Ecological Modelling

SUPPLEMENTARY MATERIAL

A high-resolution model of bat diversity and endemism for continental Africa

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Appendix A   Accessed natural history collections

A total of 54 public natural history collections were accessed directly for this study. Listed acronyms are not necessarily official and have in some cases been modified or created by us to avoid ambiguity. Previous names of institutions / collections and alternative acronyms are not shown. Data access through: 1 = GBIF, 2 = MaNIS, 3 = ARCTOS, 4 = website of institution, 5 = direct communication with curator.

Table A.1.   List of natural history collections accessed for this study

Acronym	Institution / Collection	Place	Country				
AMNH	American Museum of Natural History	New York	U.S.A.			4	5
BPBM	Bernice P. Bishop Museum	Honolulu	U.S.A.		2		
CAS	California Academy of Sciences	San Francisco	U.S.A.		2	4	
CM	Carnegie Museum of Natural History	Pittsburgh	U.S.A.			4	
CUMV	Cornell University Museum of Vertebrates	Ithaca	U.S.A.		2		
EBD	Estacion Biologica de Doñana	Sevilla	Spain	1			5
FLMNH	Florida Museum of Natural History	Gainesville	U.S.A.		2		
FMNH	Field Museum of Natural History	Chicago	U.S.A.		2		5
HZM	Harrison Zoological Museum	Sevenoaks	U.K.				5
IRSNB	Institut Royal des Sciences Naturelles de Belgique	Brussels	Belgium			4	5
ISEZ	Institute of Systematics and Evolution of Animals	Cracow	Poland	1			
KU	University of Kansas, Museum of Natural History	Lawrence	U.S.A.		2	4	
LACM	Los Angeles County Museum of Natural History	Los Angeles	U.S.A.		2	4	5
LSUMZ	Louisiana State University, Museum of Natural Science	Baton Rouge	U.S.A.		2		
MCZ	Museum of Comparative Zoology at Harvard University	Cambridge	U.S.A.		2		5
MHP	Sternberg Museum of Natural History at Fort Hays State University	Hays	U.S.A.		2		
MMNH	University of Minnesota, J.F. Bell Museum of Natural History	Minneapolis	U.S.A.		2		
MNHN	Muséum National d'Histoire Naturelle	Paris	France				5
MRAC	Musée Royal de l'Afrique Centrale	Tervuren	Belgium				5

Code	Name	City	Country	1	2	3	4	5
MRIPAS	Mammal Research Institute at the Polish Academy of Sciences	Bialowieza	Poland	1				
MSB	University of New Mexico, Museum of Southwestern Biology	Albuquerque	U.S.A.	1	2	3		
MSUM	Michigan State University Museum	East Lansing	U.S.A.	1	2			
MVZ	Museum of Vertebrate Zoology	Berkeley	U.S.A.	1	2			
MZLU	Lund Museum of Zoology	Lund	Sweden	1				
NHMB	Naturhistorisches Museum Basel	Basel	Switzerland				4	
NMMNH	New Mexico Museum of Natural History and Science	Albuquerque	U.S.A.		2			
NMR	Natural History Museum Rotterdam	Rotterdam	Netherlands	1				
NRM	Naturhistoriska Riksmuseet	Stockholm	Sweden	1				
OMNH	Sam Noble Oklahoma Museum of Natural History	Norman	U.S.A.		2			
PSM	James R. Slater Museum of Natural History	Tacoma	U.S.A.	1	2			
RMMU	Redpath Museum at McGill University	Montreal	Canada				4	
ROM	Royal Ontario Museum	Toronto	Canada	1	2			5
SAMA	South Australian Museum	Adelaide	Australia	1				
SBMNH	Santa Barbara Museum of Natural History	Santa Barbara	U.S.A.		2			
SDNHM	San Diego Natural History Museum	San Diego	U.S.A.		2			
SMF	Forschungsinstitut und Naturmuseum Senckenberg	Frankfurt a.M.	Germany	1				5
SMNS	Staatliches Museum für Naturkunde Stuttgart	Stuttgart	Germany	1				5
TM	Transvaal Museum	Pretoria	South Africa					5
TTU	Museum of Texas Tech University	Lubbock	U.S.A.	1	2			
UAM	University of Alaska Museum	Fairbanks	U.S.A.		2	3		
UCM	University of Colorado Museum of Natural History	Boulder	U.S.A.	1	2			
UMMZ	University of Michigan Museum of Zoology	Ann Arbor	U.S.A.	1	2			
UMNH	Utah Museum of Natural History	Salt Lake City	U.S.A.		2			
UNSM	University of Nebraska State Museum	Lincoln	U.S.A.		2			
USNM	National Museum of Natural History	Washington D.C.	U.S.A.	1	2			5
UTEP	Centennial Museum at the University of Texas at El Paso	El Paso	U.S.A.		2			
UWBM	University of Washington Burke Museum of Natural History & Culture	Seattle	U.S.A.	1	2		4	
VMO	Vlastivědné Muzeum v Olomouci	Olomouc	Czech Republic	1	2			
WNMU	Western New Mexico University	Silver City	U.S.A.		2	3		
YPM	Peabody Museum of Natural History at Yale University	New Haven	U.S.A.	1	2		4	
ZFMK	Zoologisches Forschungsmuseum Alexander Koenig	Bonn	Germany	1				5
ZMA	Zoologisch Museum Amsterdam	Amsterdam	Netherlands					5
ZMB	Zoologisches Museum Berlin	Berlin	Germany	1				5
ZSM	Zoologische Staatssammlung München	Munich	Germany	1				

Appendix B   Georeferencing of species occurrence data

For georeferencing locality names the following sources were used:

> Online gazetteers such as the NGA GNS gazetteer (available http://geonames.nga.mil/ggmagaz; accessed 2007-2011) and the JRC fuzzy gazetteer (available http://dma.jrc.it/services/fuzzyG/; accessed 2007-2011);

> several other gazetteers included in – often rather old – African vertebrate publications, e.g. Loveridge (1929), Hill and Carter (1941), Moreau et al. (1946), Swynnerton and Hayman (1951), Aellen (1952), Chapin (1954), Hayman (1963), Davis and Misonne (1964), Rosevear (1965), de Witte et al. (1966), Hayman et al. (1966), Kock (1969), Largen et al. (1974), Koopman (1975), Osborn and Helmy (1980), Rautenbach (1982), Aggundey and Schlitter (1984), Qumsiyeh (1985), Robbins et al. (1985), Happold (1987), Happold et al. (1988), Kowalski and Rzebik-Kowalska (1991), Bergmans (1998), Grubb et al. (1998), Pearch et al. (2001), Bergmans and van Strien (2004), Dean et al. (2006), Schmidt et al. (2008), Thorn and Kerbis Peterhans (2009), Monadjem et al. (2010) and Dalhoumi et al. (2011);

> a range of topographic maps (1:500k to 1:50k) including the base maps provided by the AfricaMap project of Harvard University (available http://worldmap.harvard.edu/africamap/; accessed 2007-2011) and the Perry-Castañeda Library Map Collection at the University of Texas (available http://www.lib.utexas.edu/maps/africa.html; accessed 2007-2011);

> occasional internet searches for context and travel routes of specific expeditions and collecting activities by individual researchers, and

> satellite imagery and digital maps provided by Google Earth™, Google Maps™ and the Open Street Map contributors (available http://www.openstreetmap.org; accessed 2007-2011).

Coordinates given in older gazetteers and topographic maps were in most cases checked for accuracy according to newer topographic maps and satellite imagery, and adjusted where necessary. Coordinates already assigned to records (by museum catalogue managers or authors of the concerned publication) were often re-evaluated too, as part of the process of associating differently spelled locality names with a single unique locality name and coordinates.

Given the fine spatial grain of our study (1 km^2), we paid special attention to accurate georeferencing localities situated on mountain slopes (Feeley and Silman, 2010). We evaluated the taxonomic plausibility and comprehensiveness of the compiled data by overlap analysis with published distribution maps (e.g. taxon or country reviews), the ACR (van Cakenberghe and Seamark, 2009) and IUCN Red List range maps (IUCN, 2009).

Drawing on expert knowledge of the species biology we also scrutinized outliers in terms of habitat category and elevation using GLC2000 (Mayaux et al., 2004) and SRTM90 data (USGS JPL, 2005, p. 90),

respectively. We also re-examined spatial outliers not supported by preliminary SDMs built including these (Raxworthy et al., 2007).

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Appendix C   Taxonomy employed and statistics of individual SDMs

Since Simmons (2005) more than 30 continental African bat species have been described as new, either based on a re-examination of existing data or in the wake of new fieldwork. Further, several taxa have been assigned new names following taxonomic revisions. To account for these changes in our study we employed an updated version of Simmons's taxonomy.

Below we list all affected taxa, briefly describe the type of change(s) made, and provide corresponding references. The affected taxa are **numbered** in their order of appearance in Table C.1.; unnumbered taxa have not changed in name and definition since Simmons (2005).

Note that we could not estimate the geographic distribution of all species included in the updated taxonomy. Some species listed here were simply described (or removed from synonymy) after we had completed our analyses. These are marked (below and in Table C.1.) with the symbol **E**.

More often however a taxon was found to comprise one or more cryptic species – but very few presence records of the involved species were examined. In these cases, unless the cryptic species was convincingly shown to be distributed allopatrically, we decided to build a single SDM that represented all species involved rather than to exclude all affected species entirely from our study. We also built SDMs representing a species complex when a large number of occurrence records pertaining to frequently misidentified species could not be reliably allocated among these. In the list below we have marked all taxa treated as a species complex with the symbol **X**.

Finally, the updated taxonomy below also includes some taxa which we decided to treat provisionally as distinct species based on our synthesis of fragmented evidence rather than a single authoritative reference. In all these cases we provide a brief justification or supportive references. In the list below we have marked all taxa treated as provisionally distinct species with the symbol **P**.

Update to the taxonomy of Simmons (2005)

1   For the genus *Cistugo* – comprising *C. lesueuri* and *C. seabrae* – the new family Cistugidae has been erected (Lack et al., 2010).

2   The Somalian population of *Asellia tridens* has been found to constitute the cryptic species *Asellia italosomalica* sp. nov. (Benda et al., 2011) effectively restricting the African distribution of *A. tridens* to the region north of Ethiopia.

3   The *Hipposideros caffer-ruber* complex was found to comprise at least seven species (A1, A2, B1, B2, C1, C2 and D), with A1 corresponding to *Hipposiders caffer* s.s. and A2 to *Hipposideros caffer tephrus*; the latter was consequently assigned species rank (Vallo et al., 2008). Based on further genetic analyses using additional material however we treated lineages B1 and B2 as likely constituting a single species only, while accepting the subclades D1, D2 and D3 as distinct species, because the very homogenous subclade D2 was found to occur at least partially in

sympatry with subclades D1 and (elsewhere) with D3 while genetic distances in both cases were near 5% (Hauslaib-Haidn, 2011). Given the complexity of this group of cryptic species, we trained SDMs only with records genetically examined by either these two studies. The exception to this rule were some records from Southern Africa and the Sahara/Sahel zone, which we allocated to lineage A1 (*H. caffer*) and A2 (*H. tephrus*), respectively, based on the combination of being considerably smaller in most measurements relative to the rest of the group, their geographic peripheral location and support by preliminary habitat suitability models built with genetically lineage data only. Further note that the taxon listed in Simmons (2005) as *Hipposideros ruber* is currently referable to the taxon listed here as *H. ruber* B (and possibly lineage B2 only).

4 P   *Hipposideros fuliginosus* comprises two morphometrically different populations, of which the one in central African likely represents an unnamed species (Fahr, 2013a). For the purpose of this study we provisionally treat the latter as the distinct species *Hipposideros* aff. *fuliginosus*.

5 P   In this study we accept as distinct species the hitherto undescribed taxon provisionally dubbed "*Hipposideros* sp. nov. Ethiopia" which is represented by the specimens SMF 45008-45010 and was reported in Largen et al. (1974) as the first *Hipposideros fuliginosus* material east of the Ituri region in DRC.

6   *Triaenops persicus afer* has been raised to species rank, with *majusculus* retained as subspecies (Benda and Vallo, 2009).

7 P   *Chaerephon bemmeleni cisturus* appears to merit species rank, but more data from West Africa representing the nominate subspecies are needed to resolve this question (Fahr, 2013b). For the purpose of this study we provisionally raise the subspecies *cisturus* to full species rank.

8 P   SDMs created for the two – geographically clearly separated – subspecies of *Chaerephon nigeriae* (Cotterill and Happold, 2013a) predict markedly different, quite complimentary distribution areas. This suggests that the ecological niche of *C. nigeriae* (if treated as a single species) is characterized by substantial spatial non-stationarity. This would violate a fundamental assumption of correlative SDMs. For the purpose of this study we therefore raised *Chaerephon nigeriae spillmani* to full species rank.

9 P   SDMs created separately for the two – geographically well separated – subspecies of *Mops brachypterus* (Happold, 2013a) predict distribution areas that barely overlapped; moreover, discrepancies are largest for the records situated geographically mid-way (in eastern DRC and Uganda) of each apparent centre of distribution. This result casts doubt on the existence of a corridor between eastern and western populations and suggests that the ecological niche of *M. brachypterus* (if treated as a single species) is characterized by substantial spatial non-stationarity. This would violate a fundamental assumption of correlative SDMs. This finding also supports the earlier conclusions of Freeman (1981) who considered the West African populations to represent a distinct species. For the purpose of this study we therefore raised *Mops brachypterus leonis* to full species rank.

10   In central Africa, new fieldwork has yielded *Casinycteris campomaanensis* sp. nov. (Hassanin, 2014). While this study was published after we had completed our analyses, the species is included in our study because we knew of two presence localities referable to this – then undescribed – species. The type locality in Cameroon however was hence unavailable when training the SDM.

11   *Scotonycteris ophiodon* is now grouped with *Casinycteris* (Hassanin, 2014).

12   *Lissonycteris angolensis* is now referable to *Myonycteris angolensis* (Nesi et al., 2013).

13   The West African population of *Megaloglossus woermanni* has been found to constitute the cryptic species *Megaloglossus azagnyi* sp. nov. (Nesi et al., 2013).

14   *Myonycteris torquata leptodon* has been raised to species rank (Nesi et al., 2013).

15   *Rousettus lanosus* is now referable to *Stenonycteris lanosus* (Nesi et al., 2013).

16 X   *Scotonycteris zenkeri* is now considered to form a species complex comprising at least two cryptic species: *S. occidentalis* in West Africa and *S. bergmansi* in the Congo basin, with the range of *S. zenkeri* reduced to eastern Nigeria and south-western Cameroon (Hassanin et al., 2015). At the time of this publication however we had already completed our analyses for this species group. The SDM used here hence represents a species complex.

17   *Rhinopoma hardwickii cystops* has been been raised to species rank (Hulva et al., 2007).

18 P   SDMs built for each of the three recognized, geographically very isolated subspecies of *Rhinolophus blasii* do not predict the other subspecies' known presence localities. While raising these subspecies to full species rank has not been suggested so far (Happold, 2013b), this result suggests that the ecological niche of *R. blasii* (if treated as a single species) is characterized by substantial spatial non-stationarity. This would violate a fundamental assumption of correlative SDMs. For the purpose of this study we therefore raised *R. blasii andreinii* (Ethiopian region) and *R. blasii empusa* (Southern Africa) to full species rank.

19 X   *Rhinolophus clivosus* is now considered a species complex (Bernard and Happold, 2013), that comprises at least *Rhinolophus horaceki* from Libya (Benda and Vallo, 2012) and the Southern African species *Rhinolophus geoffroyi* (Stoffberg et al., 2012). At the time of these publications however we had already completed our analyses for this species group, and the potential allocation of many published *R. clivosus* records to these cryptic species remains somewhat unclear. For the purpose of this study we thus treated these taxa as a species complex and created a single SDM.

20 PX   The SDM built using the isolated Nigerian localities of *R. darlingi* only fails to predict the distribution of the remaining *R. darlingi* localities (in southern Africa) and vice versa. This suggests that the ecological niche of *R. darlingi* (if treated as a single species) is characterized by substantial spatial non-stationarity. This would violate a fundamental assumption of correlative SDMs. The apparent discrepancy in terms of ecological niche conforms with notable differences

of morphometric measures between the Nigerian and the remaining *R. darlingi* population (Cotterill and Happold, 2013b). Further note that the southern African population of *R. darlingi* has recently been shown to comprise the cryptic species *R. damarensis* (Jacobs et al., 2013), which increases the likelihood that the far more distant Nigerian population constitutes a distinct species as well (although morphometric differences are small; Cotterill and Happold, 2013b). Against this background we treated the Nigerian population of *R. darlingi* as the distinct species *Rhinolophus* aff. *darlingi*. The cyptic species *R. damarensis* however could not be accounted for as we had already completed our analyses at the time of its description; the SDM of *Rhinolophus* darl*i*ngi hence represents a species complex.

21 P   The two subspecies of *R. denti* are geographically separated by about 2000 kilometres and the presumably inhospitable rainforest zone, and considerable morphometric differences exist (Cotterill, 2013). Further, SDMs created separately for each subspecies predict markedly different distribution areas. This suggests that the ecological niche of *R. denti* (if treated as a single species) is characterized by substantial spatial non-stationarity. This would violate a fundamental assumption of correlative SDMs. For the purpose of this study we therefore raised the West African subspecies *Rhinolophus denti knorri* to full species rank.

22 X   *Rhinolophus hildebrandtii* has been found to constitute a species complex comprising four species (*R. cohenae*, *R.mabuensis*, *R. mossambicus* and *R. smithersi*), all occurring in Southern Africa (Taylor et al., 2012). At the time of this publication however we had already completed our analyses of the species group. Also, the potential allocation of many published *R. hildebrandtii* records to these cryptic species remains somewhat unclear. For the purpose of this study we thus treated these taxa as a species complex and created a single SDM.

23 P   The SDM built using records representing the northwest African population of *Rhinolophus hipposideros* only (i.e. *escalerae*) clearly fails to predict the known localities of the putative subspecies *minimus* in Sudan, Ethiopia, Eritrea and Djibouti – also if the Egyptian records (of debated status) are included in the training data. Likewise, the SDM built using only *minimus* records largely fails to predict the known presences in northwest Africa, and the SDM trained with all African *hipposideros* records does not predict the *minimus* records in Sudan and Ethiopia either. These results suggest that the ecological niche of the African populations of *R. hipposideros* (if treated as a single species) is characterized by substantial spatial non-stationarity. This would violate a fundamental assumption of correlative SDMs. For the purpose of this study we therefore created a separate SDM for the northwest African *R. hipposideros* population, to which we provisionally assigned the Egyptian records too, as these were predicted by the SDM trained with northwest African records only. For *R. hipposideros minimus* no reasonably accurate SDM could be produced (also when the Egyptian records were included); we hence used a buffer model (see main text) to represent this taxon's distribution. Note that our treatment of *minimus* as a distinct species agrees with the assessment of Zagorodniuk (1999), which both Simmons (2005) and Gaisler (2013) recognize as plausible – although both retain *minimus* as a ssp. pending further evidence. Clearly, consideration of records outside our study area (e.g. from southwest Arabia and the Levante) would substantially improve the prospects of

creating a reasonable SDM for *R. h. minimus* and may help resolve the taxonomic status of the Egyptian records of *R. hipposideros*.

24   In the Albertine Rift region, new fieldwork has yielded *Rhinolophus willardi* sp. nov. (Kerbis Peterhans et al., 2013).

25 P   In this study we accept as distinct species the hitherto undescribed taxon provisionally dubbed "*Rhinolophus* sp. nov." from Mozambique represented by the three specimens MHNG 1971.067 – 1971.069.

26   *Eptesicus serotinus isabellinus* has been raised to species rank (Ibáñez et al., 2006, and Mayer et al., 2007).

27 X   *Nycticeinops schlieffeni* comprises at least two cryptic species (Koubínová et al., 2013). The number of records representing the cryptic species however is currently very low. For the purpose of this study we thus treated these taxa as a species complex and created a single SDM.

28 X   *Scotoecus hirundo*, *Scotoecus hindeii* and *Scotoecus albigula* are listed as distinct species in Simmons (2005), but uncertainty regarding the allocation of dark-winged Scotoecus records to either of these taxa is high, in part because of pronounced sexual dimorphism. We hence followed (Happold, 2013c) and grouped all records of dark-winged *Scotoecus* provisionally with *S. hirundo*. Also note that *Scotoecus hirundo* itself appears to comprise at least one cryptic species (Koubínová et al., 2013). For the purpose of this study we thus treated these taxa as a species complex and created a single SDM.

