., Suu-Ire, R., Weiss, R. & Fooks, A., 2010 Virus neutralising activity of african fruit bat (*Eidolon helvum*) sera against emerging lyssaviruses. *Virology* **408**, 183–189.
- [2] Bininda-Emonds, O., Cardillo, M., Jones, K., MacPhee, R., Beck, R., Grenyer, R., Price, S., Vos, R., Gittleman, J. & Purvis, A., 2007 The delayed rise of present-day mammals. *Nature* **446**, 507.