

Supplementary Information

Morphofunctional segregation in molossid bat species (Chiroptera: Molossidae) from the South American Southern Cone

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Appendix S1. Additional molossid specimens from South America.

Cynomops abrasus (5). Brazil: Para State, Tapajos River, Igarape Brabo (AMNH 94624, ♀; AMNH 94626, ♀; AMNH 94628, ♀). Paraguay: Guaira State, Villarica (AMNH 239235, ♂); Sapucay (AMNH 23800, ♂).

Cynomops paranus (7). Brazil: Para State, Faro, Amazon River, north bank, Piratucu River mouth (AMNH 93881, ♀); Para State, Aveiro, Caxiricatuba, Tapajos River (AMNH 94644, ♀); Para State, Tapajos River, Igarape Brabo (AMNH 94649, ♀; AMNH 94650, ♀; AMNH 94652, ♂). Bolivia, Santa Cruz State, Robore (AMNH 260261, ♂). French Guiana: Cayenne State, Sinnamary, Paracou (AMNH 267535, ♂).

Cynomops planirostris (6). Brazil: Sao Paulo State, Urupes (AMNH 236221, ♂). Paraguay: Alto Paraguay State, Fuerte Olimpo (AMNH 234455, ♀; AMNH 234456, ♂; AMNH 234457, ♂; AMNH 234458, ♀). Venezuela: Bolivar State, Sucre, Maripa (AMNH 17096, ♀).

Eumops auripendulus (6). Bolivia: State Santa Cruz, Ichillo, 4.5 km of Buen Retiro 300 m (AMNH 261849, ♂; AMNH 260305, ♀). Brazil: Para State, Tapajos River, Limoal (AMNH 95476, ♂); Para State, Faro, Amazon River north bank (AMNH 93856 ♀). Peru: Amazonas State, Santa Rosa de Huayabamba (AMNH 10125, ♀; AMNH 10126, ♀).

Eumops bonariensis (5). Brazil: Rio Grande do Sul State, Rio Grande, Quinta (AMNH 235418, ♀); Rio Grande do Sul State, Uruguiana, 135 km NE of Bella Union (AMNH 235959, ♂). Uruguay: Rio Negro State, 15 km S of Paysandu, Arroyo Negro (AMNH 205660, ♂; AMNH 205661, ♀); Artigas State, Cuareim River, Paso Ramos (AMNH 235964, ♀).

Eumops glaucinus (6). Brazil: Para State, Faro, Amazon River, north bank (AMNH 93857, ♂). Venezuela: Falcon State, Bolivar, Tocuyo River (AMNH 130700, ♀; AMNH 130700, ♂; AMNH 130703, ♀). Colombia: Tolima State, Honda (AMNH 69185, ♀); La Guajira State, Riohacha, Bahia Honda (AMNH 70540).

Eumops patagonicus (4). Paraguay: Central State, Auncion (AMNH 148668, ♀); Alto Paraguay State, Pablo Lagerenza, 65 km N of Fortin Madrejon (AMNH 248384, ♂). Bolivia: Beni State, Moxos, Tijamuchi River (AMNH 261850, ♂); Santa Cruz State, Sara, 7 km N of Santa Rosa del Sara (AMNH 246420 ♀).

Eumops perotis (3). Argentina: Jujuy Province, Ledesma, Yuto, San Francisco (AMNH 185208, ♂). Paraguay: Alto Paraguay State, Pablo Lagerenza, 170 km by road of Bahia Negra, Agua Dulce (AMNH 248390, ♂; AMNH 248391, ♀).

Nyctinomops laticaudatus (14). Brazil: Santa Catarina, Joinville, Empresul (AMNH 75892; AMNH 75893); Amazonas State, Ihla Grande, Iaunari, Negro River (AMNH 79497, ♂); Rondonia State, Alta Floresta, Pedras Negras (AMNH 209881, ♀). Bolivia: Tarija State, Gran Chaco, 8 km S and 10 km E of Villamontes (AMNH 246653, ♂); Santa Cruz State, Chiquitos, Robore (AMNH 260270, ♂; AMNH 260271, ♂; AMNH 260272, ♂). Paraguay: (AMNH 23793, ♂); Central State, Asunción (AMNH 234468, ♀); Alto Paraguay State, Fuerte Olimpo (AMNH 234695). Venezuela:

Bolivar State, Sucre, Maripa (AMNH 17012, ♂); Amazonas State, Casiquiare, Casiquiare River, Quemapure (AMNH 77481, ♂); Amazonas State, Atabapo, Orinoco River, Cano Paripari (AMNH 78201, ♀).