29 X   *Scotophilus dinganii* has recently been shown to constitute a species complex (Trujillo et al., 2009) that comprises at least two East African forms distinct from South African *S. dinganii* s.s., and to incldue *S. colias* (Vallo et al., 2011), but the designation of most published records remains unclear. For the purpose of this study we thus treated these taxa as a species complex and created a single SDM.

30 P   SDMs created separately for the nominate form of *Scotophilus leucogaster* north of the Equator and *S. leucogaster damarensis* in Southern Africa predict markedly different distribution areas that barely overlap. This suggests that the ecological niche of *S. leucogaster* (if treated as a single species) is characterized by substantial spatial non-stationarity. This would violate a fundamental assumption of correlative SDMs. Further, despite the use of a more than 100 training localities, the joint SDM displays some abrupt step-like suitability predictions extending across relatively large areas – a typical indication of poor model performance. For the purpose of this study we therefore raised *S. leucogaster damarensis* to full species rank. Note that in light of prevailing confusion regarding published records of *S. leucogaster* (Van Cakenberghe and Happold, 2013a) we largely restricted the SDM training data to material examined in Robbins et al. (1985) and specimens collected and/or examined by one of us (J.F.), which resulted in most East African records being excluded (for this region several cryptic *Scotophilus* species have recently been reported, see e.g. Trujillo et al. (2009) and Vallo et al. (2011).

31 X   *Scotophilus nigrita alvenslebeni* from southern Africa has recently been raised to species rank (Vallo et al., 2015). At the time of this publication however we had already completed our analyses. The SDM used here hence represents a species complex.

32 X   *Scotophilus viridis* may also form a species complex potentially containing a cryptic species in Kenya (Trujillo et al., 2009). As with other *Scotophilus* taxa however, the designation of many published records of *S. viridis* remains unclear. For the purpose of this study we thus treated these taxa as a species complex and created a single SDM.

33 P   *Pipistrellus* (*Hypsugo*) *crassulus bellieri* is now considered "probably a distinct species" (Fahr, 2013c) on morphometric grounds, and SDMs produced separately for the nominate form in central Africa and *bellieri* in West Africa support this notion, as they predict essentially non-overlapping distribution and thus suggest some ecological niche differentiation too. In both cases the Dahomey Gap emerged as an area of unsuitable habitat separating West African *bellieri* from *crassulus* in central Africa. Against this background, and also to avoid violating the assumption of stationarity, we treated *bellieri* as a distinct species. Also note that both *crassulus* and *bellieri* are now placed in the genus *Pipistrellus* rather than *Hypsugo* (Fahr, 2013c).

34   *Hypsugo eisentrauti* is now placed in the genus *Pipistrellus* (Van Cakenberghe and Happold, 2013b).

35 X   *Neoromicia flavescens* is now referred to as *Pipistrellus grandidieri*, and so is *Eptesicus capensis angolensis*, together with some material of *Neoromicia capensis* with which the former was synonymized temporarily (Thorn et al., 2007). Meanwhile, new fieldwork in West Africa has yielded *Pipistrellus* aff. *grandidieri* (Weber and Fahr, 2007, Monadjem and Fahr, 2007, Weber and Fahr, 2009, and Fahr and Kalko, 2011; also SMF 843399). Because the Cameroon records of *P. grandidieri* included in Thorn et al. (2007) group at least as closely with the new West African records than with the remaining ones, there remains uncertainty regarding the specific status of either form. Against this background, we created a single SDM that predicts the distribution of *P. grandidieri* and *P.* aff. *grandidieri* as a species complex.

36   The *Pipistrellus pipistrellus* population in Cyrenaica is now referable to *Pipistrellus hanaki* sp. nov. (Benda et al., 2004a).

37 X   *Pipistrellus hesperidus* has been shown to comprise several cryptic species (Koubínová et al., 2013). The number of records representing these species however is currently very low. For the purpose of this study we thus treated these taxa as a species complex and created a single SDM.

38   *Pipistrellus kuhlii* and *Pipistrellus deserti* are listed as distinct species in Simmons (2005) and Van Cakenberghe and Benda (2013), but a recent genetic analysis suggests that *P. deserti* is best regarded a junior synonym of *P. kuhlii* (Benda et al. (2014). We hence chose to build a single SDM only. Also note that *Pipistrellus kuhlii* is currently listed in Simmons (2005) as a species that according to Kock (2001) does not occur in Africa at all. Kock however merely re-assigned sub-Saharan *Pipistrellus* cf. *kuhlii* records to *Pipistrellus hesperidus* – not those from North Africa. *Pipistrellus kuhlii* hence does occur in continental Africa.

39 P   In this study we accept as distinct species the hitherto undescribed taxon provisionally dubbed "*Pipistrellus* sp. nov. Tai NP" from Ivory Coast based on two specimens in the collection of J. Fahr (RCJF 679, RCJF 680).

40 P   In this study we accept as distinct species the hitherto undescribed taxon provisionally dubbed "*Pipistrellus* sp. nov. *Uganda*" represented by the specimen FMNH 165169.

41   *Plecotus austriacus christii* has been raised to species rank (Benda et al., 2004b).

42   The north-west African population of *Plecotus kolombatovici* has been described as *gaisleri* ssp. nov. (Spitzenberger et al., 2006) and is now considered distinct at the species level (Mayer et al., 2007).

43 X   *Glauconycteris beatrix* and *Glauconycteris humeralis* are listed as distinct species in Simmons (2005), and this assessment is still followed by (Happold, 2013d) pending further analyses. Several authors however consider *G. humeralis* to be a subspecies of *G. beatrix* only (e.g. (Eger and Schlitter, 2001). Against this background and because the allocation of most records from the Congo Basin to either *beatrix* (from Sierra Leone to Gabon) or *humeralis* (from easternmost DRC to western Kenya) is rather unclear, we created a single SDM to represent both taxa.

44   For *Glauconycteris superba* the new genus *Niumbaha* has been erected (Reeder et al., 2013).

45 X   *Laephotis botswanae* and *Laephotis angolensis* are still regarded as distinct species by Kearney (2013b) – in agreement with Simmons (2005) – but records of the latter taxon are so few that the inherent morphometric variability cannot be assessed adequately (Kearney, 2013a); differences are thus possibly insignificant implying subspecies status only. Against this background and because the SDM built using only *L. angolensis* records was rather poor, we created a single SDM using records of both taxa.

46   *Pipistrellus helios* is now referred to as *Neoromicia* "cf. *helios*", because the holotype – but not all specimens currently assigned to this form – was found to be conspecific with *Neoromicia nana* (Happold and Van Cakenberghe, 2013).

47   *Pipistrellus melckorum* is now referred to as *Neoromicia* "*cf. melckorum*", because the type series – but not all specimens currently assigned to this form – was found to be conspecific with *Neoromicia capensis* (Kearney, 2013b).

48 X   *Neoromicia nana* comprises at least one cryptic species (Koubínová et al., 2013). The number of records representing the cryptic species however is currently very low. For the purpose of this study we thus treated these taxa as a species complex and created a single SDM.

49 X   *Neoromicia somalica* comprises at least one cryptic species (Koubínová et al., 2013). The number of records representing the cryptic species however is currently very low. For the purpose of this study we thus treated these taxa as a species complex and created a single SDM.

50   In West Africa, new fieldwork has yielded *Neoromicia roseveari* sp. nov. (Monadjem et al., 2013).

51 P   In this study we accept as distinct species the hitherto undescribed taxon provisionally dubbed "*Neoromicia sp*. nov. 1" from Ivory Coast represented by the specimen RCFJ 775 in the research collection of J. Fahr (Fahr, 2008).

52 P   In this study we accept as distinct species the hitherto undescribed taxon provisionally dubbed "*Neoromicia* sp. nov. 2" from Sierra Leone represented by the two specimens ZFMK 2006.159 and ZFMK 2006.160 (Decher et al., 2010).

53   *Myotis dieteri* sp. nov. has been described from old material hitherto referred to as *Myotis megalopus* (Happold, 2005). As a second occurrence locality we accept the one reported for *M. megalopus* in Vattier-Bernard (1970).

54   The North African population of *Myotis nattereri* is now considered specifically distinct and referred to as *Myotis* sp. B (aff. *nattereri*) (García-Mudarra et al., 2009, and Salicini et al., 2013).

55 P   In this study we accept as distinct species the hitherto undescribed taxon provisionally dubbed "*Kerivoula* sp. nov. *Bukavu*" from eastern DRC represented by the specimen MRAC 23172 which Hayman et al. (1966) list as *Kerivoula ?aerosa*.

E   *Scotophilus mhlanganii* has recently been presented as a cryptic species within South African *Scotophilus* (Jacobs et al. 2006); a formal description however has not been given (yet) and some authors regard the specimens in question to represent *S. viridis*, e.g. Monadjem et al., (2010) and Van Cakenberghe and Happold (2013c). We hence did not consider this species in the present study.

E   The genus *Miniopterus* has been raised to family status (Miller-Butterworth et al., 2007).

E   The primarily European bat species *Pipistrellus pygmaeus* has recently been collected in Ceuta raising the possibility of a wider presence in north-west Africa (López-Baucells et al., 2012). We hence did not consider this species in the present study however, as we had completed our analyses at the time of this publication.

E   In the Albertine Rift region, new fieldwork has yielded *Rhinolophus kahuzi* sp. nov. (Kerbis Peterhans et al., 2013). We have not however included this species in the present study.

SDM statistics:

In addition to specifying the taxonomy employed in this study, Table C.1 lists a range of SDM performance (AUC and omission error) and uncertainty measures (fraction of predicted presence area affected by clamping), as well as some context data such as the number of training points, the threshold used to obtain the binary map, and the species' predicted prevalence (at 1 km^2 grain) within continental Africa. For further details please consult the legend below the table.

Reasonable MaxEnt SDMs could be produced for 226 out of 241 species (~94%) included in this study. For the remaining 15 species no (reasonable) SDM could be produced; these are marked with "b" in the second column of Table C.1. Ten of these species are currently known from only a single locality, another three species from only two localities and two other species have been recorded from three localities and four localities, respectively. Most of these 15 species appear to be clearly range-restricted species, i.e. their poor representation in collections seems mostly due to their small range, with low detectability playing a secondary role. We therefore estimated their spatial distribution using a different method that produced a locally constrained, habitat-specific prediction (see the paragraph on 'buffer models' in Section 2.2 of the main text).

Table C.1.　　　Taxonomic specifications and statistics of individual SDMs

taxo-nomic remarks §1	SDM remarks §2	ende-mic to Africa? §3	Taxon name	trai-ning localities used	non-zero coefficients §4	trai-ning AUC	test AUC (mean) §5	AUC diff (train - mean test)	test AUC assoc. std. dev.	chosen logistic thresh-hold	deviation from highest MaxEnt threshold §6	omission rate [1 km tolerance] §7	omission rate [10 km tolerance] §7	preva-lence of final SDM §8	fraction affected by clamping §9
				[count]	[count]	[0.xxx]	[0.xxx]	[in %]	[0.xxx]	[0.xxx]	[0.xxx]	[in %]	[in %]	[in %]	[in %]
1	s	Y	*Cistugo lesueuri*	18	18	990	966	2.42	027	480	-46	0.00	0.00	0.939	0.000
1		Y	*Cistugo seabrae*	13	9	997	993	0.40	004	540	-1	0.00	0.00	0.703	0.000
		Y	*Saccolaimus peli*	65	19	940	917	2.45	012	370	-1	0.11	0.03	8.129	0.023
		Y	*Taphozous hamiltoni*	12	8	990	971	1.92	023	480	-3	0.17	0.08	2.466	0.000
	s	Y	*Taphozous hildegardeae*	18	18	999	993	0.60	012	250	-134	0.00	0.00	0.055	0.000
		Y*	*Taphozous mauritianus*	230	68	811	810	0.12	no repl.	350	4	0.19	0.03	14.706	0.077
		N	*Taphozous nudiventris*	67	18	926	918	0.86	022	400	147	0.25	0.13	28.129	7.801
		N	*Taphozous perforatus*	111	59	890	813	8.65	no repl.	260	-2	0.15	0.09	20.204	1.440
		Y*	*Coleura afra*	82	32	886	842	4.97	012	440	-3	0.18	0.09	8.907	0.050
		Y*	*Asellia patrizii*	8	6	977	967	1.02	018	480	-3	0.00	0.00	0.472	0.000
2		[Y*]	*Asellia italosomalica*	5	5	997	971	2.61	011	560	-5	0.00	0.00	0.946	0.000
2		[N]	*Asellia tridens*	119	62	983	971	1.22	no repl.	170	3	0.08	0.03	27.515	11.782
	s	Y	*Cloeotis percivali*	34	25	941	950	-0.96	002	550	79	0.22	0.00	3.467	0.000
		Y	*Hipposideros abae*	65	31	923	878	4.88	016	600	237	0.43	0.23	1.717	0.006
		Y	*Hipposideros beatus*	64	16	947	923	2.53	014	330	-2	0.08	0.03	6.776	0.110
3		[Y]	*Hipposideros caffer*	37	16	977	962	1.54	007	320	2	0.05	0.00	1.116	0.008
		Y	*Hipposideros camerunensis*	5	3	970	843	13.09	219	700	90	0.60	0.20	0.675	0.000
	s	Y	*Hipposideros curtus*	15	13	990	964	2.63	019	500	75	0.20	0.10	0.359	0.000
		Y	*Hipposideros cyclops*	186	73	914	886	3.06	no repl.	250	-75	0.09	0.02	11.314	0.169
4 P		Y	*Hipposideros fuliginosus*	29	17	965	936	3.01	026	340	5	0.07	0.03	2.342	0.000
4 P		Y	*Hipposideros* aff. *fuliginosus*	6	6	966	948	1.86	032	460	-2	0.00	0.00	5.787	0.000
		Y	*Hipposideros gigas*	65	26	940	867	7.77	028	260	-56	0.05	0.00	6.963	0.000
		Y	*Hipposideros jonesi*	48	20	937	914	2.45	005	500	222	0.29	0.15	2.466	0.010

taxo-nomic remarks §1	SDM remarks §2	ende-mic to Africa? §3	Taxon name	training localities used	non-zero coefficients §4	training AUC	test AUC (mean) §5	AUC diff (train - mean test)	test AUC assoc. std. dev.	chosen logistic thresh-hold	deviation from highest MaxEnt threshold §6	omission rate [1 km tolerance] §7	omission rate [10 km tolerance] §7	preva-lence of final SDM §8	fraction affected by clamping §9
				[count]	[count]	[0.xxx]	[0.xxx]	[in %]	[0.xxx]	[0.xxx]	[0.xxx]	[in %]	[in %]	[in %]	[in %]
		Y	*Hipposideros lamottei*	2	7	992	n/a	n/a	n/a	600	-94	0.00	0.00	0.002	0.000
		Y	*Hipposideros marisae*	7	7	989	976	1.31	022	800	272	0.29	0.14	0.088	0.059
	s	Y*	*Hipposideros megalotis*	20	17	962	916	4.78	085	400	55	0.05	0.05	1.418	0.002
3	s	[Y]	*Hipposideros ruber* B	13	5	948	909	4.11	048	510	-3	0.09	0.00	4.287	0.002
3		[Y]	*Hipposideros* aff. *ruber* C1	26	13	921	806	12.49	087	450	5	0.08	0.00	7.713	0.000
3		[Y]	*Hipposideros* aff. *ruber* C2	9	5	964	947	1.76	031	480	1	0.00	0.00	5.786	0.000
3		[Y]	*Hipposideros* aff. *ruber* D1	11	7	950	911	4.11	028	500	0	0.09	0.00	7.235	0.000
3	s	[Y]	*Hipposideros* aff. *ruber* D2	21	14	984	960	2.44	046	450	-70	0.05	0.05	1.051	0.000
3	b	[Y]	*Hipposideros* aff. *ruber* D3	3	n/a	n/a	n/a	n/a	n/a	n/a	n/a	0.00	0.00	0.003	0.000
3		[N]	*Hipposideros tephrus*	34	18	907	849	6.39	053	600	163	0.35	0.15	15.581	0.000
		Y	*Hipposideros vittatus*	82	37	882	795	9.86	020	450	2	0.10	0.05	14.381	0.125
5 P		[Y]	*Hipposideros* sp. nov. Ethiopia	4	7	996	995	0.10	002	710	1	0.00	0.00	0.065	0.000
6		[Y]	*Triaenops afer*	67	25	866	794	8.31	010	450	51	0.27	0.06	10.875	0.002
		Y	*Cardioderma cor*	86	45	951	934	1.79	007	310	58	0.08	0.01	6.065	0.015
		Y	*Lavia frons*	230	65	896	853	4.80	no repl.	340	-2	0.11	0.03	14.305	0.031
		Y	*Chaerephon aloysiisabaudiae*	15	7	906	831	8.28	032	400	-80	0.07	0.07	12.239	0.000
		Y	*Chaerephon ansorgei*	53	23	842	740	12.11	021	450	1	0.19	0.02	14.030	0.000
7 P		Y	*Chaerephon bemmeleni*	5	3	887	640	27.85	277	580	48	0.20	0.20	7.516	0.006
7 P		[Y]	*Chaerephon* (*bemmeleni*) *cisturus*	18	10	958	912	4.80	037	380	-4	0.11	0.00	5.533	0.001
		Y	*Chaerephon bivittatus*	31	16	902	890	1.33	023	460	1	0.06	0.00	9.490	0.000
		Y	*Chaerephon chapini*	10	5	862	777	9.86	103	530	-2	0.10	0.10	12.334	0.000
	b	Y	*Chaerephon gallagheri*	1	n/a	n/a	n/a	n/a	n/a	n/a	n/a	0.00	0.00	0.001	0.000
		Y	*Chaerephon major*	55	23	902	870	3.55	006	420	-2	0.11	0.04	18.631	0.026

taxo-nomic remarks §1	SDM remarks §2	ende-mic to Africa? §3	Taxon name	trai-ning localities used	non-zero coefficients §4	trai-ning AUC	test AUC (mean) §5	AUC diff (train - mean test)	test AUC assoc. std. dev.	chosen logistic thresh-hold	deviation from highest MaxEnt threshold §6	omission rate [1 km tolerance] §7	omission rate [10 km tolerance] §7	preva-lence of final SDM §8	fraction affected by clamping §9
				[count]	[count]	[0.xxx]	[0.xxx]	[in %]	[0.xxx]	[0.xxx]	[0.xxx]	[in %]	[in %]	[in %]	[in %]
8 P		Y	*Chaerephon nigeriae*	37	17	892	799	10.43	035	460	-2	0.14	0.05	14.024	0.002
8 P	[Y]		*Chaerephon (nigeriae) spillmani*	25	15	948	898	5.27	049	300	1	0.04	0.04	11.793	0.000
		Y*	*Chaerephon pumilus*	536	81	810	769	5.06	no repl.	210	-209	0.02	0.00	40.787	0.068
	s, w	Y	*Chaerephon russatus*	7	3	957	941	1.67	051	520	-2	0.00	0.00	5.054	0.001
		Y	*Chaerephon shortridgei*	16	9	973	950	2.36	012	430	53	0.00	0.00	5.759	0.000
9 P		Y	*Mops brachypterus*	5	3	954	891	6.60	114	540	0	0.00	0.00	1.371	0.000
9 P		[Y]	*Mops (brachypterus) leonis*	34	15	937	899	4.06	005	360	3	0.06	0.00	6.890	0.000
		Y	*Mops condylurus*	287	71	842	800	4.99	no repl.	250	-156	0.06	0.00	28.412	0.082
		Y	*Mops congicus*	8	5	929	918	1.18	047	460	-50	0.13	0.00	8.416	0.003
		Y	*Mops demonstrator*	30	14	946	875	7.51	054	370	1	0.10	0.03	8.843	0.033
		Y*	*Mops midas*	58	21	881	817	7.26	060	460	4	0.19	0.05	12.637	0.002
	w	Y	*Mops nanulus*	39	17	903	862	4.54	027	280	-74	0.10	0.08	14.347	0.061
	b	Y	*Mops niangarae*	1	n/a	n/a	n/a	n/a	n/a	n/a	n/a	0.00	0.00	0.001	0.000
		Y	*Mops niveiventer*	21	18	957	914	4.49	019	400	3	0.10	0.00	9.138	0.000
	w	Y	*Mops petersoni*	8	4	967	958	0.93	046	520	86	0.13	0.13	4.667	0.001
		Y	*Mops spurrelli*	37	27	973	931	4.32	016	390	-36	0.00	0.00	1.432	0.009
		Y	*Mops thersites*	58	28	940	901	4.15	007	320	-17	0.07	0.00	6.438	0.005
	s, w	Y	*Mops trevori*	13	8	913	820	10.19	085	550	5	0.08	0.08	8.812	0.000
		Y	*Myopterus daubentonii*	8	4	871	816	6.31	140	570	0	0.25	0.13	9.461	0.000
		Y	*Myopterus whitleyi*	15	9	934	879	5.89	082	510	-2	0.13	0.07	7.163	0.016
		Y*	*Otomops martiensseni*	51	27	861	837	2.79	027	260	-95	0.14	0.06	16.136	0.004
		Y	*Platymops setiger*	26	15	984	972	1.22	016	250	-4	0.08	0.04	3.417	0.000
		Y	*Sauromys petrophilus*	36	16	952	942	1.05	032	370	5	0.08	0.06	4.920	0.000
		N	*Tadarida aegyptiaca*	163	68	878	820	6.61	no repl.	340	2	0.12	0.03	16.080	0.025

taxo-nomic remarks §1	SDM remarks §2	ende-mic to Africa? §3	Taxon name	trai-ning localities used	non-zero coefficients §4	trai-ning AUC	test AUC (mean) §5	AUC diff (train - mean test)	test AUC assoc. std. dev.	chosen logistic thresh-hold	deviation from highest MaxEnt threshold §6	omission rate [1 km tolerance] §7	omission rate [10 km tolerance] §7	preva-lence of final SDM §8	fraction affected by clamping §9
				[count]	[count]	[0.xxx]	[0.xxx]	[in %]	[0.xxx]	[0.xxx]	[0.xxx]	[in %]	[in %]	[in %]	[in %]
	w	Y	*Tadarida fulminans*	23	10	902	798	11.53	089	520	0	0.13	0.00	6.551	0.003
		Y	*Tadarida lobata*	10	7	931	787	15.47	059	530	-2	0.00	0.00	6.168	0.001
		N	*Tadarida teniotis*	15	16	991	956	3.53	041	300	-2	0.00	0.00	1.837	0.000
	w	Y	*Tadarida ventralis*	18	10	887	829	6.54	077	400	2	0.11	0.00	8.055	0.002
		Y	*Nycteris arge*	143	54	926	898	3.02	no repl.	220	-75	0.04	0.02	11.242	0.000
		Y	*Nycteris aurita*	19	12	968	939	3.00	063	270	3	0.11	0.00	5.887	0.000
		Y	*Nycteris gambiensis*	72	25	945	917	2.96	016	310	4	0.07	0.06	6.424	0.000
		Y	*Nycteris grandis*	145	69	891	802	9.99	no repl.	260	-152	0.09	0.01	12.026	0.001
		Y	*Nycteris hispida*	461	92	811	778	4.07	no repl.	200	-232	0.02	0.00	41.939	0.000
		Y	*Nycteris intermedia*	21	12	900	836	7.11	060	370	-90	0.10	0.05	13.282	0.293
		Y	*Nycteris macrotis*	328	75	822	813	1.09	no repl.	270	-134	0.06	0.02	33.817	0.052
		Y	*Nycteris major*	12	6	923	879	4.77	035	480	-1	0.00	0.00	8.150	0.001
		Y	*Nycteris nana*	61	19	915	871	4.81	010	390	-32	0.07	0.05	11.106	0.000
		Y	*Nycteris parisii*	6	5	974	935	4.00	068	410	4	0.00	0.00	6.597	0.000
		Y*	*Nycteris thebaica*	621	79	783	728	7.02	no repl.	250	-185	0.05	0.02	48.903	0.343
	b	Y	*Nycteris vinsoni*	1	n/a	n/a	n/a	n/a	n/a	n/a	n/a	0.00	0.00	0.001	0.000
		Y	*Nycteris woodi*	20	11	956	893	6.59	042	550	41	0.10	0.00	4.521	0.000
		Y	*Casinycteris argynnis*	19	12	969	964	0.52	008	320	-93	0.00	0.00	5.811	0.000
10		[Y]	*Casinycteris campomaanensis*	2	7	999	n/a	n/a	n/a	740	-1	0.00	0.00	0.029	0.000
11	s	Y	*Casinycteris (Scotonycteris) ophiodon*	19	14	983	958	2.54	028	350	4	0.05	0.05	1.184	0.000
		Y*	*Eidolon helvum*	473	96	810	782	3.46	no repl.	200	-171	0.07	0.02	35.183	0.061
		Y	*Epomophorus angolensis*	22	14	986	968	1.83	027	550	139	0.18	0.05	1.111	0.000
	s	Y	*Epomophorus anselli*	3	4	966	789	18.32	137	610	2	0.00	0.00	0.006	0.000

taxo-nomic remarks §1	SDM remarks §2	ende-mic to Africa? §3	Taxon name	trai-ning localities used	non-zero coefficients §4	trai-ning AUC	test AUC (mean) §5	AUC diff (train - mean test)	test AUC assoc. std. dev.	chosen logistic thresh-hold	deviation from highest MaxEnt threshold §6	omission rate [1 km tolerance] §7	omission rate [10 km tolerance] §7	preva-lence of final SDM §8	fraction affected by clamping §9
				[count]	[count]	[0.xxx]	[0.xxx]	[in %]	[0.xxx]	[0.xxx]	[0.xxx]	[in %]	[in %]	[in %]	[in %]
		Y	*Epomophorus crypturus*	105	70	951	936	1.58	no repl.	310	-17	0.06	0.02	6.845	0.000
		Y	*Epomophorus gambianus*	296	71	932	917	1.61	no repl.	240	-55	0.05	0.01	9.581	0.000
		Y	*Epomophorus grandis*	2	6	976	n/a	n/a	n/a	630	2	0.00	0.00	0.001	0.000
		Y	*Epomophorus labiatus*	144	70	912	855	6.25	no repl.	300	-4	0.09	0.03	7.808	0.004
		Y	*Epomophorus minimus*	23	17	977	923	5.53	051	370	-2	0.00	0.00	4.731	0.000
		Y	*Epomophorus wahlbergi*	303	72	898	862	4.01	no repl.	340	5	0.11	0.02	8.213	0.000
		Y	*Epomops buettikoferi*	97	49	964	940	2.49	007	270	-10	0.06	0.04	1.660	0.000
		Y	*Epomops dobsonii*	22	13	958	914	4.59	052	380	5	0.09	0.05	7.273	0.000
		Y	*Epomops franqueti*	315	66	921	915	0.65	no repl.	220	-105	0.05	0.03	11.997	0.000
		Y	*Hypsignathus monstrosus*	187	62	920	871	5.33	no repl.	250	-99	0.05	0.02	11.248	0.000
12		Y	*Myonycteris angolensis*	198	62	889	863	2.92	no repl.	280	-3	0.14	0.05	8.344	0.000
13		Y	*Megaloglossus azagnyi*	87	42	971	949	2.27	012	240	-101	0.02	0.02	1.708	0.000
13		Y	*Megaloglossus woermanni*	136	66	962	958	0.42	no repl.	180	-51	0.04	0.01	7.677	0.000
		Y	*Micropteropus intermedius*	3	5	992	936	5.65	041	690	-2	0.00	0.00	0.654	0.000
		Y	*Micropteropus pusillus*	421	81	882	872	1.13	no repl.	270	-115	0.08	0.02	17.387	0.000
	s	Y	*Myonycteris relicta*	16	16	997	965	3.21	025	660	1	0.00	0.00	0.172	0.000
14		Y	*Myonycteris leptodon*	85	33	957	934	2.40	009	250	-47	0.08	0.01	2.262	0.369
14		Y	*Myonycteris torquata*	77	28	928	899	3.13	006	230	-156	0.04	0.04	11.462	0.000
		Y	*Nanonycteris veldkampii*	152	64	939	875	6.82	no repl.	210	-61	0.05	0.02	5.261	0.000
		Y	*Plerotes anchietae*	8	4	986	927	5.98	157	640	80	0.00	0.00	2.927	0.000
		N	*Rousettus aegyptiacus*	310	81	818	795	2.81	no repl.	300	-57	0.11	0.02	15.268	0.145
15		Y	*Stenonycteris lanosus*	32	13	955	884	7.43	027	290	0	0.09	0.09	1.845	0.000
16 X		Y	*Scotonycteris zenkeri*	90	36	956	918	3.97	018	300	37	0.06	0.01	3.999	0.249
17		N	*Rhinopoma cystops*	81	34	980	943	3.78	017	310	4	0.04	0.02	14.068	0.000
	s	Y	*Rhinopoma macinnesi*	11	7	994	993	0.10	003	570	-2	0.25	0.08	2.043	0.006

taxo-nomic remarks §1	SDM remarks §2	ende-mic to Africa? §3	Taxon name	trai-ning localities used	non-zero coefficients §4	trai-ning AUC	test AUC (mean) §5	AUC diff (train - mean test)	test AUC assoc. std. dev.	chosen logistic thresh-hold	deviation from highest MaxEnt threshold §6	omission rate [1 km tolerance] §7	omission rate [10 km tolerance] §7	preva-lence of final SDM §8	fraction affected by clamping §9
				[count]	[count]	[0.xxx]	[0.xxx]	[in %]	[0.xxx]	[0.xxx]	[0.xxx]	[in %]	[in %]	[in %]	[in %]
		N	*Rhinopoma microphyllum*	33	12	961	919	4.37	014	320	3	0.09	0.03	25.599	0.000
		Y	*Rhinolophus adami*	2	9	1000	n/a	n/a	n/a	730	0	0.00	0.00	0.002	0.000
		Y	*Rhinolophus alcyone*	76	27	893	873	2.24	011	390	3	0.14	0.04	7.897	0.005
18 P		N	*Rhinolophus blasii*	19	12	991	980	1.11	008	430	-15	0.05	0.00	0.972	0.000
18 P		N	*Rhinolophus (blasii) andreinii*	9	4	935	881	5.78	102	660	78	0.33	0.00	1.953	0.000
18 P		[Y]	*Rhinolophus (blasii) empusa*	54	25	956	924	3.35	006	400	90	0.11	0.02	2.270	0.000
		Y	*Rhinolophus capensis*	17	12	993	961	3.22	053	500	-14	0.06	0.00	0.437	0.000
19 X		N	*Rhinolophus clivosus*	204	76	887	811	8.57	no repl.	380	-4	0.12	0.04	9.629	0.283
20 PX		Y	*Rhinolophus darlingi*	71	20	928	898	3.23	013	340	0	0.11	0.01	7.083	0.000
20 PX		[Y]	*Rhinolophus* aff. *darlingi*	8	5	940	887	5.64	070	640	55	0.38	0.00	0.619	0.000
		Y	*Rhinolophus deckenii*	22	20	992	976	1.61	017	320	-159	0.00	0.00	1.070	0.000
21 P		Y	*Rhinolophus denti*	19	15	984	966	1.83	018	390	-70	0.05	0.00	4.233	0.000
21 P		[Y]	*Rhinolophus (denti) knorri*	10	8	980	953	2.76	051	500	-2	0.10	0.00	1.174	0.000
		Y	*Rhinolophus eloquens*	54	15	953	942	1.15	007	220	-4	0.02	0.00	3.736	0.000
		N	*Rhinolophus euryale*	10	9	993	988	0.50	006	450	-113	0.00	0.00	0.454	0.000
		N	*Rhinolophus ferrumequinum*	32	13	991	982	0.91	002	280	4	0.00	0.00	1.030	0.000
		Y	*Rhinolophus fumigatus*	196	64	857	789	7.93	no repl.	410	4	0.17	0.07	12.911	0.019
		Y	*Rhinolophus guineensis*	31	18	988	971	1.72	021	300	-55	0.03	0.03	0.830	0.000
22 X		Y	*Rhinolophus hildebrandtii*	122	66	902	815	9.65	no repl.	410	5	0.09	0.02	9.717	0.003
		Y	*Rhinolophus hilli*	2	6	1000	n/a	n/a	n/a	640	2	0.00	0.00	0.001	0.000
	s	Y	*Rhinolophus hillorum*	17	16	995	984	1.11	008	340	-309	0.00	0.00	0.573	0.000

taxo-nomic remarks §1	SDM remarks §2	ende-mic to Africa? §3	Taxon name	trai-ning localities used	non-zero coefficients §4	trai-ning AUC	test AUC (mean) §5	AUC diff (train - mean test)	test AUC assoc. std. dev.	chosen logistic thresh-hold	deviation from highest MaxEnt threshold §6	omission rate [1 km tolerance] §7	omission rate [10 km tolerance] §7	preva-lence of final SDM §8	fraction affected by clamping §9
				[count]	[count]	[0.xxx]	[0.xxx]	[in %]	[0.xxx]	[0.xxx]	[0.xxx]	[in %]	[in %]	[in %]	[in %]
23 P		N	*Rhinolophus hipposideros*	20	11	983	961	2.24	022	570	46	0.10	0.00	1.178	0.000
23 P	b	[Y]	*Rhinolophus (hipposideros) minimus*	4	n/a	n/a	n/a	n/a	n/a	n/a	n/a	0.00	0.00	0.004	0.000
		Y	*Rhinolophus landeri*	205	66	813	680	16.36	no repl.	430	4	0.21	0.06	14.362	0.027
	s	Y	*Rhinolophus maclaudi*	6	9	995	976	1.91	034	650	48	0.00	0.00	0.203	0.022
	s	Y	*Rhinolophus maendeleo*	5	4	933	904	3.11	117	640	-1	0.20	0.20	0.040	0.000
		N	*Rhinolophus mehelyi*	29	12	985	969	1.62	013	350	-100	0.00	0.00	1.468	0.000
	s	Y	*Rhinolophus ruwenzorii*	14	10	996	994	0.20	004	200	-124	0.07	0.00	0.425	0.006
	b	Y	*Rhinolophus sakejiensis*	1	n/a	n/a	n/a	n/a	n/a	n/a	n/a	0.00	0.00	0.001	0.000
		Y	*Rhinolophus silvestris*	4	4	959	868	9.49	141	600	57	0.50	0.00	0.121	0.000
		Y	*Rhinolophus simulator*	79	27	882	815	7.60	011	440	80	0.18	0.13	4.583	0.001
		Y	*Rhinolophus swinnyi*	40	17	928	840	9.48	007	320	48	0.10	0.00	8.411	0.000
		Y	*Rhinolophus ziama*	3	6	999	996	0.30	002	700	2	0.00	0.00	0.013	0.000
24		[Y]	*Rhinolophus willardi*	2	10	1000	n/a	n/a	n/a	610	-1	0.00	0.00	0.001	0.000
25 P		[Y]	*Rhinolophus sp. nov.*	2	9	1000	n/a	n/a	n/a	830	-3	0.00	0.00	0.001	0.000
	s	N	*Eptesicus bottae*	6	6	999	983	1.60	037	400	-35	0.00	0.00	0.258	0.015
	s	Y	*Eptesicus floweri*	11	9	996	991	0.50	006	520	4	0.00	0.00	3.964	0.000
		Y	*Eptesicus hottentotus*	31	14	909	820	9.79	032	350	-46	0.10	0.06	6.599	0.001
26		N	*Eptesicus isabellinus*	35	20	984	977	0.71	003	380	5	0.09	0.03	1.446	0.000
27 X		Y	*Nycticeinops schlieffeni*	191	66	872	837	4.01	no repl.	380	5	0.17	0.04	23.102	0.056
		Y	*Scotoecus albofuscus*	26	12	886	822	7.22	044	420	4	0.15	0.00	13.103	0.005
28 X		Y	*Scotoecus hirundo & hindei & albigula*	104	54	879	794	9.67	no repl.	360	-48	0.05	0.01	16.420	0.000
29 X		Y	*Scotophilus dinganii*	156	70	841	739	12.13	no repl.	350	-68	0.05	0.00	21.286	0.004
30 P		Y	*Scotophilus leucogaster*	92	26	951	932	2.00	016	250	-21	0.03	0.00	10.899	0.000

taxonomic remarks §1	SDM remarks §2	endemic to Africa? §3	Taxon name	training localities used	non-zero coefficients §4	training AUC	test AUC (mean) §5	AUC diff (train - mean test)	test AUC assoc. std. dev.	chosen logistic threshold	deviation from highest MaxEnt threshold §6	omission rate [1 km tolerance] §7	omission rate [10 km tolerance] §7	prevalence of final SDM §8	fraction affected by clamping §9
				[count]	[count]	[0.xxx]	[0.xxx]	[in %]	[0.xxx]	[0.xxx]	[0.xxx]	[in %]	[in %]	[in %]	[in %]
30 P		[Y]	*Scotophilus (leucogaster) damarensis*	40	17	961	949	1.25	021	230	-103	0.03	0.00	8.365	0.000
31 X		Y	*Scotophilus nigrita*	18	9	851	775	8.93	111	500	-1	0.22	0.11	15.359	0.000
	s	Y	*Scotophilus nucella*	10	9	963	949	1.45	031	600	36	0.18	0.00	1.872	0.000
		Y	*Scotophilus nux*	32	14	952	930	2.31	011	360	-1	0.06	0.00	5.639	0.000
32 X		Y	*Scotophilus viridis*	153	54	903	870	3.65	no repl.	330	1	0.11	0.04	9.824	0.000
		N	*Nyctalus lasiopterus*	3	3	999	995	0.40	004	700	-54	0.00	0.00	0.064	0.000
	s	N	*Nyctalus leisleri*	6	4	988	980	0.81	008	660	1	0.00	0.00	0.606	0.000
		Y	*Pipistrellus aero*	7	5	983	955	2.85	057	600	51	0.14	0.00	0.721	0.006
33 P	s	[Y]	*Pipistrellus (crassulus) bellieri*	16	11	988	886	10.32	108	430	5	0.00	0.00	0.455	0.000
33 P		Y	*Pipistrellus crassulus*	18	10	940	910	3.19	023	460	-4	0.06	0.00	7.186	0.013
34		Y	*Pipistrellus eisentrauti*	5	6	998	996	0.20	004	580	-1	0.00	0.00	0.036	0.297
35 X		Y	*Pipistrellus grandidieri* & aff. *grandidieri*	20	11	865	813	6.01	106	440	4	0.25	0.10	9.947	0.044
36	s	Y	*Pipistrellus hanaki*	10	11	1000	992	0.80	014	530	-76	0.00	0.00	0.014	0.000
37 X		Y	*Pipistrellus hesperidus*	96	49	917	855	6.76	022	390	-3	0.14	0.05	4.132	0.000
		Y	*Pipistrellus inexspectatus*	13	8	939	918	2.24	016	460	-26	0.00	0.00	8.173	0.011
38 X		[N]	*Pipistrellus kuhlii* & *deserti*	93	37	981	974	0.71	no repl.	280	-1	0.05	0.00	6.491	15.051
		Y	*Pipistrellus nanulus*	70	30	887	810	8.68	044	390	-2	0.24	0.06	13.387	0.012
	b	Y	*Pipistrellus permixtus*	1	n/a	n/a	n/a	n/a	n/a	n/a	n/a	0.00	0.00	0.001	0.000
		N	*Pipistrellus pipistrellus*	16	8	986	978	0.81	006	340	5	0.00	0.00	1.765	0.003
		Y*	*Pipistrellus rueppellii*	107	58	875	765	12.57	no repl.	280	-2	0.09	0.02	23.163	2.349
		Y	*Pipistrellus rusticus*	66	21	847	766	9.56	036	440	1	0.18	0.05	14.744	0.000
39 P	s	[Y]	*Pipistrellus* sp. nov. Tai NP	2	13	1000	n/a	n/a	n/a	500	-238	0.00	0.00	0.001	0.000
40 P	b	[Y]	*Pipistrellus* sp. nov. Uganda	1	n/a	n/a	n/a	n/a	n/a	n/a	n/a	0.00	0.00	0.001	0.000