Nyctinomops macrotis (4). Bolivia: Chuquisaca State, Luis Calvo, 1 km S of Camatindi (AMNH 264088, ♂). Dominican Republic, Distrito Nacional, Santo Domingo (AMNH 244933, ♀; AMNH 242934, ♀; AMNH 244936, ♂).

Molossops temminckii (4). Brazil: Mato Grosso do Sul State, Maracaju (AMNH 134918, ♂). Bolivia: Beni State, Mamore, ca. 20 km SW of San Joaquin, Estancia Yotiole (AMNH 211255, ♀); Tarija State, Gran Chaco, Estancia Bolivar (AMNH 264112, ♂). Uruguay: Rio Negro State, 15 km S of Paysandu, Arroyo Negro (AMNH 205651, ♀).

Promops nasutus (5). Argentina: Jujuy Province, Ledesma, Yuto (AMNH 184647, ♀; AMNH 184648, ♀; AMNH 184649, ♀). Bolivia: Santa Cruz State, Caballero, 3 km by road SE of Comarapa (AMNH 260306, ♀); Santa Cruz State, Ichilo, 4.5 km N and 1.5 km E of Cerro Amboro, Pitasama River (AMNH 261851, ♀).

Promops centralis (6). Bolivia: Santa Cruz State, Chiquitos, Robore (AMNH 260273, ♂; AMNH 260274, ♂). Honduras: La Paz State, Santa Elena, El Pedrero (AMNH 126855, ♀). Panama: Panama State, Arraijan, Fort Clayton (AMNH 183866, ♀). Trinidad and Tobago: Trinidad State, Victoria County, George Village (AMNH 175652, ♀); Trinidad State, Saint George County, Port of Spain (AMNH 178692, ♂).

Table S2. Results of Redundancy Analysis for molossid bats from Argentina. Values significant at the $P = 0.01$.

Analysis	Variables	Variance	<i>F</i> value	<i>P</i> value
Individual	Southern Andean Yungas	0.057	22.533	0.0002
	Low Monte	0.030	11.712	0.0018
	Humid Pampa	0.015	5.895	0.0138
Forward stepwise selection	Southern Andean Yungas	0.057	22.533	0.0002
	Low Monte	0.021	8.410	0.0040
	Humid Pampas	0.012	4.804	0.0252

Table S3. Results of Redundancy Analysis for molossid bats from Argentina, dataset corrected size. Values significant at the $P = 0.01$.

Analysis	Variables	Variance	<i>F</i> value	<i>P</i> value
Individual	Southern Andean Yungas	0.056	22.301	0.0002
	Humid Pampa	0.013	5.071	0.0172
Forward stepwise selection	Southern Andean Yungas	0.056	22.301	0.0002
	Dry Chaco	0.012	4.997	0.0144

Table S4. Results of Canonical Phylogenetic Ordination (CPO) for molossid bats from Argentina (dataset corrected and not corrected size), total variation explained by the final model.

Dataset not corrected size					
Axes	1	2	3	4	Total Variance
Eigenvalues	0.880	0.019	0.004	0.001	1.000
Species-phylogenetic variables correlations	0.959	0.934	0.867	0.611	
Cumulative percentage variance					
Of species data	88.0	89.9	90.3	90.4	
Of species-phylogenetic variables relation	97.2	99.3	99.7	99.8	
Sum of all eigenvalues					1.000
Sum of all canonical eigenvalues					0.906
Dataset corrected size					
Axes	1	2	3	4	Total Variance
Eigenvalues	0.832	0.038	0.007	0.000	1.000
Species-phylogenetic variables correlations	0.992	0.749	0.707	0.192	
Cumulative percentage variance					
Of species data	83.2	87.0	87.7	87.7	
Of species-phylogenetic variables relation	94.8	99.1	99.9	100.0	
Sum of all eigenvalues					1.000
Sum of all canonical eigenvalues					0.877