taxo-nomic remarks §1	SDM remarks §2	ende-mic to Africa? §3	Taxon name	trai-ning localities used	non-zero coefficients §4	trai-ning AUC	test AUC (mean) §5	AUC diff (train - mean test)	test AUC assoc. std. dev.	chosen logistic thresh-hold	deviation from highest MaxEnt threshold §6	omission rate [1 km tolerance] §7	omission rate [10 km tolerance] §7	preva-lence of final SDM §8	fraction affected by clamping §9
				[count]	[count]	[0.xxx]	[0.xxx]	[in %]	[0.xxx]	[0.xxx]	[0.xxx]	[in %]	[in %]	[in %]	[in %]
		N	*Barbastella barbastellus*	6	5	981	972	0.92	021	640	100	0.17	0.00	1.199	0.007
		N	*Barbastella leucomelas*	2	7	1000	n/a	n/a	n/a	590	4	0.00	0.00	0.027	0.000
		N	*Otonycteris hemprichii*	36	19	989	985	0.40	003	300	150	0.11	0.03	7.479	1.721
	s	Y	*Plecotus balensis*	6	5	996	991	0.50	009	570	-4	0.00	0.00	0.241	0.000
41		Y	*Plecotus christii*	19	15	997	994	0.30	005	400	117	0.11	0.00	0.487	0.000
42		[Y]	*Plecotus gaisleri*	23	11	985	976	0.91	009	330	-1	0.04	0.00	2.415	0.203
	s	Y	*Glauconycteris alboguttata*	9	4	975	926	5.03	123	420	-1	0.00	0.00	4.696	0.000
		Y	*Glauconycteris argentata*	60	19	908	884	2.64	009	400	4	0.10	0.05	6.238	0.005
43 X		Y	*Glauconycteris beatrix & humeralis*	29	12	955	936	1.99	028	400	-1	0.07	0.04	6.232	0.063
		Y	*Glauconycteris curryae*	6	4	959	934	2.61	040	600	95	0.17	0.17	2.809	0.001
		Y	*Glauconycteris egeria*	5	4	976	886	9.22	159	620	-4	0.00	0.00	2.218	0.000
		Y	*Glauconycteris gleni*	3	5	986	944	4.26	024	650	4	0.00	0.00	2.457	0.000
	b	Y	*Glauconycteris kenyacola*	1	n/a	n/a	n/a	n/a	n/a	n/a	n/a	0.00	0.00	0.001	0.000
	b	Y	*Glauconycteris machadoi*	1	n/a	n/a	n/a	n/a	n/a	n/a	n/a	0.00	0.00	0.001	0.000
		Y	*Glauconycteris poensis*	59	26	922	859	6.83	015	320	5	0.11	0.07	5.162	0.156
		Y	*Glauconycteris variegata*	91	34	822	715	13.02	007	390	-4	0.14	0.08	20.449	0.013
44		Y	*Niumbaha* (*Glauconycteris*) *superba*	5	4	911	773	15.15	217	600	67	0.20	0.00	5.167	0.000
		Y	*Hypsugo anchietae*	40	15	939	928	1.17	004	400	3	0.08	0.00	7.250	0.000
		N	*Hypsugo ariel*	2	5	999	n/a	n/a	n/a	620	1	0.00	0.00	0.133	0.000
		Y	*Hypsugo musciculus*	5	5	908	792	12.78	218	540	5	0.20	0.00	8.360	0.002
		N	*Hypsugo savii*	16	12	993	983	1.01	005	500	7	0.06	0.00	0.677	0.008
45 X		Y	*Laephotis botswanae & angolensis*	30	14	933	894	4.18	024	400	1	0.03	0.00	8.927	0.000
	s	Y	*Laephotis namibensis*	7	3	994	991	0.30	009	570	-2	0.00	0.00	1.639	0.000

taxo-nomic remarks §1	SDM remarks §2	ende-mic to Africa? §3	Taxon name	trai-ning localities used	non-zero coefficients §4	trai-ning AUC	test AUC (mean) §5	AUC diff (train - mean test)	test AUC assoc. std. dev.	chosen logistic thresh-hold	deviation from highest MaxEnt threshold §6	omission rate [1 km tolerance] §7	omission rate [10 km tolerance] §7	preva-lence of final SDM §8	fraction affected by clamping §9
				[count]	[count]	[0.xxx]	[0.xxx]	[in %]	[0.xxx]	[0.xxx]	[0.xxx]	[in %]	[in %]	[in %]	[in %]
		Y	*Laephotis wintoni*	12	3	946	912	3.59	064	500	101	0.25	0.08	2.098	0.000
		Y	*Mimetillus moloneyi*	110	62	867	783	9.69	no repl.	390	2	0.18	0.09	8.576	0.156
		Y	*Neoromicia brunnea*	25	14	950	923	2.84	037	410	38	0.08	0.08	2.950	0.001
		Y	*Neoromicia capensis*	318	63	854	797	6.67	no repl.	220	-133	0.07	0.04	21.827	0.001
		Y	*Neoromicia guineensis*	103	59	929	894	3.77	no repl.	220	-71	0.08	0.03	11.457	0.186
46		Y	*Neoromicia* "cf. *helios*"	4	3	991	858	13.42	140	600	0	0.00	0.00	2.985	0.000
47		Y	*Neoromicia* "cf. *melckorum*"	21	15	961	918	4.47	039	450	5	0.14	0.00	4.215	0.000
48 X		Y	*Neoromicia nana*	434	80	784	734	6.38	no repl.	200	-251	0.01	0.00	43.135	0.061
		Y	*Neoromicia rendalli*	95	47	870	766	11.95	003	320	-60	0.09	0.00	21.741	0.020
49 X		Y	*Neoromicia somalica*	129	54	892	849	4.82	no repl.	320	-56	0.06	0.03	14.510	0.058
		Y	*Neoromicia tenuipinnis*	108	64	917	894	2.51	no repl.	200	-98	0.06	0.00	14.022	0.234
		Y	*Neoromicia zuluensis*	76	21	929	881	5.17	009	260	-39	0.09	0.03	10.069	0.000
50		Y	*Neoromicia roseveari*	2	12	999	n/a	n/a	n/a	810	-5	0.00	0.00	0.001	0.000
51 P	b	Y	*Neoromicia* sp. nov. 1	1	n/a	n/a	n/a	n/a	n/a	n/a	n/a	0.00	0.00	0.001	0.000
52 P	b	Y	*Neoromicia* sp. nov. 2	2	n/a	n/a	n/a	n/a	n/a	n/a	n/a	0.00	0.00	0.002	0.000
		Y*	*Myotis bocagii*	139	58	864	778	9.95	no repl.	350	-1	0.11	0.01	10.528	0.150
	s	N	*Myotis capaccinii*	6	8	990	983	0.71	007	680	-1	0.00	0.00	0.472	0.000
53	b	Y	*Myotis dieteri*	2	n/a	n/a	n/a	n/a	n/a	n/a	n/a	0.00	0.00	0.002	0.000
		N	*Myotis emarginatus*	10	5	985	975	1.02	016	470	1	0.00	0.00	1.010	0.009
	b	Y	*Myotis morrisi*	2	n/a	n/a	n/a	n/a	n/a	n/a	n/a	0.00	0.00	0.002	0.000
	s	N	*Myotis mystacinus*	7	3	985	978	0.71	015	590	3	0.00	0.00	1.501	0.000
54		[Y]	*Myotis* sp. B (aff. *nattereri*)	5	4	991	988	0.30	004	590	-4	0.00	0.00	0.429	0.000
		Y*	*Myotis punicus*	46	19	986	976	1.01	003	240	-141	0.00	0.00	1.788	0.005
	s	Y	*Myotis scotti*	8	3	978	916	6.34	162	490	-2	0.00	0.00	0.522	0.002

taxo-nomic remarks §1	SDM remarks §2	ende-mic to Africa? §3	Taxon name	trai-ning localities used	non-zero coefficients §4	trai-ning AUC	test AUC (mean) §5	AUC diff (train - mean test)	test AUC assoc. std. dev.	chosen logistic thresh-hold	deviation from highest MaxEnt threshold §6	omission rate [1 km tolerance] §7	omission rate [10 km tolerance] §7	preva-lence of final SDM §8	fraction affected by clamping §9
				[count]	[count]	[0.xxx]	[0.xxx]	[in %]	[0.xxx]	[0.xxx]	[0.xxx]	[in %]	[in %]	[in %]	[in %]
		Y	*Myotis tricolor*	89	35	914	900	1.53	005	330	-4	0.09	0.06	4.625	0.016
		Y	*Myotis welwitschii*	47	19	884	834	5.66	033	400	-4	0.13	0.02	9.733	0.002
		Y	*Kerivoula africana*	2	9	999	n/a	n/a	n/a	820	-4	0.00	0.00	0.004	0.000
		Y	*Kerivoula argentata*	44	18	880	850	3.41	033	290	-103	0.05	0.00	20.235	0.023
	s	Y	*Kerivoula cuprosa*	9	5	937	915	2.35	082	400	-63	0.11	0.00	8.611	0.011
		Y	*Kerivoula lanosa*	57	19	761	671	11.83	020	400	-170	0.14	0.02	21.322	0.034
		Y	*Kerivoula phalaena*	10	8	952	727	23.63	191	550	-39	0.10	0.10	6.559	0.004
		Y	*Kerivoula smithii*	16	12	938	904	3.62	055	360	-4	0.13	0.06	6.929	0.014
55 P	b	[Y]	*Kerivoula* sp. nov. Bukavu	1	n/a	n/a	n/a	n/a	n/a	n/a	n/a	0.00	0.00	0.001	0.000
	z	Y	*Eptesicus platyops*	2	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
	z	Y	*Kerivoula eriophora*	1	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
			MEAN	60	24	936	893	4.65	40	428	-13	0.087	0.028	7.067	0.187
			STANDARD DEVIATION	96	23	52	76	4.23	48	144	73	0.091	0.043	8.277	1.335
			MEDIAN	21	15	948	912	3.43	23	400	-1	0.072	0.002	5.162	0.000

Note that all values in all columns reporting AUC values must not be compared across species or in terms of their absolute value (without considering the specific examined suitability distribution; available from authors upon request). See main text and Appendix I for a discussion.

Legend:

§1   the indicated taxa were renamed and/or removed from synonymy or described as new since Simmons (2005). Numbers refer to a brief account of the taxonomic change provided just above this Table C.1.

§2   the indicated species were modelled with non-standard SDM settings (s, w), or by means of a 'buffer model' instead of a MabEnt SDM (b); in two cases their distribution could not be considered at all (z).

     s   SDM includes spatially non-independent records (i.e. spatial distance for same-habitat records of 20-40 km not enforced) due to low number of independent training localities (typically < 10, if reducing an extreme regional collection bias, also sometimes > 10).

     w   SDM built without use of freshwater proximity predictor (strong riverine sample bias evident and if included, SDM would clearly assign it too much importance, e.g. high-flying molossids captured disproportionately often when descending to drink).

     b   Not possible to build a (reasonable) SDM given low sample size; a habitat-adjusted circular area with 10 km radius around known localities was used to represent the species' realized distribution ('buffer model').

     z   Neither a (reasonable) SDM nor a 'buffer model' could be created for this species because the description of all presence localities is too imprecise (> 10 km) given the fine grain of our study.

§3   Y = species is endemic to continental Africa; Y* = endemic to continental Africa or the African islands including Madagascar; N = species' range extends beyond continental Africa or associated islands; letters in [square brackets] indicate that the assigned endemism status differs from Simmons (2005) because of the use of our updated taxonomy.

§4   model complexity expressed as the number of non-zero coefficients retained in final MaxEnt model

§5   test AUC values were computed differently depending on the number of training points used (n). For common species (n >= 100) the AUC obtained for a single 33% test data partition was deemed sufficient. For species with n = 31 to 100 the mean AUC obtained for 33% test partitions of three separate runs were taken. For species with n = 10 to 30 the mean AUC obtained for a 5-fold cross-validation was taken. For species with n = 3 to 9 the mean AUC obtained for an n-fold cross validation was taken. If an SDM was built for species with n = 2, no test AUC is available. Note that in order to facilitate a comparison of training vs. test AUCs for the entire set of species, all three SUMMARY statistics for the column "AUC training" were calculated excluding those species for which it was not possible to compute a test AUC (the differences for average and median values however were < 0.003 and for the standard deviation <0.000).

§6   as described in the main text (Section 2.5) we used a multi-criteria approach to threshold-setting when converting the continuous MaxEnt output into binary format. Here we report for each species how strongly our finally selected threshold deviated from the highest logistic

threshold statistic provided by MaxEnt. Negative values indicate that the latter was deemed too restrictive in light of expert knowledge of the species biology, the overall sampling effort in the area surrounding its presence localities, other presence localities not used for either training or testing SDMs, and the sensitivity of the MaxEnt statistics to small georeferencing errors / inaccurate locality descriptions given the fine grain employed. Positive values indicate that the highest logistic threshold was regarded as rendering a too liberal distribution prediction.

§7   as elaborated in the main text (Section 2.6), we not only calculated omission rates based on our "crisp" fine-grained 1 km^2 prediction, but also based on a fuzzier view of predicted range boundaries (i.e. expanding these for evaluation purposes by 10 km). Here we report the corresponding omission rates obtained for each SDM. Note that some of the presence points used for training could no longer plot into the predicted presence area, once we clipped all SDMs with a detailed water mask. To ensure that omission rates remained unaffected by this post-modelling step, we did not count presence points plotting outside of the predicted distribution by less than 1 km as error of omission. Summary statistics for this column are based only on those species for which SDMs were successfully produced.

§8   with the final analysis mask in place (i.e. after exclusion of water surfaces and no-data areas), the size of our study area amounted to 28,931,267 km^2.

§9   proportion of the predicted presence area were clamping of at least one predictor took place (after threshold-setting and biogeographic clipping).

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Appendix D   Defining the area for background sampling

SDM techniques such as MaxEnt contrast environmental conditions found at species presence sites with the average conditions in the entire study area. Inferred habitat preferences can hence be misleading if average conditions relate to a geographic area that has not been available to the species, because in this case habitat preference could not be articulated.

In a first step, we therefore explored whether environmental conditions in areas where African bats (as a group) have been found differ from the average conditions found across entire continental Africa, which would justify the use of a target group background (Ponder et al., 2001; Phillips et al., 2009).

Given substantial amounts of multicollinearity among the 18 predictor variables, we first removed redundancy in environmental space by means of a Principal Component Analysis (PCA). The PCA was performed in ArcGIS™ Desktop 9.1 (ESRI, 1999) after rescaling all predictors to values [0-1000]. For each of the eight principal components featuring the highest eigenvalues (which together explained 98.8% of total variance) we then carried out the comparison.

As shown in Fig. D.1, we found that habitat conditions at known bat sampling sites (top row associated with each PC) differed strongly from the mean conditions across continental Africa (bottom row associated with each PC). The difference was strongest along the first PC, which contrasted the environment characterizing the Sahara desert with conditions in more vegetated and more stable regions in terms of temperature. This result confirmed the need to use a TG background.

For reasons given in the main text (Section 2.4), we chose to use a kernel density estimate around all documented bat localities to represent the effectively sampled area. We used the Fixed Kernel Density Estimator in Hawth's Tools (available: http://www.spatialecology.com/htools/kde.php; accessed 2010-07-15) for ArcGIS™ Desktop 9.1 (ESRI, 1999). As we performed all MaxEnt SDMs using predictors in geographic projection (to avoid resampling original cell values), we produced the kernel density estimate polygon in an equal area projection to control for latitude-invoked areal distortions. We chose a fixed kernel type (as probability of sampling does not extend infinitely from reference point), a quartic kernel shape (deemed an appropriate decay function in sampling probability from reference point; choice not found to influence the outcome essentially), a scaling factor of 1,000,000 (to ensure smooth decay curves), a raster cell size of 5 (a finer one was impossible due to computer memory limitations), and a single parameter smoothing factor of 50. As final delineation we selected the 95 percent volume contour, because this allowed for a markedly reduced buffer size around sampling points without excluding even the most isolated one. The resulting polygon file was projected back to our default WGS84 geographic projection and used to clip all predictors.

Fig. D.1 shows that the environmental conditions contained in the resulting background extent (middle row) closely resemble those found at documented bat localities (top row). Hence the training group background defined by the kernel density estimate sufficiently mirrored and thus cancelled the environmental bias contained in the (exact) bat presence localities, relative to entire continental Africa.
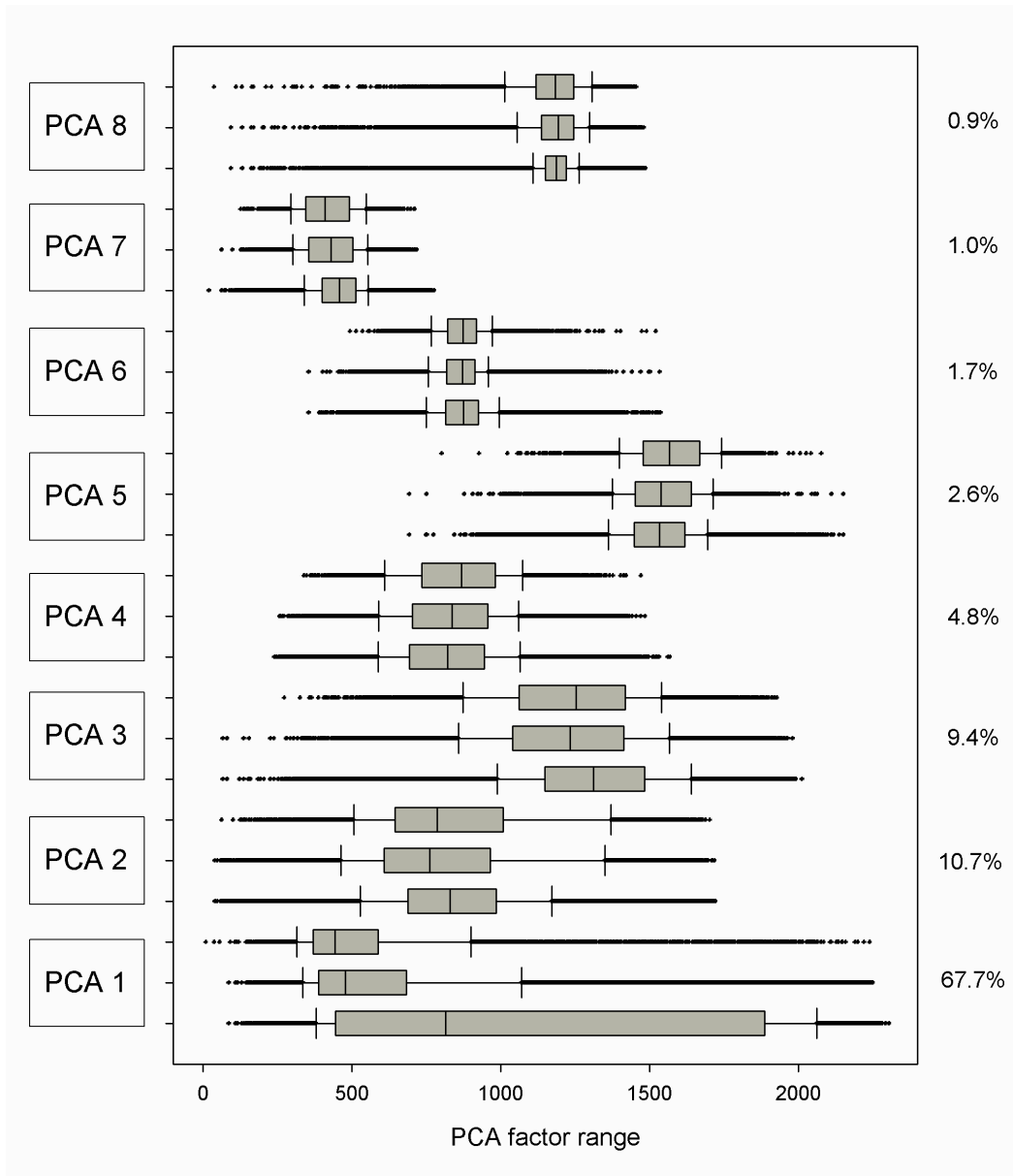
Figure D.1.   Environmental space of continental Africa as quantified by the first eight principal components (PC) extracted from the entire set of predictor variables (excluding freshwater proximity, as our interest was on purely local habitat conditions). Together these eight PCs account for 98.8% of environmental variability. Individual PC loadings are shown on the right Y axis. For each PC, three box plots are shown: the full distribution of values across continental Africa (bottom row), the distribution of values associated with documented bat presence localities only (top row), and the distribution of values as captured by the kernel density estimate created to delineate the background used for MaxEnt modelling (middle row).

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Appendix E   Sources and pre-processing of environmental predictors

The final set of 18 environmental predictors described below was selected to represent a comprehensive and balanced set of factors known to determine habitat suitability of African bats in general.

Climate

All 10 climate variables of the present study are based on the WorldClim 1.4 dataset (available http://www.worldclim.org/current; accessed 2007-07-25). This dataset features a grain of 30 arc seconds (ca. 1 km^2) and was created by topographically sensitive interpolation of average monthly climate values measured by a (rather irregular) global network of weather stations primarily over the time period 1960 – 1990 (Hijmans et al., 2005). Details on how we produced the predictors are given in the main text (Section 2.3). All computations were carried out in ArcGIS™ 9.1 (ESRI, 2005). Precipitation variables were retained in mm. Temperature values were multiplied by 10 prior to stacking the 12 monthly average grids to reduce loss of precision when converting from continuous to integer data format.

Topography

The two terrain ruggedness predictors were generated from SRTM30 V2 data (available http://dds.cr.usgs.gov/srtm/version2_1/SRTM30; accessed 2007-08-06). The majority of these data was acquired in 2000 and features a native spatial resolution of 1 arc second subsequently coarsened to a 30 arc seconds grain (Farr et al., 2007). While datasets with higher resolution exist for Africa (USGS JPL, 2005), the selected one matches best the grain and generality of the other chosen predictor variables which characterize vegetation, hydrology and land cover. All computations were carried out in ArcGIS™ 9.1 (ESRI, 2005). Note that some artefacts in the SRTM30 (and SRTM90) datasets affecting areas in the Sahara have only recently been removed (Danielson and Gesch, 2011). This improvement could not be considered here. Predicted ranges of about 17 species (~7% of all considered) are affected by this data issue, but in each case only a marginal part of the range is concerned.

Hydrology

The single freshwater proximity predictor was generated as follows. We first removed all features contained in the HydroSHEDS river network dataset (WWF WCP, 2007) that were situated within "desert-like" or "hard saltpan" classes 22-25 of the GLC2000 dataset (Mayaux et al., 2004). The HydroSHEDS data are available at http://hydrosheds.cr.usgs.gov/index.php (accessed 2011-04-28) and the GLC2000 data at available http://forobs.jrc.ec.europa.eu/products/glc2000/glc2000.php (accessed 2007-04-01). Next we combined the result with the rivers and lakes shapefiles contained in the SWBD dataset (USGS EROS Center, 2002), which is available at https://lta.cr.usgs.gov/srtm_water_body_dataset (accessed 2011-04-28). HydroSHEDS features by definition might not carry water, and can be assumed to represent dry streams in nearly all cases if situated in desert environments. SWBD features located in such "desert-like" GLC2000 classes were accepted, however, not only because their larger size suggests the permanent presence of water but also as the SWBD dataset was compiled to represent true water surfaces. SWBD features identified as "hard

saltpan" in GLC2000 on the other hand were not admitted as it can be assumed that they contain very little freshwater only - if any. Next, 20 buffer polygons were created around the resulting freshwater network, up to a distance of 10 km using an interval of 0.5 km. Finally, this distance map was converted into a raster grid matching the grain of the other predictors. Cells containing freshwater received the value 20; neighbouring cells received an accordingly lower value. All cells located 10 km or further from freshwater cells obtained the value 0. This sill was established assuming that the resource value of freshwater beyond this distance is close to zero for the majority of studied species.

Vegetation

As a continuous measure of difference in vegetation structure (Wiens, 2002) we derived three vegetation variables from the MODIS Vegetation Continuous Fields dataset (MOD44B) Collection 3 (Hansen et al., 2003b): tree, herb cover and bare ground (available: http://glcf.umd.edu/data/vcf [link to Collection 3]; accessed 2007-08-15). The data were acquired between November 2000 and November 2001 and are available at 500 m spatial resolution. The data are based on monthly composites of the MOD09A1 Surface Reflectance 8 day product (Hansen et al., 2003a). In light of some presumed minor artefacts (somewhat speckled appearance in cloudy forest regions, reduced in later version of this product), we smoothed these data by extracting for each cell the mean within a 4x4 rectangular neighbourhood using the Focal Statistics tool in the Spatial Analyst extension of ArcView™ 3.2 (ESRI, 1999). Finally all three variables were resampled to 30 arc second resolution to match the grain of our coarser predictors. Note that the employed Collection 3 is no longer retrievable online and has been replaced by MOD44B Collection 5, which however does not contain the herb and bare ground layers yet (available https://lpdaac.usgs.gov/products/modis_products_table/mod44b; accessed 2013-11-23). We recognize that the remotely sensed QSCAT data recently made available could prove a valuable vegetation structure parameter for habitat suitability modelling (Buermann et al., 2008), but we were unable to consider this dataset for the present study.

Land cover

Finally, to allow niche inference with respect to vegetation density (regardless of structure) as well as to different less-vegetated surfaces, we included two land cover variables taken from the SPOT-VEGETATION composite image available for download at the JRC website (http://forobs.jrc.ec.europa.eu/products/vgt_mosaic_africa/africa_spot_vgt.php; accessed 2007-08-16). This imagery is based on data collected daily throughout the year 2000 at 30 arc-seconds spatial resolution, has been corrected for cloud and haze effects and subjected to a local contrast stretch to enhance certain features (Mayaux et al., 2004). We extracted both band 2 (green) and band 3 (red) from the .tif image, which essentially correspond to the annual average of spectral response values in the Near-Infrared channel (NIR) (0.78–0.89 µm), and the Red channel (0.61–0.68 µm) of the VEGETATION sensor on board SPOT 4, respectively (pers. comm. P. Mayaux 2008-02-17).

To train models with original predictor data, we retained their native projection (geographic/WGS 84) when building SDMs, and resampled all predictors to an equal area projection only afterwards when casting projections across entire Africa. Not using an equal area grid could have translated into spatial

bias, as cells in subtropical regions were likely to contain more training data than cells closer to the equator. We controlled for this effect by (a) enforcing a minimum distance among occurrence records much larger than 1 km, and (b) using an equal area projection when computing the kernel density estimate (see Appendix D) used to delimit the background data sampled by MaxEnt.

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Appendix F   Assessment of multicollinearity among environmental predictors

To assess multicollinearity of candidate predictor variables, we computed pairwise Pearson correlation coefficients (in geographic projection) using BioMapper 3.2 (Hirzel et al., 2004) available for download at http://www2.unil.ch/biomapper/products.html (accessed 2008-01-29). Only those variables ultimately selected are shown in the table below. See the main text (Section 2.3) for a discussion.

Table F.1.   Pairwise Pearson correlation coefficients for all 18 environmental predictors at continental extent.

	land_specnir	land_specred	land_vcfbare	land_vcfherb	land_vcftree	hydr_prox	topo_v9x9	topo_c3x3	clim_tnstd	clim_tnmin	clim_tnmax	clim_txstd	clim_txmin	clim_txmax	clim_pstd	clim_pmin	clim_pmax	clim_psum
clim_psum	-0.62	-0.77	-0.83	0.54	0.83	0.58	0.27	0.30	-0.78	0.55	-0.38	-0.72	0.37	-0.57	0.86	0.56	0.92	1.00
clim_pmax	-0.61	-0.71	-0.84	0.66	0.66	0.59	0.22	0.24	-0.74	0.55	-0.31	-0.73	0.47	-0.47	0.98	0.32	1.00	
clim_pmin	-0.21	-0.39	-0.33	0.01	0.67	0.25	0.12	0.14	-0.44	0.32	-0.22	-0.34	0.10	-0.36	0.14	1.00		
clim_pstd	-0.62	-0.69	-0.83	0.70	0.57	0.57	0.21	0.23	-0.67	0.49	-0.31	-0.70	0.45	-0.44	1.00			
clim_txmax	0.63	0.68	0.63	-0.49	-0.50	-0.48	-0.49	-0.46	0.58	-0.03	0.88	0.64	0.16	1.00				
clim_txmin	-0.21	-0.23	-0.40	0.35	0.27	0.24	-0.25	-0.22	-0.60	0.84	0.33	-0.66	1.00					
clim_txstd	0.65	0.71	0.80	-0.66	-0.58	-0.56	-0.18	-0.18	0.91	-0.67	0.42	1.00						
clim_tnmax	0.55	0.55	0.49	-0.43	-0.31	-0.38	-0.47	-0.44	0.36	0.28	1.00							
clim_tnmin	-0.25	-0.36	-0.46	0.30	0.46	0.31	-0.08	-0.05	-0.79	1.00								
clim_tnstd	0.60	0.70	0.76	-0.57	-0.64	-0.55	-0.23	-0.24	1.00									
topo_c3x3	-0.33	-0.37	-0.24	0.15	0.27	0.28	0.92	1.00										
topo_v9x9	-0.36	-0.37	-0.23	0.16	0.23	0.28	1.00											
hydr_prox	-0.59	-0.64	-0.66	0.58	0.43	1.00												
land_vcftree	-0.46	-0.67	-0.64	0.20	1.00													
land_vcfherb	-0.72	-0.65	-0.88	1.00														
land_vcfbare	0.78	0.84	1.00															
land_specred	0.94	1.00																
land_specnir	1.00																	

Reference:

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Appendix G   Selection of presence localities for model training

The basic principles and procedures have been outlined already in the main text. Here we provide more details on the steps taken to simultaneously overcome the following two challenges:

(1) use only species occurrence data with a high level of spatiotemporal quality and taxonomic reliability while retaining a sufficient sample size, and
(2) achieve statistical independence among presence records while retaining critical information on the full width of a species' ecological niche.

At least for rare species (i.e. when sample size is small) these two aims become intimately related, and an optimal solution involves some trade-off between the two, in addition to the trade-off requirements inherent to each aim.

Aim (1) Addressing the trade-off between data quality and sample size

As stated in the main text (Section 2.2), for model training we only used records featuring a spatial uncertainty lower than 5 km and a collection date more recent than 1960 – but we made a few exceptions: in regions characterized by rather stable land cover types, such as deserts or current old growth tropical forest, we tolerated a spatiotemporal mismatch larger than 5 km and a collection date before 1960. However, we critically examined all records plotting to densely populated areas (> 5000 people / km^2 as per the LandScan™ 2006 dataset (ORNL, 2006) even if georeferencing accuracy was better than 5 km. Records of species known to use urban habitat were always accepted but those of other species only if a similar human presence at the time of collection could be assumed owing to a fairly recent collection date or the particular location (e.g. a mosque in downtown Cairo).

If following the procedure outlined above and in the main text (Section 2.2) resulted in less than 15 records for a given species, we generated a set of alternative SDMs, now incorporating additional records that were either spatially somewhat dependent (i.e. with a minimum distance to each other of less than ~30 km; see spatial filter details outlined below), or were collected before 1960 and/or were found to carry a spatial uncertainty larger than 5 km.

We added candidate records iteratively in sets of similar data quality levels. The aim here was to trade a still acceptable amount of data quality for an increase in sample size, thus improving model robustness in exchange for some model accuracy.

This iterative approach of tentatively including records of lower spatiotemporal quality was also applied for some species with more than 15 reliable training points available if the initial SDM failed to predict the entire region surrounding geographical outliers that we regarded as correctly identified but excluded from model building due to their old age or spatial uncertainty above 5 km. In such cases, the aim was to explore whether these records were truly inadequate data (e.g. possibly misidentified or sampled prior to recent drastic land cover change), or constituted somewhat old/inaccurate but valuable material from

undersampled environmental space, in which case their inclusion could have arguably improved the overall quality of the SDM.

In summary, we proceeded as follows:

(a) If for a given species, 15 or more records of top quality (as defined above) were left after application of the spatial filter, and the prediction covered at least the general area surrounding all taxonomically reliable records (i.e. seemed plausible), we accepted this model as the final one. This was the most common case.

(b) If for a given species, less than 15 records of top quality were left after application of the spatial filter, and one of the additionally produced models using data of somewhat lesser spatiotemporal quality (dated 1930-1960 or spatial uncertainty 5-10 km) yielded a clearly more plausible prediction, we chose the latter over the former.

(c) If for a given species, less than 15 records were left after application of the spatial filter and after using additional data of somewhat lesser spatiotemporal quality (as described above) – we no longer enforced the spatial filter.

(d) If for a given species, less than 15 records were left despite the inclusion of somewhat lesser spatiotemporal quality (as described above) and not enforcing the spatial filter, we accepted the model as the best achievable, as long as its prediction was not completely implausible as judged by expert knowledge; if the latter was the case however, we did not produce any SDM for this species.

Records discarded during the above selection process due to insufficient spatial accuracy or old age were later used as fuzzy context data when assessing the plausibility of results, when choosing a threshold to obtain binary predictions, and when cropping habitat patches predicted as suitable but located implausibly far from known occurrences. None of these records were used in the statistical evaluation of model performances.

We did not require SDMs to use a certain minimum number of training localities. Here we provide further reasons complementing those laid out in the main text (Section 2.2). We acknowledge that from a statistical perspective, models using less presence localities than predictors tend to be overparameterized (Guisan and Thuiller, 2005), which may be the main reason why many MaxEnt studies do not use less than about 15 localities (Yackulic et al., 2013, Fig. 1). However, MaxEnt reduces the number of predictors effectively used if trained with few localities only, and in addition, we raised the regularization parameter above default. These two measures help avoid model overfitting (Phillips and Dudík, 2008). Our results confirm this effect as SDMs built with < 10 localities were only moderately overparameterized and about as robust as models built with more records (see Fig. G.1). The obvious exceptions are SDMs trained with two or three localities only – but for these, we manually constrained predictions to the immediate geographic vicinity. We therefore conclude that MaxEnt SDMs built with only three to nine presence records performed reasonably well, at least in terms of model complexity and robustness, despite the potentially high number of predictors used.
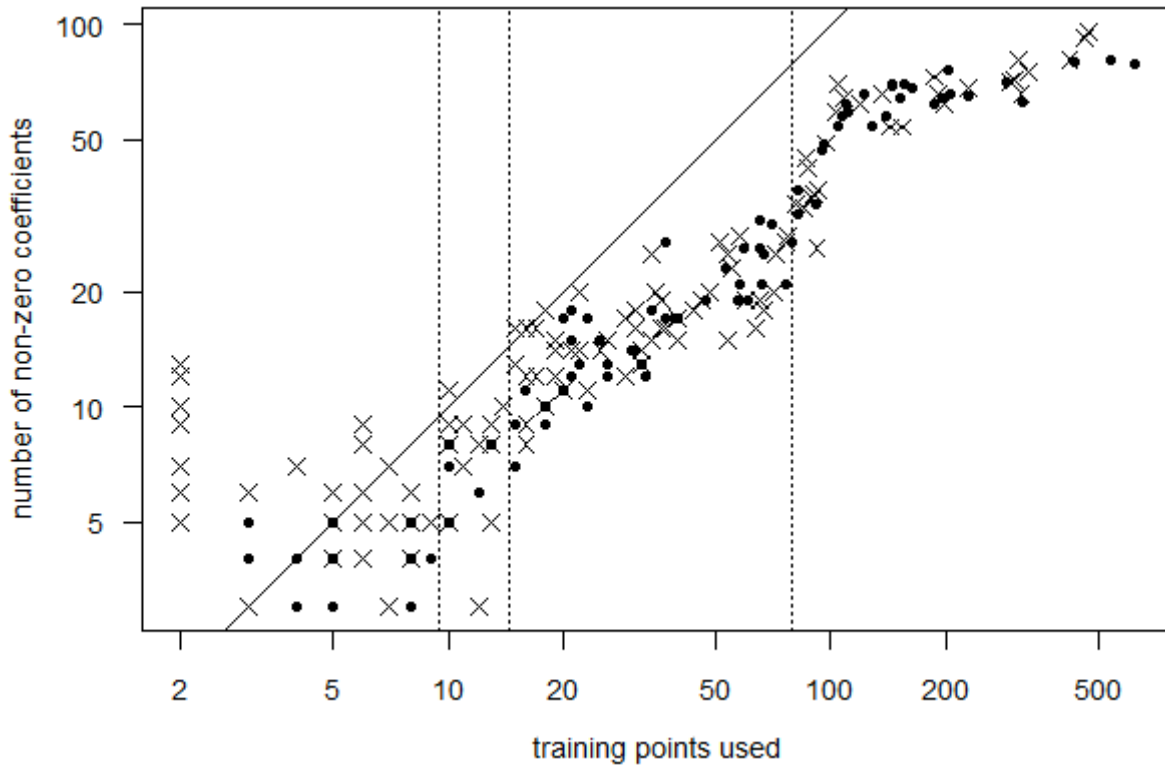
Figure G.1.   Model complexity (represented by the number of features with non-zero coefficients retained in final MaxEnt SDMs) as a function of the number of training localities used. Only about 10% (23 of 227) of the produced SDMs plot above the black 1:1 line and thus could be considered somewhat overfitted (Guisan and Thuiller, 2005). Filled circles represent less robust SDMs, as the difference in their AUC values (training minus test) was larger than the median (4.2%) (Warren and Seifert, 2011). X symbols represent the remaining, i.e. arguably more robust (but possibly overfitted) SDMs. Dashed vertical lines separate the ranges of training points treated equally by default in MaxEnt in terms of admitted feature types: 2-9 linear only, 10-14 plus quadratic, 15-79 plus hinge, >= 80 plus threshold and product features (Phillips and Dudík, 2008).

Further, overfitted MaxEnt SDM for rare species may still be useful if the study aim is restricted to reasonable predictions regarding the immediate vicinity around known localities (as opposed to transferring predictions into vastly different space). One such example is the study by Jackson and Robertson (2011) that employed MaxEnt with only four occurrence points to predict the distribution of a rare South African small mammal and successfully discovered two additional localities within a distance of about 30 km. In a similar context, Ortega Huerta (2007) created MaxEnt models of Mexican birds and mammals using only two occurrences. The relative usefulness of such SDMs could be related to the fact

that species known from a few localities only also tend to be habitat specialists, and it is generally easier to infer the ecological niche of a specialist than a generalist.

Lastly, we limited the potential impact of models built with very few presences on overall richness patterns by choosing a higher threshold during conversion to a binary map and / or by applying a narrower biogeographic clip around documented occurrence localities. Against this background we argue that dispensing with the minimum presence number requirement was acceptable.

Aim (2) Addressing the trade-off between independence of records and full gradient sampling

Spatial autocorrelation inherent to the spatial dynamics of a species' local population can result in statistically non-independent presence, which may lead to overfitted SDMs (Austin, 2002; Dormann, 2007). As the available presence records were not obtained via a sampling scheme that took into account such species-related spatial autocorrelation, we employed a spatial filter and thus retained only one presence point within a specific distance.

As the commonly employed rectangular grid would involve some directional bias (accepted distances being larger in diagonal directions), we used a hexagonal grid instead (Schipper et al., 2008). The grid was created in our custom equal area projection using the Repeating Shapes tool for ArcGIS 9.x (ESRI, 2005) (available http://www.jennessent.com/arcgis/repeat_shapes.htm; accessed 2011-05-12), choosing a hexagon diameter of 40 km, which corresponds to about 20 km edge length depending on cell latitude. This cell size is likely larger than the spatial dynamics of local population of most – although certainly not all – bat species. The specific local (spatial) sampling scheme employed was hence rendered irrelevant after application of this filter. A single hexagonal grid however would have retained spatially close records situated near the border of a cell. We therefore created two replicates of this grid, shifting the cell centre onto the two northernmost hexagon corners, respectively, using Vector Rotation & Shifting in Hawth's Tools (available http://www.spatialecology.com/htools/vectorrotation.php; accessed 2011-05-12). The consecutive application of these three hexagonal spatial filters ensured a minimum distance among admitted presence points of about 20 km.