Figure S5. Ordination diagram of the Principal Component Analysis (PCA). A) segregation of the specimens of molossid species from South America (including additional specimens outside the study area); polygons include specimens from each species. *C. abrasus* (▼), *C. paranus* (●), *C. planirostris* (▲), *E. auripendulus* (▲), *E. bonariensis* (▼), *E. dabbeni* (■), *E. glaucinus* (◇), *E. patagonicus* (○), *E. perotis* (◆), *M. neglectus* (△ black), *M. temminckii* (△ gray), *M. molossus* (●), *M. rufus* (+), *N. laticaudatus* (■), *N. macrotis* (◆), *P. centralis* (△), *P. nasutus* (□), *T. brasiliensis* (⊗). B) Vectors shown the strength of correlation of each variable to the plane of PC1 and PC2. See text for abbreviations.

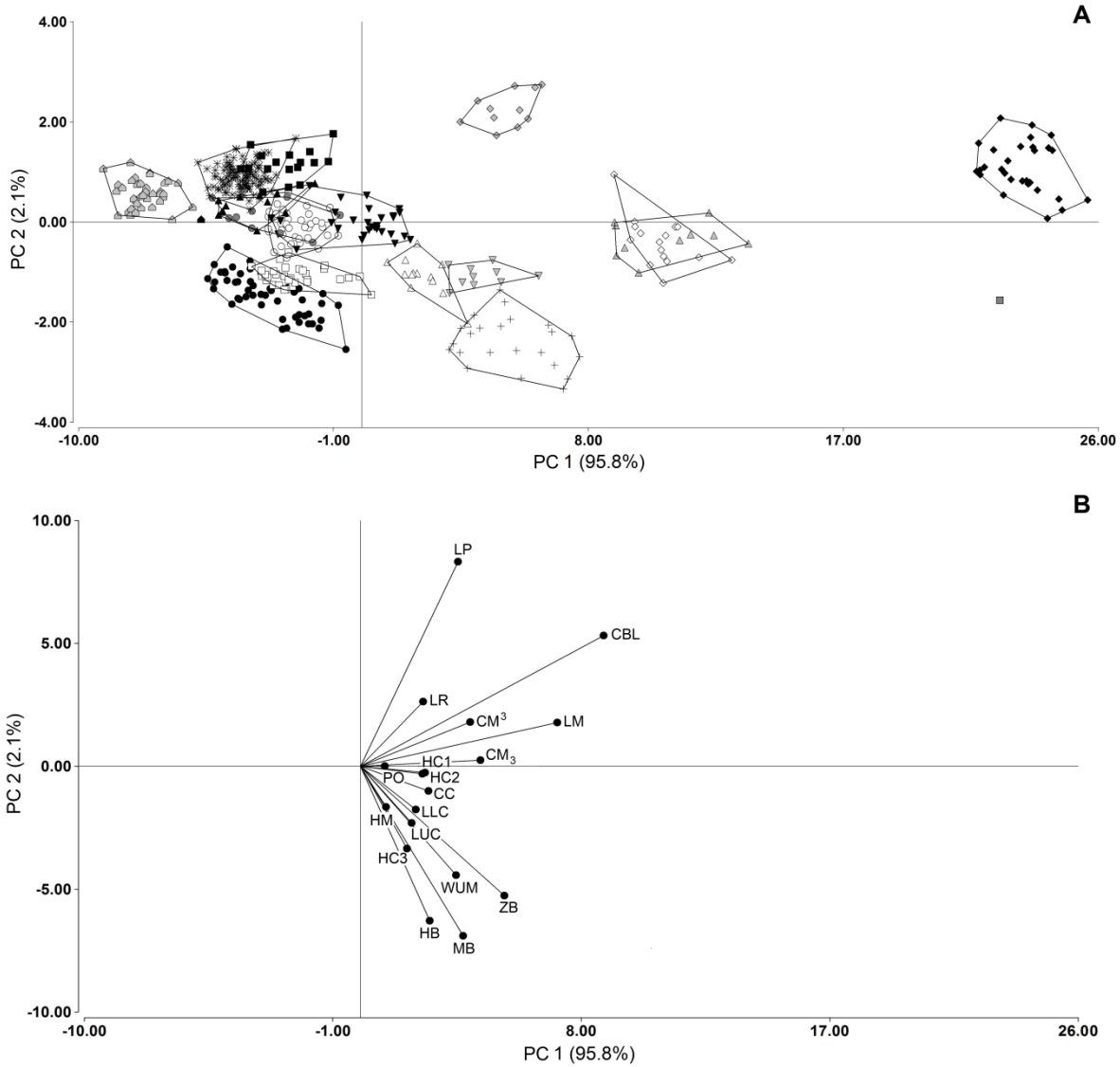


Table S6. Results of Redundancy Analysis for molossid bats including additional specimens from South America. Values significant at the $P = 0.01$.

Analysis	Variables	Variance	<i>F</i> value	<i>P</i> value
Individual	Southern Andean Yungas	0.041	18.939	0.0002
	Low Monte	0.029	13.337	0.0004
	Humid Pampa	0.016	7.359	0.005
	Lara-Falcon Dry Forest	0.011	5.184	0.0254
Forward stepwise selection	Southern Andean Yungas	0.041	18.939	0.0002
	Low Monte	0.022	10.578	0.0022
	Humid Pampas	0.014	6.846	0.0064
	Lara-Falcón Dry Forest	0.011	5.372	0.0274

Table S7. Results of Canonical Phylogenetic Ordination (CPO) for molossid bats including additional specimens from South America. Clades are numbered as in *Fig. 3*. All values significant at the $p = 0.01$

Analysis	Variables	Variance	F- value	p value
Individual	5	0.685	978.191	0.0002
	6	0.645	814.501	0.0002
	7	0.618	726.238	0.0002
	4	0.301	193.193	0.0002
	3	0.102	51.130	0.0002
	2	0.101	50.409	0.0002
	13	0.090	44.205	0.0002
	10	0.068	32.621	0.0002
	9	0.049	23.246	0.0002
	15	0.016	7.358	0.0076
	12	0.011	4.989	0.0208
	Forward stepwise selection	5	0.685	978.191
7		0.081	154.647	0.0002
13		0.043	102.051	0.0002
2		0.039	116.592	0.0002
12		0.008	24.229	0.0002
9		0.010	34.698	0.0002
10		0.008	27.443	0.0094
3		0.004	15.093	0.0058
16		0.002	6.416	0.0038

Figure S8. Ordination diagram of the Principal Component Analysis (PCA). A) segregation of the specimens of molossid species from South America (including additional specimens outside the study area) excluding species with only one specimens (*E. dabbeni* and *M. neglectus*); polygons include specimens from each species. *C. abrasus* (▼), *C. paranus* (●), *C. planirostris* (▲), *E. auripendulus* (▲), *E. bonariensis* (▼), *E. glaucinus* (◇), *E. patagonicus* (○), *E. perotis* (◆), *M. temminckii* (△ gray), *M. molossus* (●), *M. rufus* (+), *N. laticaudatus* (■), *N. macrotis* (◆), *P. centralis* (△), *P. nasutus* (□), *T. brasiliensis* (⊗). B) Vectors shown the strength of correlation of each variable to the plane of PC1 and PC2. See text for abbreviations.