Strictly enforcing this spatial filter could have resulted in the loss of valuable information about the full width of a species' niche in situations where known presence localities are few and locally clustered but distributed across a long environmental gradient in environmental space (Hirzel and Guisan, 2002). We therefore admitted multiple presence records from within a single hexagonal cell if they plotted into "very different" habitat (see Fig. G.2).
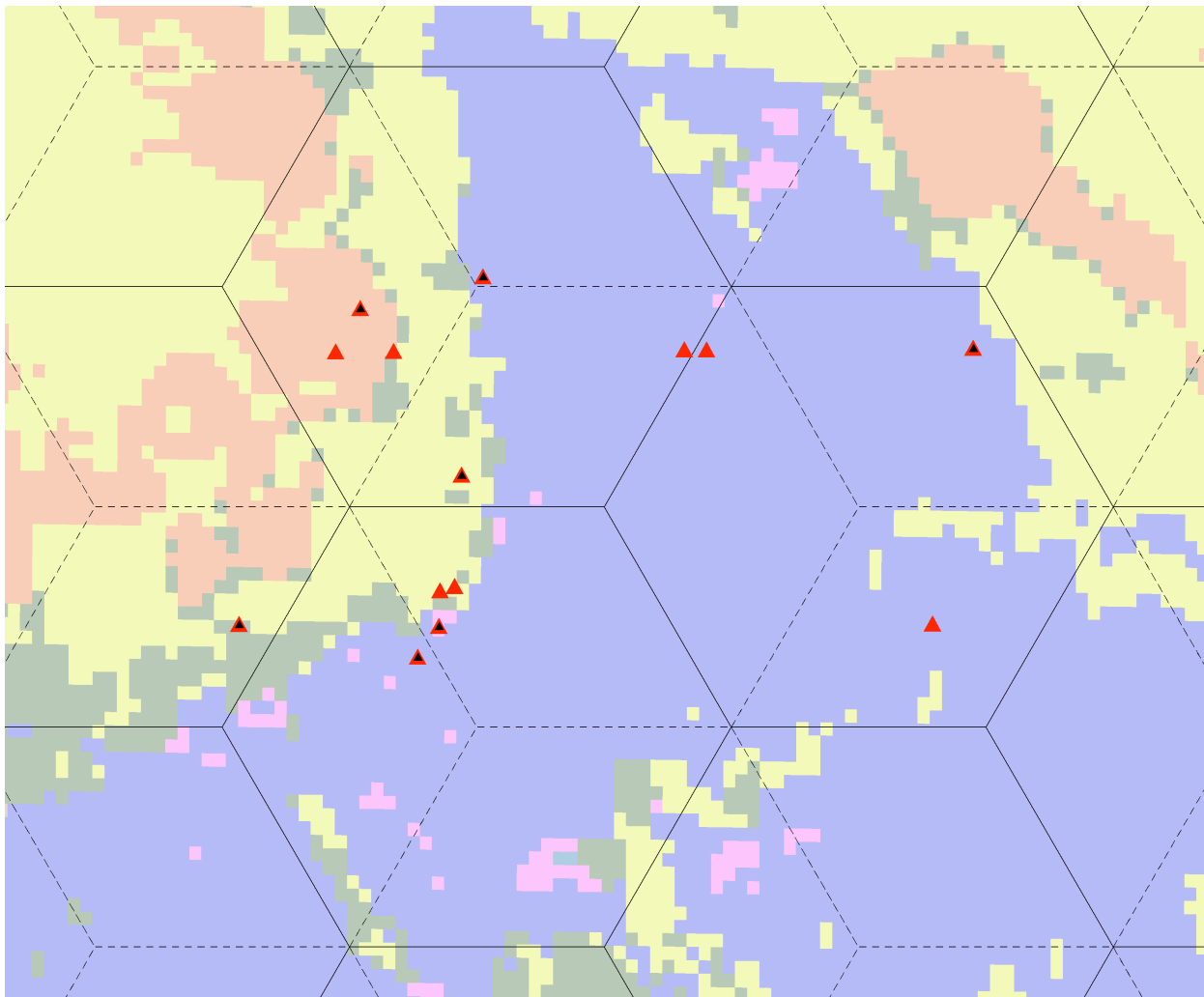
Figure G.2.   Illustration of the habitat-specific spatial filter. The differently coloured background areas represent different habitat classes. For clarity, only two of the three hexagonal grids employed are shown here (as solid and dashed lines, respectively). Red triangles denote available presence data (assessed as being of sufficient quality) for a particular bat species. As a result of the filter, only one record from each habitat class within each hexagonal cell was retained (red triangles with a black core). Only this set of records was used to train the MaxEnt model.

We quantified "very different habitat" by means of a custom-built categorical map (see Fig. G.3.); we did not use general purpose land cover maps as their categories may not be relevant to African bats. Instead, we relied on the environmental variables which we had already identified as potentially relevant predictors of bat occurrence. We excluded however the freshwater proximity predictor as the aim was to quantify only local habitat. The remaining 17 predictor variables were rescaled to values [0-1000] and subjected to a principal component analysis (PCA) using ArcGIS™ Desktop 9.1 (ESRI, 2005). We did not normalize each predictor because some exhibited extremely skewed or bimodal distributions which

could not be transformed sufficiently, and it is neither common in this context (see e.g. Metzger et al., 2013) nor is it a strict requirement for PCA (Jolliffe, 2002; Reimann et al., 2008).

Only the top eight eigenvectors of this PCA were used in further processing (cumulative explained variance 98.8%; individual contribution at least 0.9%), as the remaining eigenvectors displayed a very low signal-to-noise ratio (visual analysis). Using the ISOCLUSTER algorithm (Ball and Hall, 1965) as implemented in ERDAS IMAGINE® 9.1 (Leica Geosystems, 2003) we then performed an unsupervised classification varying the number of classes from 40 to 100. To obtain as robust class boundaries as possible we selected the map with the highest class separability in terms of two measures (Bouguessa et al., 2006). We chose the map featuring 68 classes as it ranked best in terms of Jeffreys-Matusita distance with a minimum separability between class means of 1213, and second-best in terms of the Transformed Divergence index with a minimum separability between class means of 1570 (see Swain and Davis, 1978) for a description of both indices).
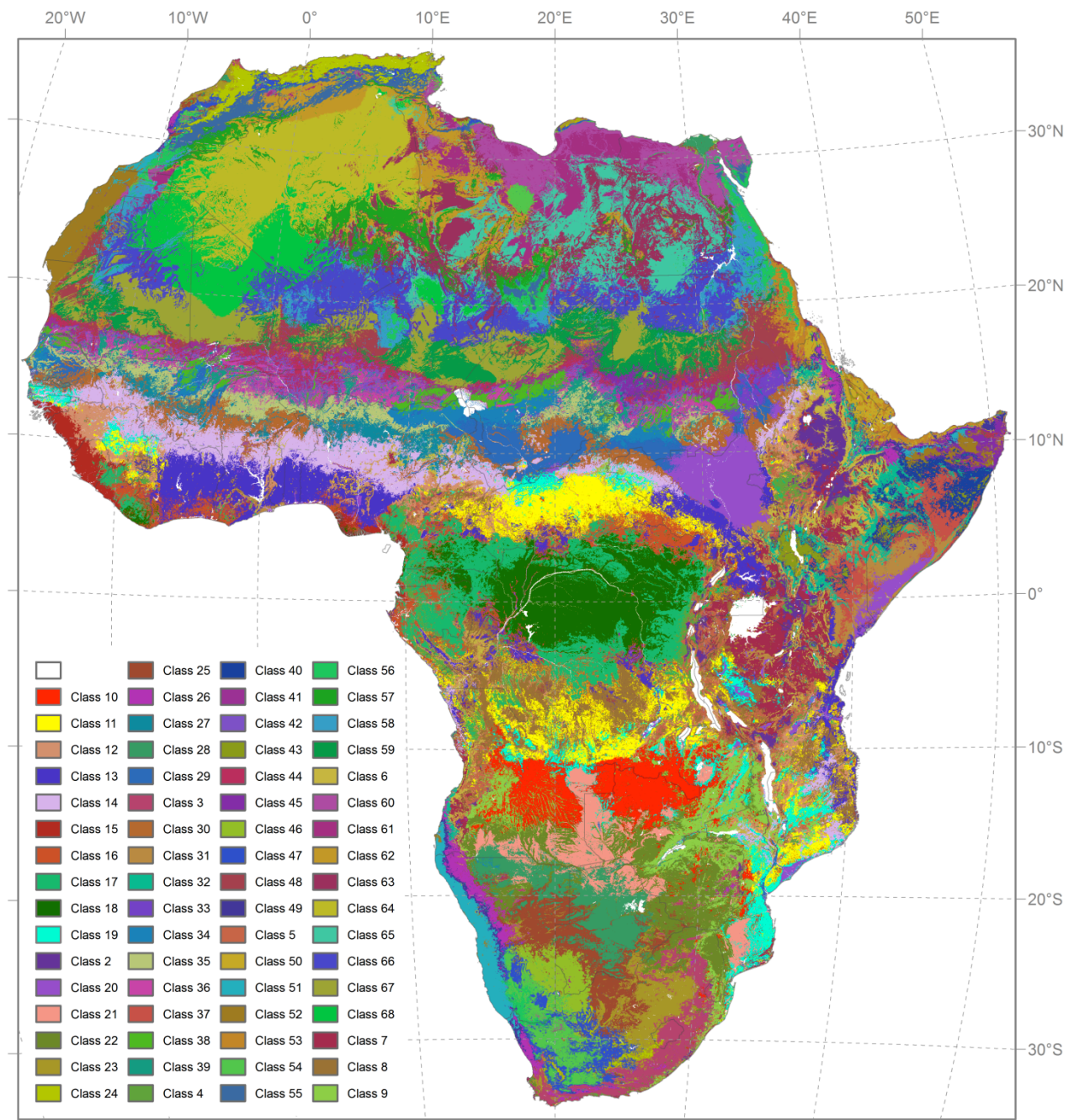
Figure G.3.   Classified habitat map (68 classes) derived from the first eight principal components based on the set of our predictor variables (excluding freshwater proximity). See text above for details.

The map was also used to evaluate the plausibility of some surprising richness coldspots; these coincide largely with the classes 10 (bright red), 11 (bright yellow) and 19 (turquoise). See Section 4.3 of the main text (and Appendix R) for results and an interpretation of the findings.

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Appendix H   Setting of binary thresholds

As stated in the main text (Section 2.5), there is still considerable debate about which criteria to use when selecting a specific threshold to convert continuous SDM predictions to binary presence-absence maps (Wilson et al., 2005; Allouche et al., 2006; Freeman and Moisen, 2008).

The perhaps most important reason here is that most statistically defined thresholds, including those examined by the commonly cited study of Liu et al. (2005) – such as equal sensitivity and specificity – are based on the confusion matrix whose components respond to changes in prevalence, irrespective of model fit (Lobo et al., 2008). The prevalence of a species within the study area however is usually not known; in fact this may be the very reason to produce the SDM.

Further, most of these statistics (implicitly) assume equal weight of omission and commission error, whereas presence-only SDMs are often developed in an application context that considers omission errors more important, also because commission error remains ultimately unknown in case of mobile species. This certainly applies to our study too.

Irrespective of the study purpose, presence-only SDMs also tend to penalize omission error more than commission error because background does not equal true absence data – typically some 'hidden' presences are contained therein (Smith, 2013).

Finally, prevalence-independent thresholds such as '10 percentile training presence' are not without caveats either: they are even more sensitive to positional error in occurrence data. In studies using a fine grain – such as the present one – a percentile threshold can easily result in too liberal predictions attempting to cover presence localities slightly misplaced into unsuitable habitat. Reversely, this threshold may also lead to overly restrictive predictions in fine-grained studies if a number of localities representing marginally suitable habitat are incorrectly georeferenced to nearby sites predicted as more suitable.

In conclusion, choosing an adequate threshold eventually depends on which relative weights are assigned to omission and commission errors, on the accuracy of employed presence data relative to the chosen spatial grain, and on typically unknown characteristics of the studied species such as true prevalence. Pending further research, we therefore consider the use of a combination of statistical metrics, auxiliary data and expert knowledge the most promising approach to threshold-setting.

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Appendix I   Evaluation of individual SDMs

Measuring model discrimination using the AUC

The AUC in the ROC plot (Fielding and Bell, 1997) is currently the most frequently used statistic to evaluate the performance of SDMs (Franklin, 2009). However, as stated in the main text, for several reasons this measure is of very limited use when absence data are lacking – but also due to some inherent properties.

Most limitations are ultimately a consequence of its rank-based nature, because unless the set of sample points on which the AUC is calculated is fully representative of the examined suitability distribution (i.e. the SDM), the AUC will be biased towards rare species relative to the study area (Jiménez-Valverde et al., 2013). This means a model representing a wide ranging species can have a low AUC value and yet discriminate excellently (Lobo et al., 2008), for in such cases the maximum AUC value attainable is less than 1 (Wiley et al., 2003). Delicately, this also means that the value of 0.5 will no longer represent discrimination better than chance (Jiménez-Valverde, 2012). The AUC measure is also not independent of model calibration success, unless in the aforementioned – very rare –situation (Jiménez-Valverde et al., 2013). Another consequence is that AUC increases in response to the addition of features in MaxEnt (Raes and Steege, 2007), which makes it sensitive to sample size unless MaxEnt default settings are altered. The AUC value hence also partially reflects model complexity (Warren and Seifert, 2011; Radosavljevic and Anderson, 2014; Boria et al., 2014).

The use of AUC to measure model discrimination success is also questionable for reasons unrelated to its ranked-based nature, if used with background data instead of true absences. For sampling the former nearly always yields a fraction of suitable but unoccupied habitat, which causes AUC values to systematically overestimate model discrimination ability (Smith, 2013). The AUC should also not be used to evaluate models aimed to estimate the potential rather than realized distribution of a species, because it weights both omission and commission error equally; it is in the nature of predicting a species potential distribution however, that suitable areas contain relatively few presences (Peterson et al., 2008; Jiménez-Valverde, 2012). As an aside, this is also the reason that we did not use any threshold-based discrimination measures such as TSS (Allouche et al., 2006): while weights could easily be added to the TSS statistics, we simply do not have sufficient knowledge of the true prevalence of most species to establish appropriate weights.

Against this background, we did not use AUC values as model selection criteria (see Section 2.5 of the main text) at any point when selecting between different SDM variants for a single species.

Given the above difficulties with evaluating the discrimination success of presence-only models, we also did not assess whether AUC values were significantly above those of a null model (see e.g.Raes and Steege, 2007; Merckx et al., 2011). Instead, we focused on assessing model calibration and overall model plausibility (realism) using omission errors and expert knowledge as described in the main text.

Generation of test SDMs

Model performance and uncertainty should ideally be evaluated using truly independent data. Such data however are costly to obtain via new field work for studies with continental extent. As is common in large-extent SDM studies, we therefore evaluated model performance using cross-validation and data resampling with randomly withheld test partitions.

For efficiency reasons we generated different types of test data depending on how many training localities (of acceptable quality) were available for a species. For common species (n => 100) we regarded a single 33% test data partition sufficient. For species with n = 31 to 100 we used the mean of three 33% test partitions. For species with n = 10 to 30 we performed a 5-fold cross-validation. For species with n = 3 to 9, we carried out an n-fold cross-validation. For SDMs built for species with n = 2, no replicate SDM i.e. no test data could be produced.

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Appendix J   Sensitivity of omission rates to range boundary precision
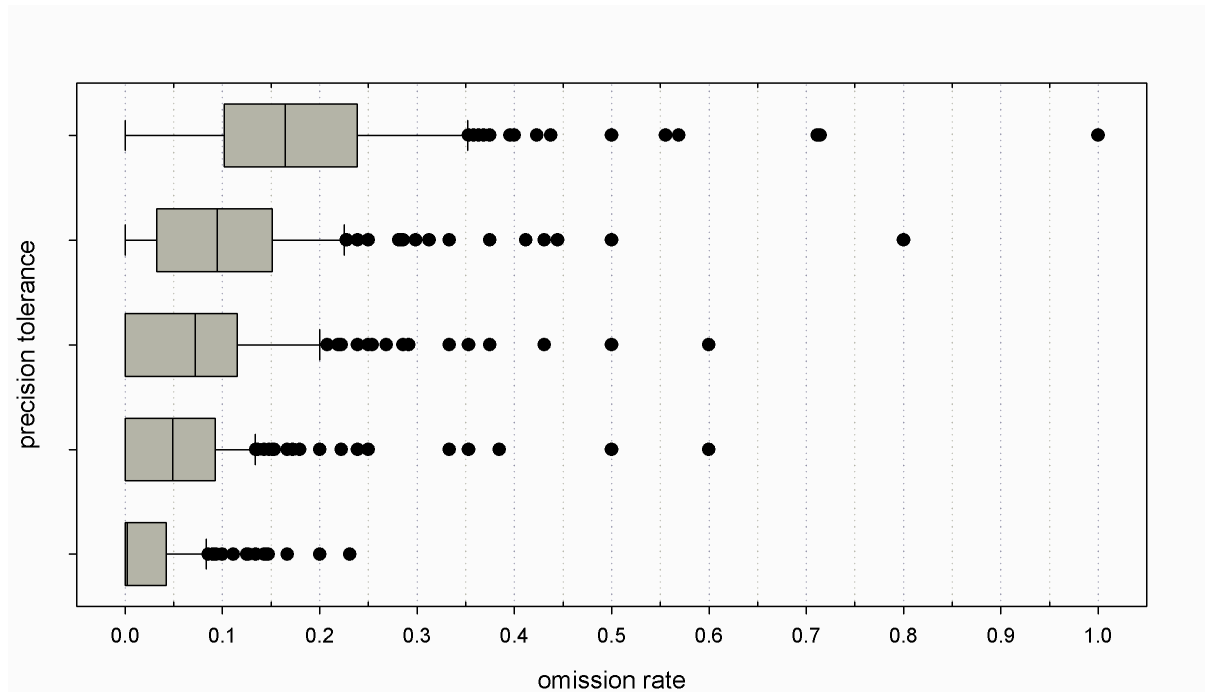
Figure J.1.   Omission rates calculated for each final SDM (n = 226) based on the full set of training localities for five different levels of potential positional error: 0 km (top row), 0.5 km, 1 km, 2 km and 10 km (bottom row). Note the substantial improvement within the first 1 km (between top and centre row). The main reason is that an improved water mask was imposed on final SDMs, which caused some localities (near rivers, lakes, and coast) to not be covered by the grid anymore. We therefore regard the 1 km level (the centre row above) as the most appropriate assessment of omission rate. However, given the mobility of bats, the 10 km tolerance level (bottom row) may also be informative when evaluating model calibration. Some SDMs still carry noticeable omission error at the 1 km^2 grain, but a more liberal threshold would have resulted in almost certain range overprediction as judged by expert opinion.

Appendix K   Reduction in richness due to biogeographic clips
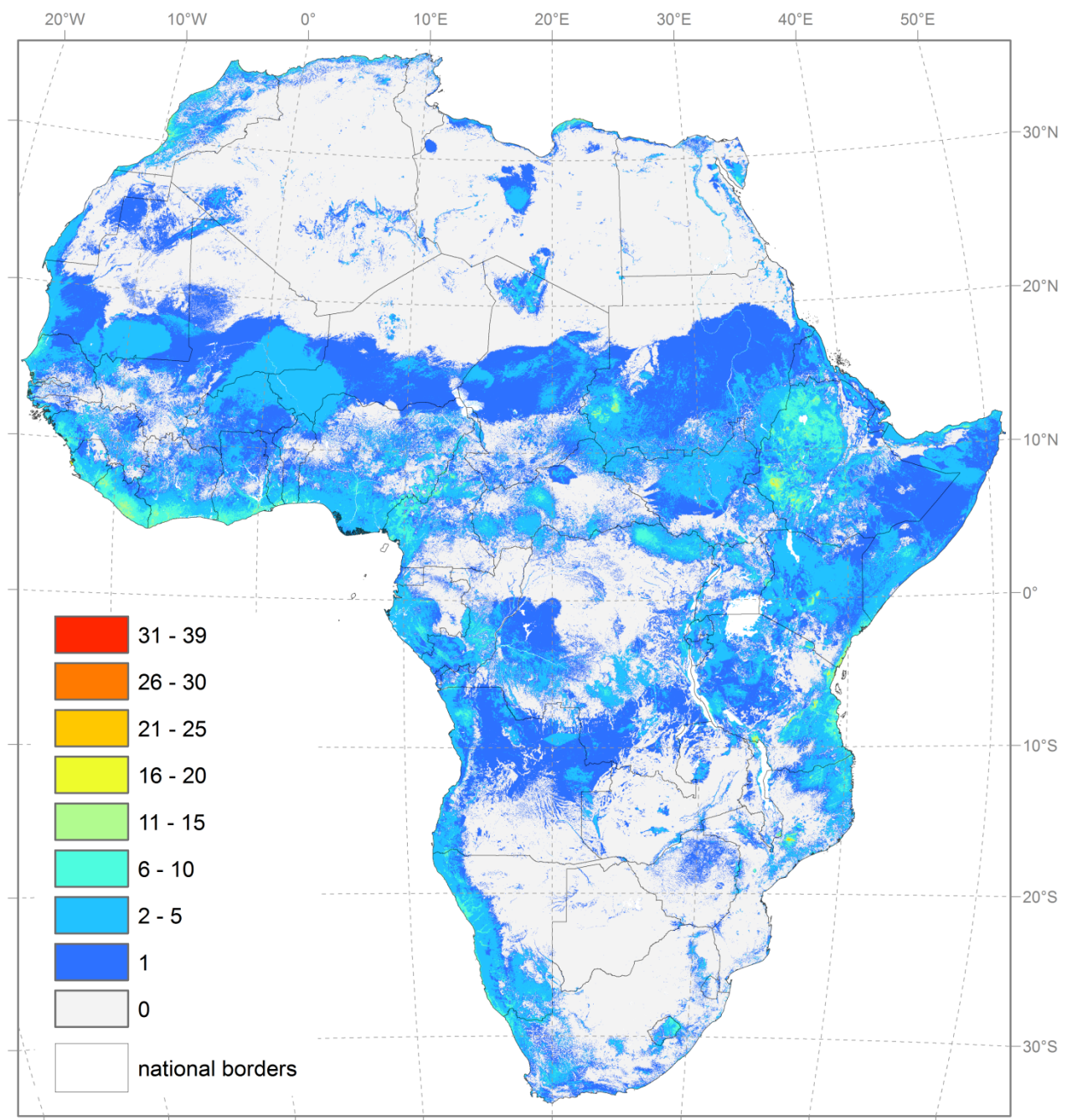
Figure K.1.   Reduction in predicted species richness (total = 226 SDMs) due to applied biogeographic clips. Not surprisingly, this reduction was strongest for (a) cells in areas with insular character like isolated mountains, e.g. the Mabu Mts in central Mozambique (reduced from 56 to 27 spp.) but also the Tibesti Mts in northern Chad (reduced from 15 to 4 spp.), and (b) for areas with species-rich habitat that is also found in the opposite hemisphere, see e.g. the central coast of Morocco (reduced from 40 to 8 spp.) or north-eastern Libya (reduced from 48 to 9 spp.). For most of the study area however, the effect

on predicted richness was rather small: a reduction by more than three species occurred only in about 8% of the total study area.