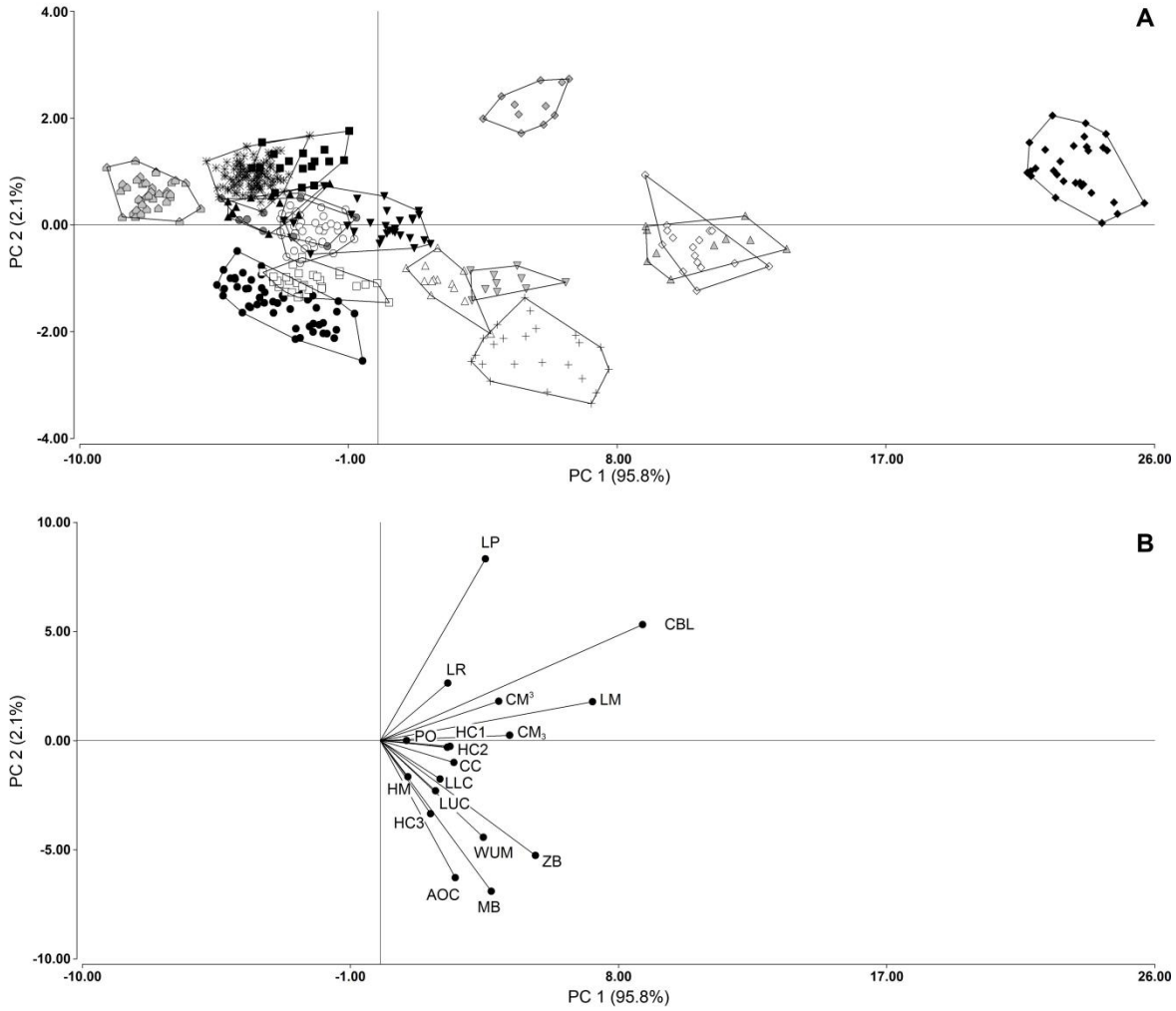


Table S9. Results of Redundancy Analysis for molossid bats including additional specimens from South America, and excluding species with only one specimen (*E. dabbenei* and *M. neglectus*). Values significant at the $P = 0.01$.

Analysis	Variables	Variance	<i>F</i> value	<i>P</i> value
Individual	Southern Andean Yungas	0.042	19.619	0.0002
	Low Monte	0.029	13.322	0.0004
	Humid Pampa	0.016	7.280	0.0076
	Lara-Falcon Dry Forest	0.012	5.303	0.0240
Forward stepwise selection	Southern Andean Yungas	0.042	19.619	0.0002
	Low Monte	0.022	10.511	0.001
	Humid Pampas	0.014	6.707	0.0076
	Lara-Falcón Dry Forest	0.011	5.523	0.210

Table S10. Results of Canonical Phylogenetic Ordination (CPO) for molossid bats including additional specimens from South America, and excluding species with only one specimen (*E. dabbenei* and *M. neglectus*). All values significant at the $p = 0.01$

Analysis	Variables	Variance	F- value	p value	
Individual	5	0.681	953.986	0.0002	
	6	0.639	791.316	0.0002	
	4	0.296	188.370	0.0002	
	3	0.102	50.599	0.0002	
	2	0.101	50.410	0.0002	
	9	0.067	31.884	0.0002	
	8	0.048	22.463	0.0002	
	13	0.016	7.365	0.0042	
	11	0.011	4.971	0.0272	
	Forward stepwise selection	5	0.681	953.986	0.0002
		13	0.030	47.133	0.0002
6		0.020	32.947	0.0002	
12		0.017	29.152	0.0002	
4		0.020	37.431	0.0002	
10		0.018	37.201	0.0002	
11		0.016	35.660	0.0002	
2		0.014	33.941	0.0002	
14		0.002	4.221	0.0282	

Figure S11. Ordination diagram of the Principal Component Analysis (PCA). A) segregation of the specimens of molossid species from South America (including additional specimens outside the study area), dataset corrected size; polygons include specimens from each species. *C. abrasus* (▼), *C. paranus* (●), *C. planirostris* (▲), *E. auripendulus* (▲), *E. bonariensis* (▼), *E. dabbeni* (■), *E. glaucinus* (◇), *E. 484 patagonicus* (○), *E. perotis* (◆), *M. neglectus* (△ black), *M. temminckii* (△ gray), *M. molossus* (●), *M. rufus* (+), 485 *N. laticaudatus* (■), *N. macrotis* (◆), *P. centralis* (△), *P. nasutus* (□), *T. brasiliensis* (⊗). B) Vectors shown the strength of correlation of each variable to the plane of PC1 and PC2. See text for abbreviations.

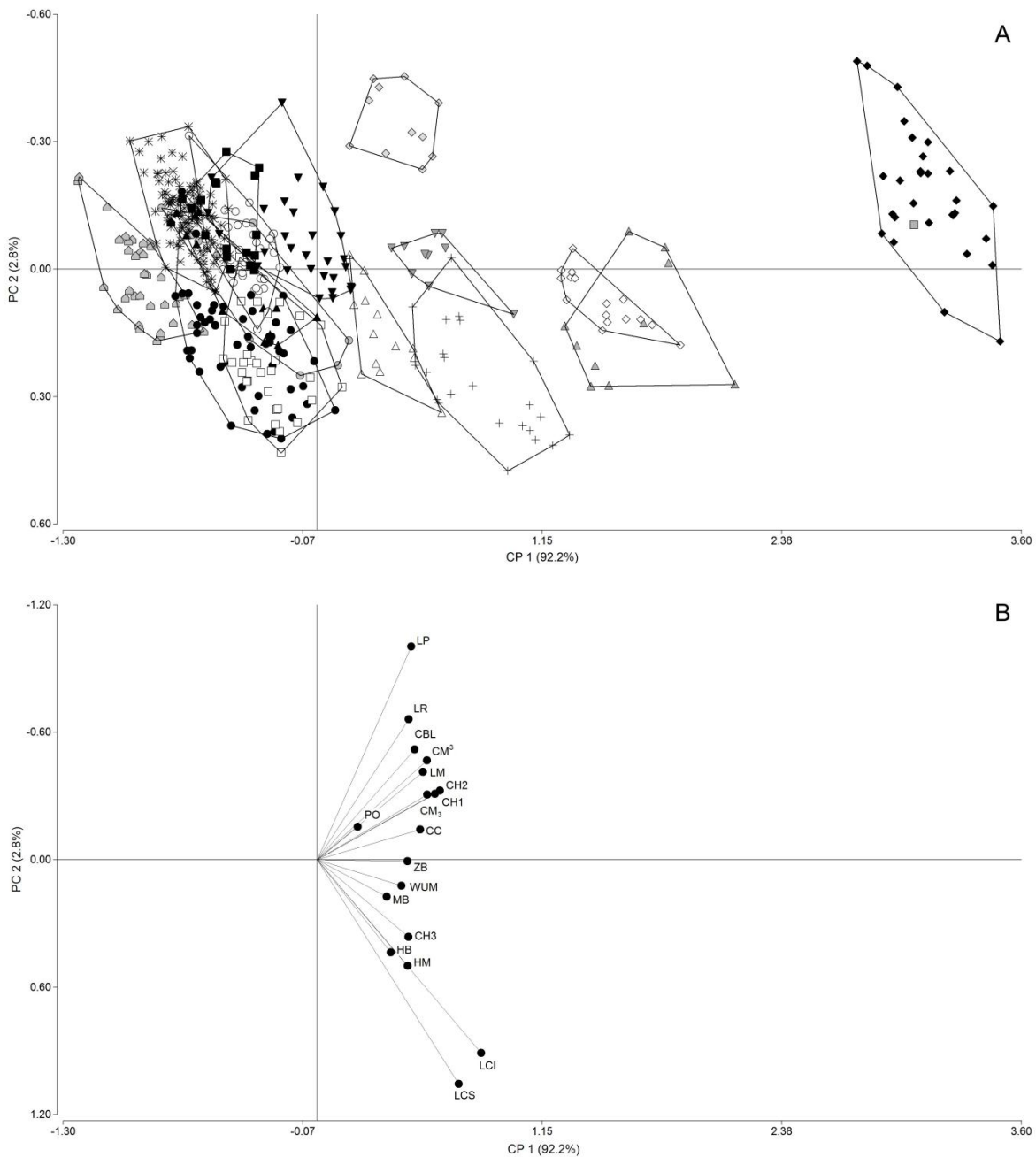


Figure S12. Ordination diagram of the Principal Component Analysis (PCA). A) segregation of the specimens of molossid species from South America (including additional specimens outside the study area) excluding species with only one specimens (*E. dabbeni* and *M. neglectus*), dataset corrected size; polygons include specimens from each species. *C. abrasus* (▼), *C. paranus* (●), *C. planirostris* (▲), *E. auri pendulus* (▲), *E. bonariensis* (▼), *E. glaucinus* (◇), *E. patagonicus* (○), *E. perotis* (◆), *M. temminckii* (△ gray), *M. molossus* (●), *M. rufus* (+), *N. laticaudatus* (■), *N. macrotis* (◆), *P. centralis* (△), *P. nasutus* (□), *T. brasiliensis* (⊗). B) Vectors shown the strength of correlation of each variable to the plane of PC1 and PC2. See text for abbreviations.