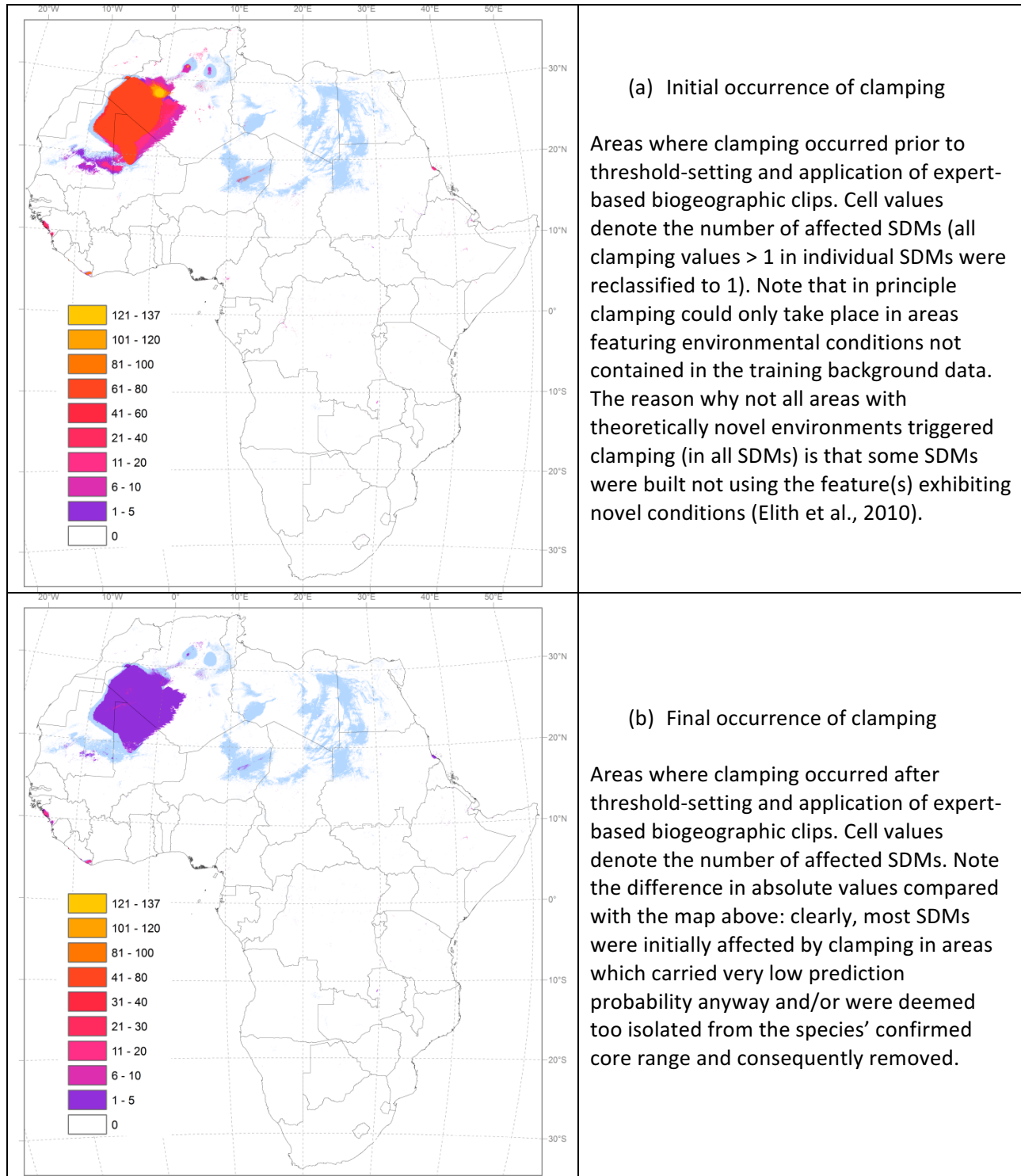## Appendix L   Clamping-related uncertainty in final species richness model

(a) Initial occurrence of clamping

Areas where clamping occurred prior to threshold-setting and application of expert-based biogeographic clips. Cell values denote the number of affected SDMs (all clamping values > 1 in individual SDMs were reclassified to 1). Note that in principle clamping could only take place in areas featuring environmental conditions not contained in the training background data. The reason why not all areas with theoretically novel environments triggered clamping (in all SDMs) is that some SDMs were built not using the feature(s) exhibiting novel conditions (Elith et al., 2010).

(b) Final occurrence of clamping

Areas where clamping occurred after threshold-setting and application of expert-based biogeographic clips. Cell values denote the number of affected SDMs. Note the difference in absolute values compared with the map above: clearly, most SDMs were initially affected by clamping in areas which carried very low prediction probability anyway and/or were deemed too isolated from the species' confirmed core range and consequently removed.

Figure L.1.   The difference between panels (a) and (b) shows that after threshold-setting and application of biogeographic clips, very few SDMs retained areas where clamping had taken place. Although some cells featured such novel environmental conditions that clamping occurred in as many as 137 (out of 226) SDMs, post-processing reduced this number to a maximum of 33 SDMs. The regions where clamping was most often applied were the western Sahara and some smaller areas near the West African coast featuring extreme rainfall conditions. In total, about 3% of continental Africa was found to harbour novel environmental conditions which necessitated clamping. Had we used a strict target group background definition (i.e. all bat localities as single cells instead of the custom kernel density estimate to depict sampling effort), the area of novel environmental conditions would have been much larger (shown in light blue).

We performed a similar analysis using MESS values (Elith et al., 2010) instead of clamping (also see Appendix S); results were nearly identical though, hence we report only the latter.

References:

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Appendix M   Correlation between AUC values and other SDM properties
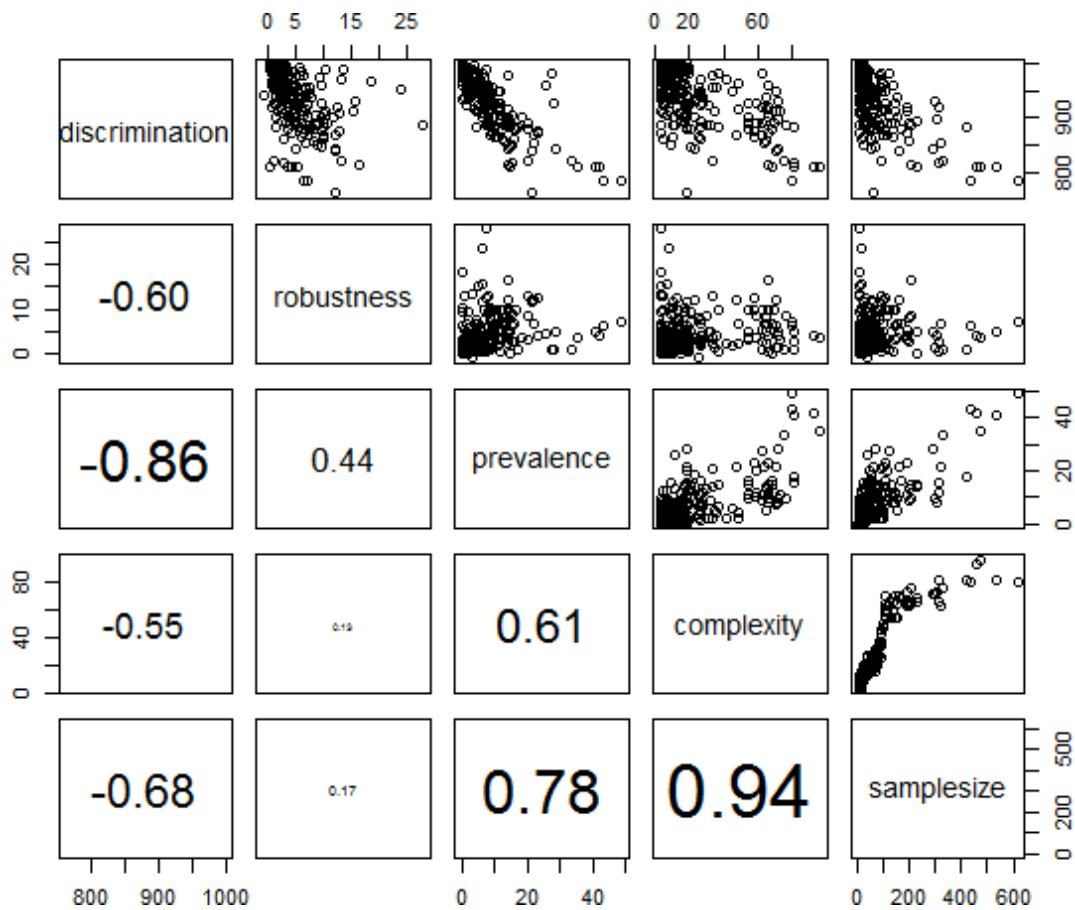
Figure M.1.   Scatterplots showing the correlation between AUC values of final SDMs ('discrimination'), the associated difference (in %) to mean AUC values obtained for test SDMs ('robustness'), the species' predicted prevalence across continental Africa ('prevalence'), the number of non-zero coefficients used to train the final SDM ('complexity') and the number of training localities used for the final SDM ('samplesize'). The lower-left half of panels contains Spearman's correlation coefficients (the normality assumption of Pearson's measure was not met and we preferred not to transform the raw data (O'Hara and Kotze, 2010). All correlations are highly significant (p-value < 0.001) except the relationships of 'robustness' with 'complexity' and 'samplesize' (p-values > 0.05). All analyses were carried out in R (R Core Team, 2014).

References:

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Appendix N   Species richness of African endemics
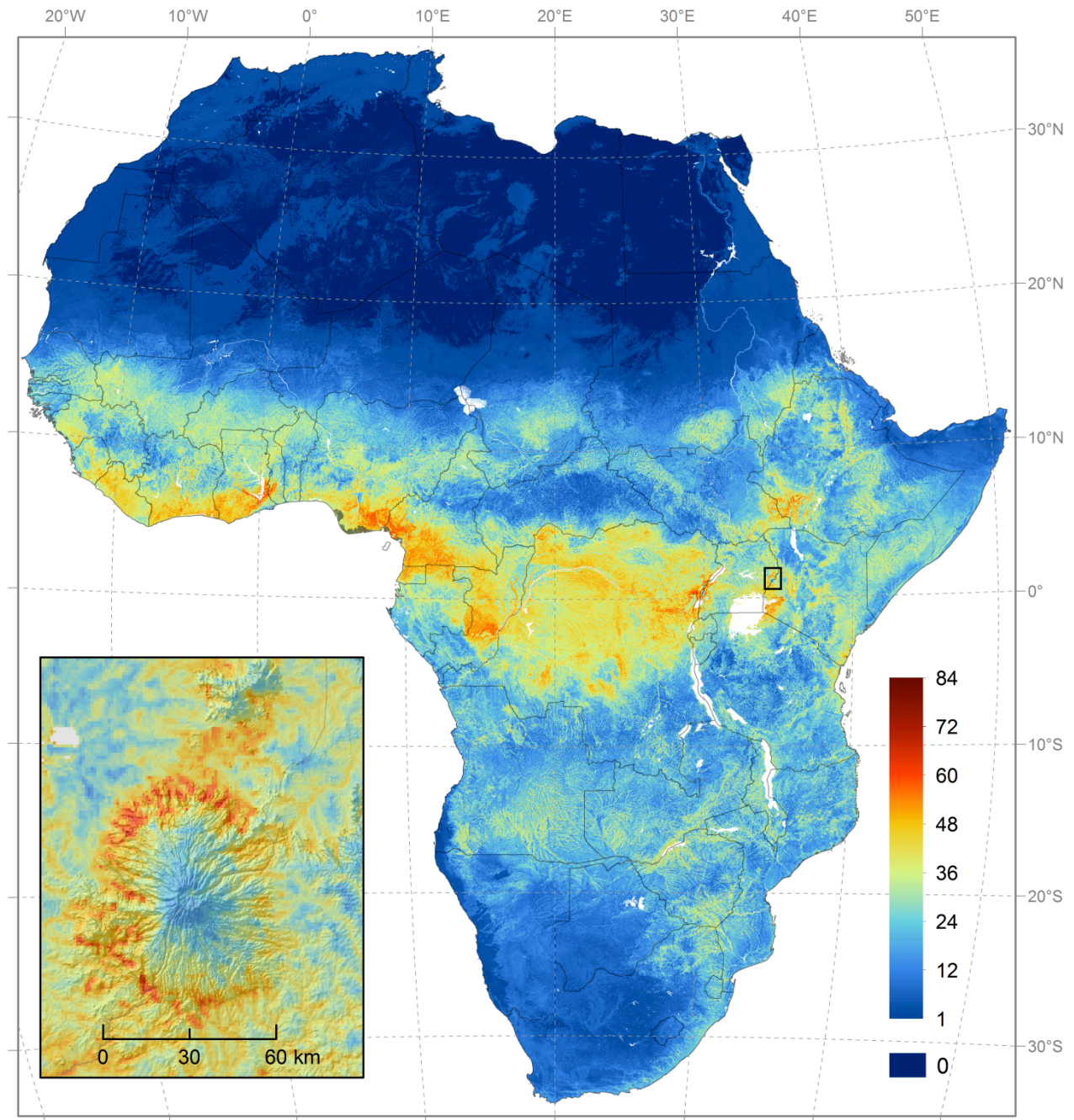
Figure N.1.   Predicted species richness of African endemics (n = 212, excluding *Miniopterus* spp.) at 1 km^2 spatial grain. The inset shows the area around Mt Elgon and illustrates the apparent association of richness with the hydrological network and/or steep sloping terrain; Topography shown by hill-shading (SRTM).

Appendix O   Summed range size rarity of African endemics
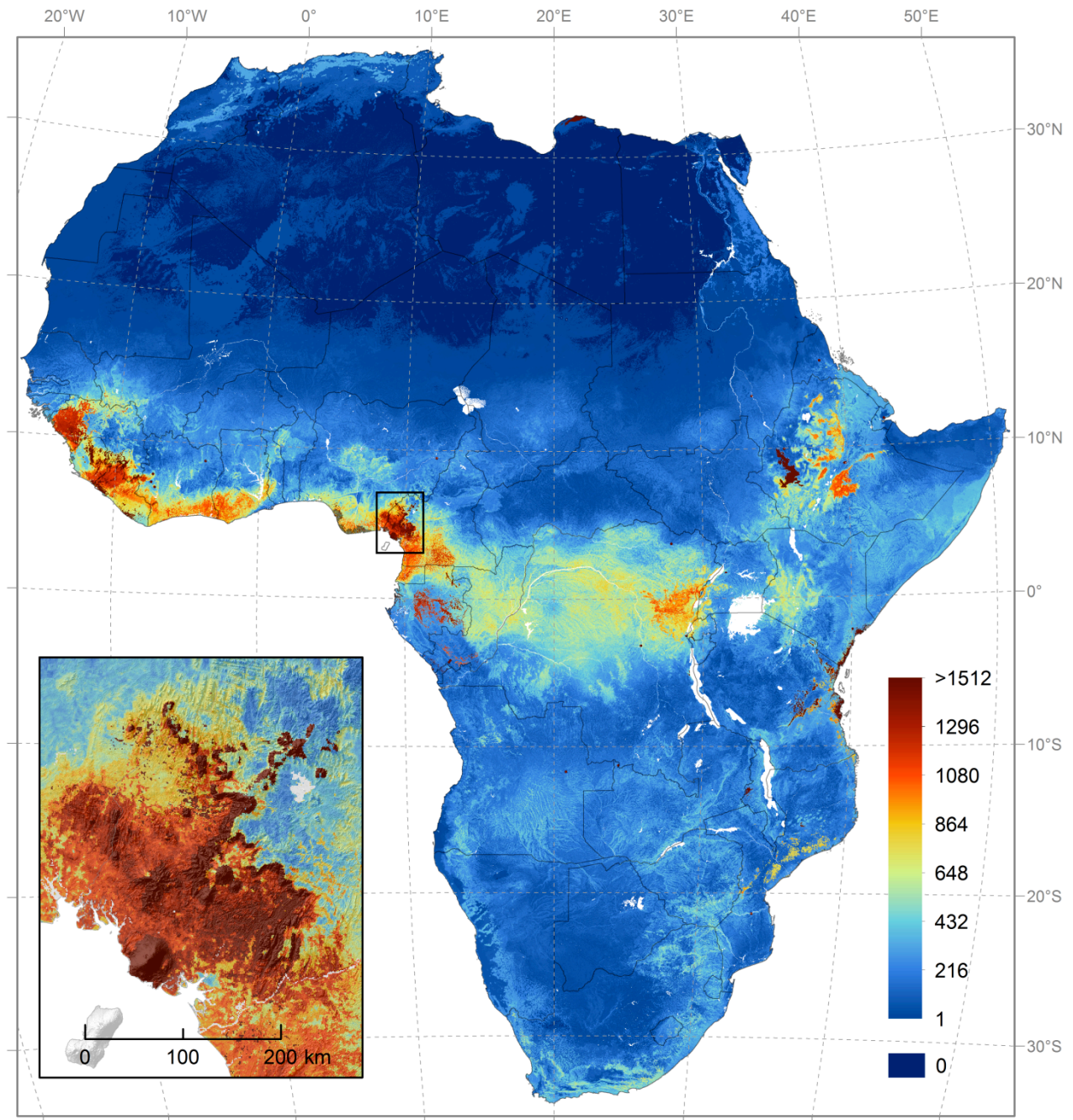
Figure O.1.   Summed range-size rarity predictions of species endemic to Africa (n = 212, excluding *Miniopterus* spp.) at 1 km^2 spatial grain. The inset zooms in on the pattern along the Cameroon volcanic line; topography shown by hill shading (SRTM). Due to the strong skewness of the distribution, data are mapped with a linear colour stretch truncated at one standard deviation (1512). Note that rarity

hotspots (brown) emerging as abrupt peaks from a background of low range size rarity values (blue), tend to be based on a single species and are thus more dependent on the quality of the SDM or buffer model than the hotspots surrounded by moderate levels of range size rarity (in orange and yellow) which typically involve more than one relatively rare species.