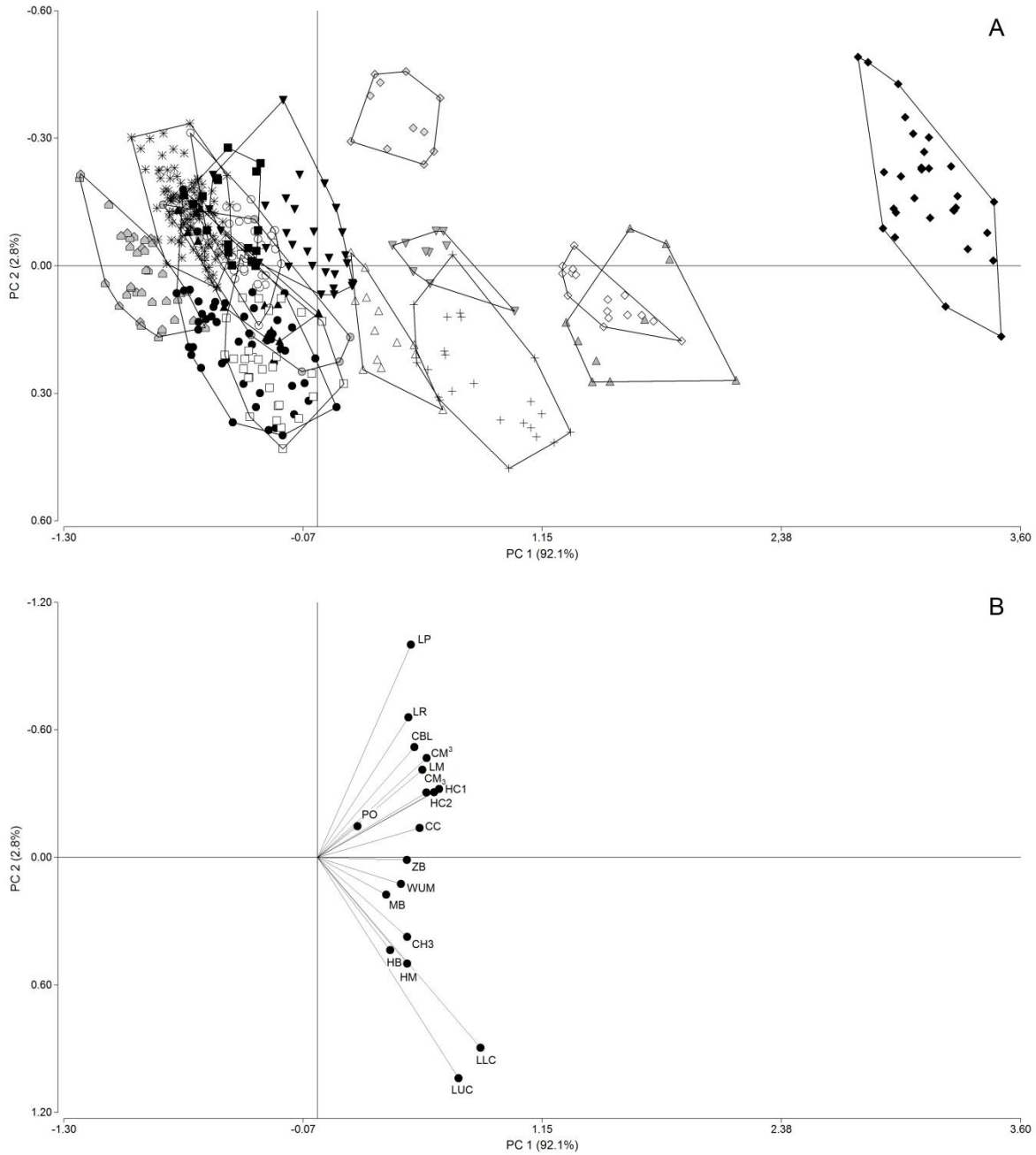


Table S13. Results of Redundancy Analysis for molossid bats including additional specimens from South America, dataset corrected size. Values significant at the $P = 0.01$.

Analysis	Variables	Variance	<i>F</i> value	<i>P</i> value
Individual	Southern Andean Yungas	0.050	23.672	0.0002
	Humid Pampa	0.010	4.673	0.0190
Forward stepwise selection	Southern Andean Yungas	0.050	23.672	0.0002
	Dry Chaco	0.020	9.526	0.0012
	Madeira-Tapajos Moist Forest	0.008	3.849	0.0326

Table S14. Results of Redundancy Analysis for molossid bats including additional specimens from South America, and excluding species with only one specimen (*E. dabbenei* and *M. neglectus*), dataset corrected size. Values significant at the $P = 0.01$.

Analysis	Variables	Variance	<i>F</i> value	<i>P</i> value
Individual	Southern Andean Yungas	0.053	24.810	0.0002
	Humid Pampa	0.016	4.581	0.0184
Forward stepwise selection	Southern Andean Yungas	0.053	24.810	0.0002
	Dry Chaco	0.022	10.547	0.0004
	Madeira-Tapajos Moist Forest	0.008	3.966	0.332

Table S15. Results of Canonical Phylogenetic Ordination (CPO) for molossid bats including additional specimens from South America, dataset corrected size. Clades are numbered as in *Fig. 3*. All values significant at the $p = 0.01$.

Analysis	Variables	Variance	<i>F</i> - value	<i>p</i> value	
Individual	7	0.802	1818.823	0.0002	
	6	0.588	639.730	0.0002	
	5	0.558	566.202	0.0002	
	4	0.201	113.178	0.0002	
	3	0.076	36.849	0.0002	
	2	0.028	12.750	0.0002	
	9	0.024	11.171	0.0008	
	15	0.023	10.736	0.0008	
	10	0.017	7.572	0.003	
	8	0.016	7.097	0.0046	
	17	0.012	5.401	0.0118	
	Forward stepwise selection	7	0.802	1818.823	0.0002
		5	0.075	275.084	0.0002
6		0.003	9.909	0.0002	
17		0.002	6.099	0.0002	

Table S16. Results of Canonical Phylogenetic Ordination (CPO) for molossid bats including additional specimens from South America, and excluding species with only one specimen (*E. dabbenei* and *M. neglectus*), dataset corrected size. All values significant at the $p = 0.01$

Analysis	Variables	Variance	F- value	p value
Individual	6	0.580	618.174	0.0002
	5	0.554	555.796	0.0002
	4	0.198	110.272	0.0002
	3	0.075	36.115	0.0002
	2	0.027	12.519	0.0002
	8	0.024	10.841	0.0018
	13	0.023	10.464	0.0008
	9	0.016	7.331	0.0062
	7	0.015	6.963	0.0046
	15	0.012	5.255	0.0148
	14	0.009	3.902	0.0290
	10	0.006	2.656	0.0664
	12	0.005	2.381	0.0814
11	0.004	1.754	0.1472	
Forward stepwise selection	6	0.580	618.174	0.0002
	5	0.043	50.607	0.0002