Appendix P   Sensitivity of hotspot congruence to changes in hotspot size and the quantification of 'endemism'
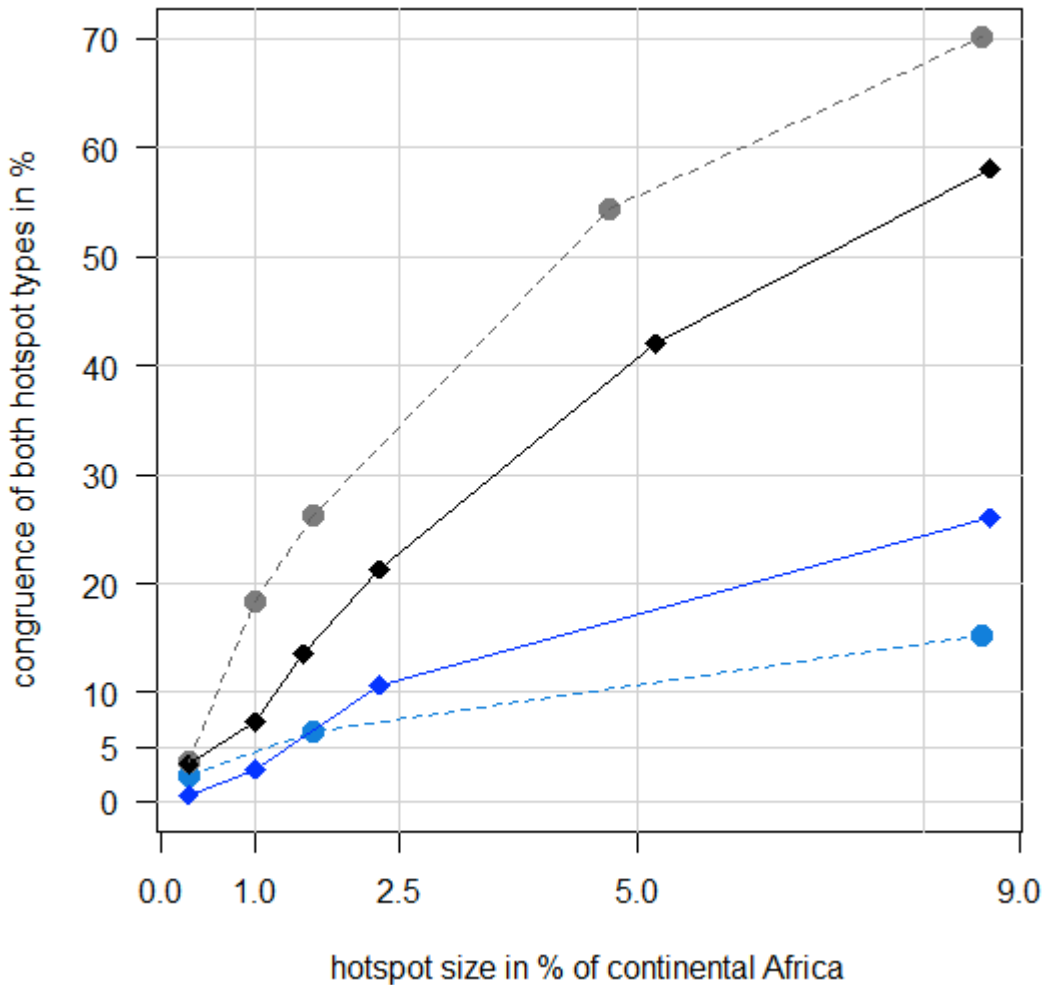
Figure P.1.   Sensitivity of hotspot congruence to definitions of hotspot size and the measure of rarity employed. In all cases the congruence between richness and rarity hotspots steadily increases as hotspot size is enlarged. This increase is much weaker though when 'rarity' is measured using the richness of the quartile of species with the smallest range sizes (blue and light blue symbols) as opposed to the principal measure employed in the present study (see Section 2.7 of the main text), i.e. each cell's summed range size rarity score (black and grey symbols). Circles (regardless of colour) denote the level of congruence when considering African endemics only (n=212), whereas diamonds indicate the level of hotspot congruence level based on all species (n=241).

Appendix Q **Spatial congruence of richness and rarity hotspots of African endemics**
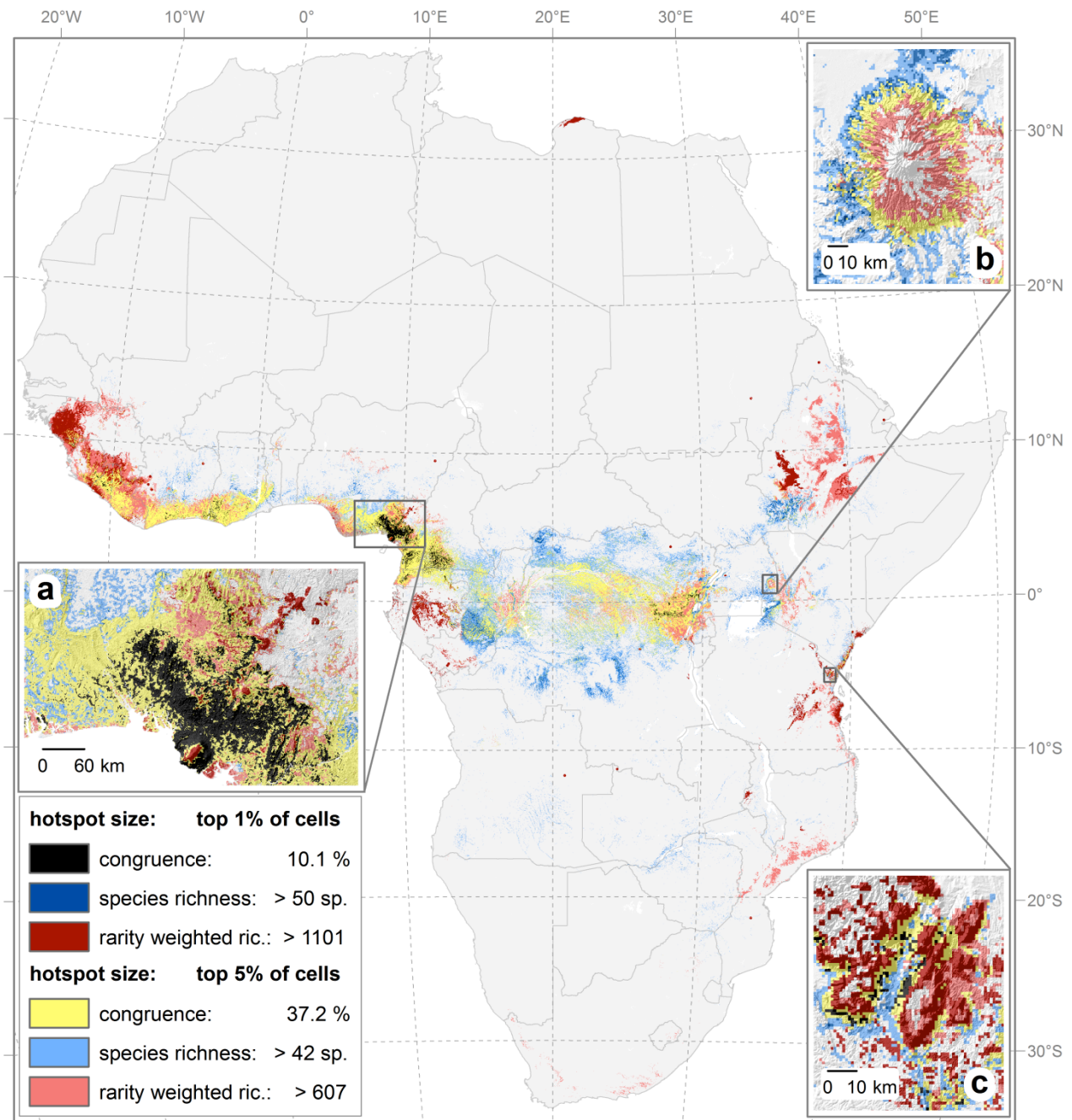

Figure Q.1. Spatial congruence between hotspots of species richness and endemism (quantified here as summed range size rarity) considering African endemics only (n=212). If hotspot size is defined as the highest ranking 1% of cells the area of congruence is very small (indicated in black). If hotspots are defined as the highest ranking 5% of cells, the area of congruence is considerably larger (in yellow). Areas shown in blue and red depict those richness and endemism hotspots, respectively, that do not overlap – neither at the 1% nor at the 5% hotspot size level.

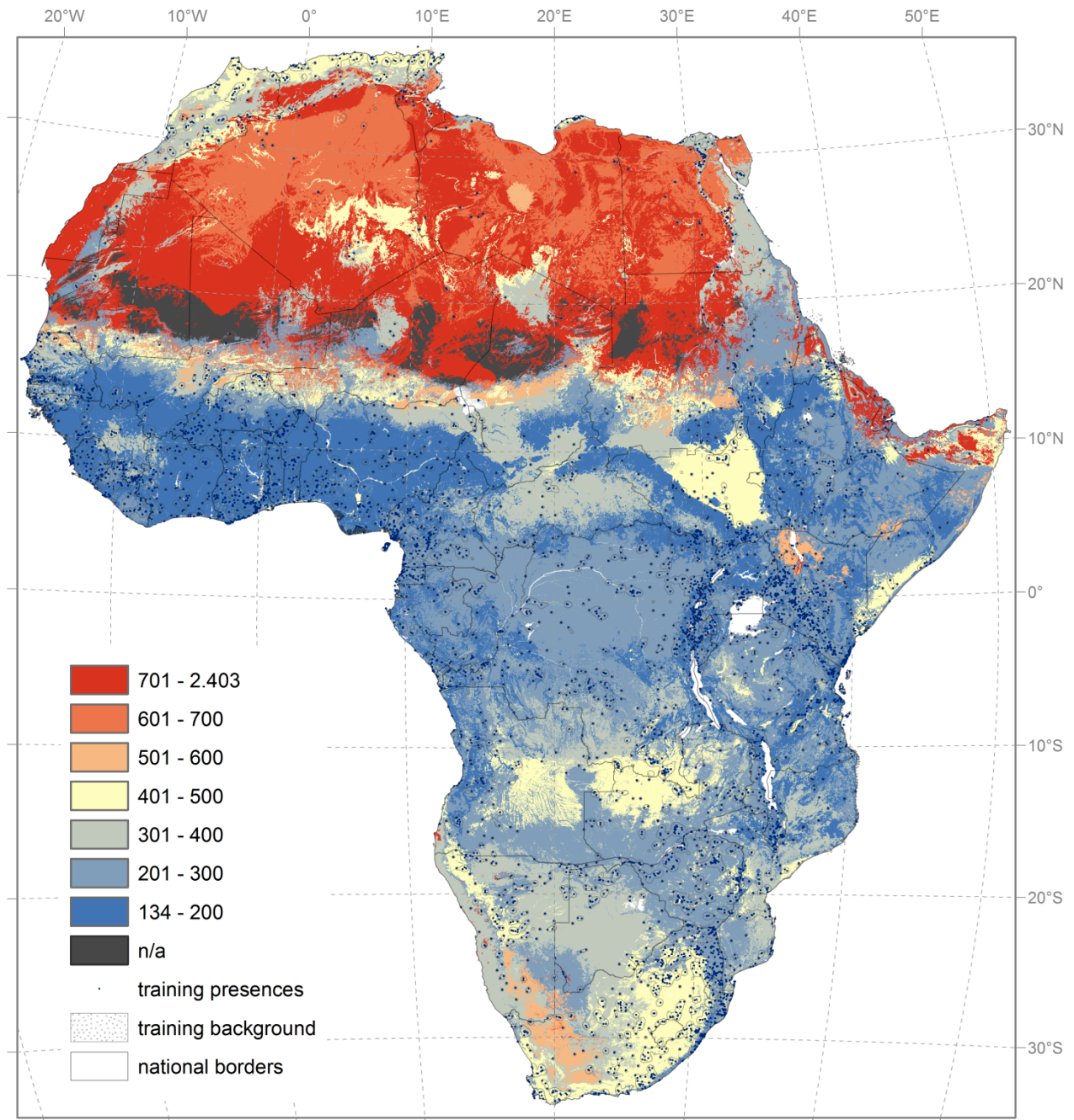## Appendix R   Plausibility of predicted richness 'coldspots'

Figure R.1.   Mean area (in km^2) represented by each presence point, calculated separately for each habitat class. Only the portion of each habitat class that overlaps with the kernel-defined background sampling area was considered in the calculation (for details on the definition of habitat classes and background delineation see Section 2.2 of the main text and Appendix G). By this measure, habitat classes shown in red have received relatively little attention by bat collectors, whereas habitat classes shown in blue have been sampled more intensely (habitats shown in dark grey do not contain any

localities used for training SDMs). Within tropical Africa several areas stand out where sampling effort has been notably lower than in the immediately surrounding habitat classes. The first group consists of savanna habitats in relatively flat terrain and comprises the Nile River flats in South Sudan as well as coastal plains in southern Somalia and central Mozambique. The second group consists of woodlands and forest-savanna mosaics in moderately rugged terrain and comprises parts of eastern Guinea, most of the Central African Republic, parts of north-eastern Angola and southern DRC, a large part of Mozambique and – most notably – the miombo woodlands in central Angola and north-western Zambia. See the main text (Section 4.3) for a discussion of these patterns.
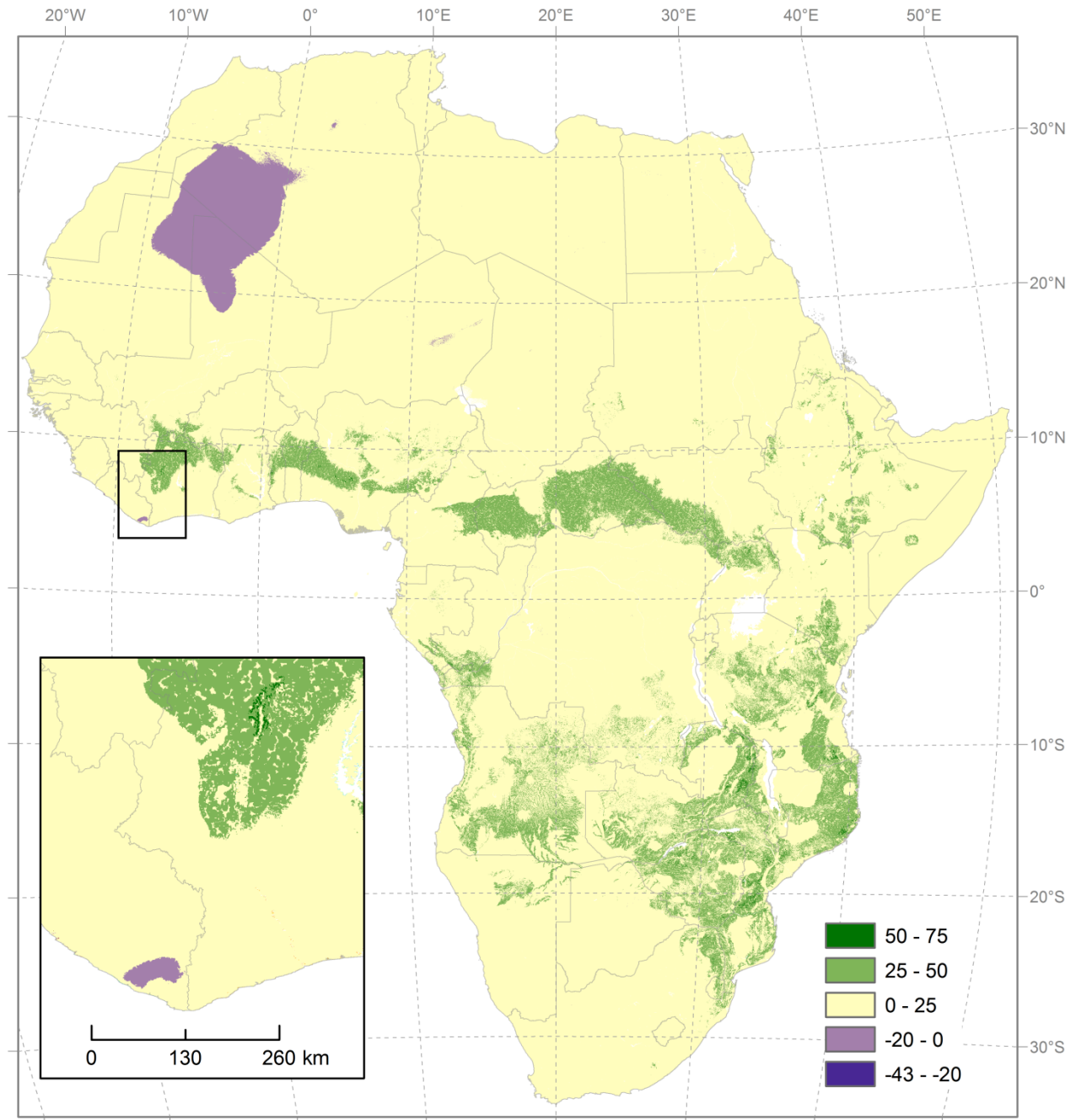
Appendix S   Multivariate Environmental Similarity Surface (MESS) output of MaxEnt

	50 - 75
	25 - 50
	0 - 25
	-20 - 0
	-43 - -20

Figure S.1.   Multivariate environmental similarity surface (MESS) showing the degree of environmental novelty encountered by MaxEnt when training the SDM for *Saccolaimus peli*

(Pteropodidae). Cells with values < 0 (purple) indicate conditions outside the training range. Positive values > (beige and green) 0 denote increasing multivariate environmental similarity. MESS maps for other species were nearly identical.

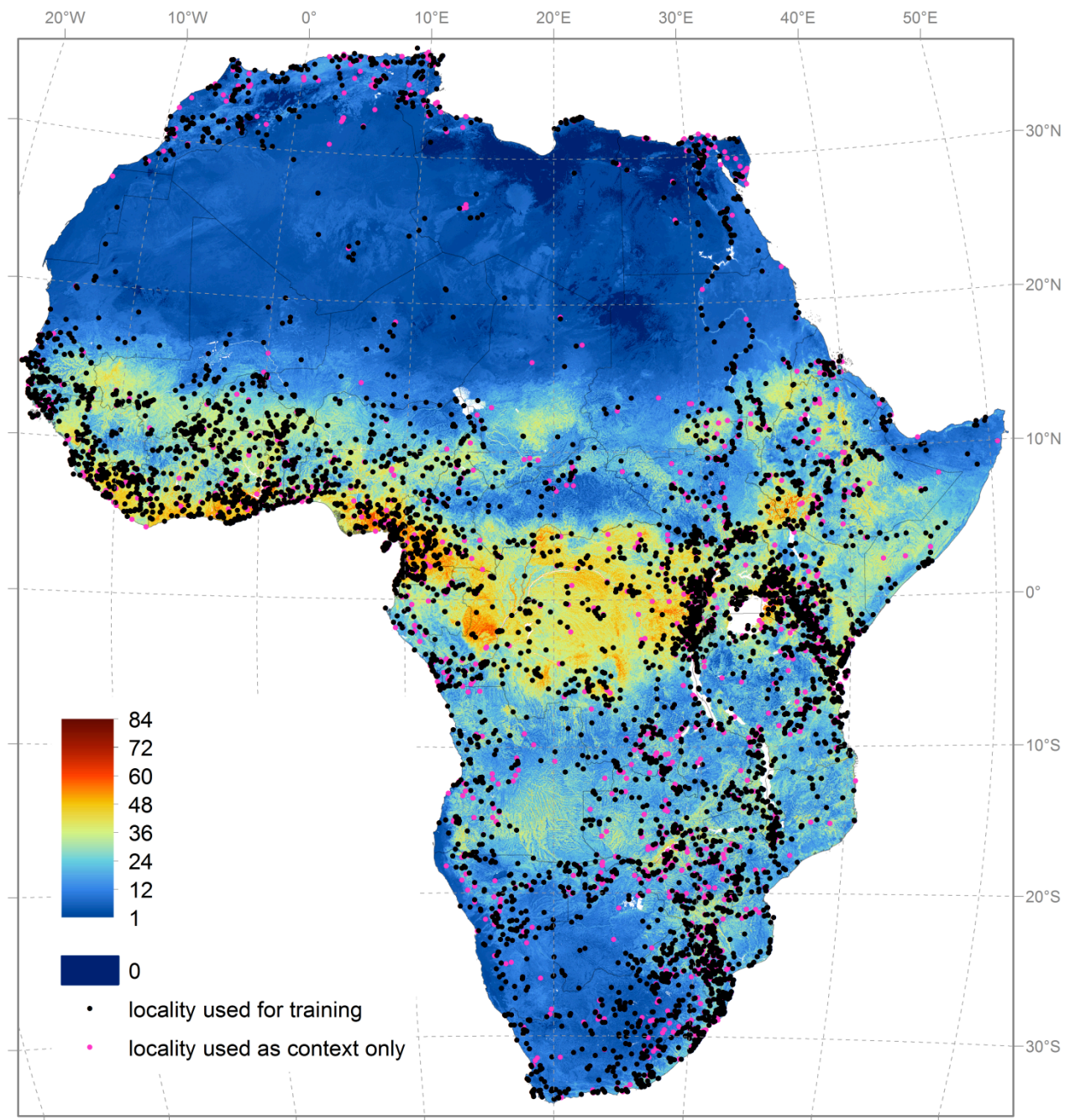**Appendix T   Survey gaps in light of predicted species richness**

Figure T.1.   Bat presence localities against the background of predicted species richness of all bat species known to occur in continental Africa (n=241) except *Miniopterus* spp. Black dots indicate localities used to train SDMs; pink dots indicate those that did not meet the specified data quality requirements (see Section 2.2 of the main text) and were only used as context information during threshold setting and biogeographic clipping (Section 2.5 of the main text). The map may be useful in planning future bat surveys (see Section 4.4 of the main text).