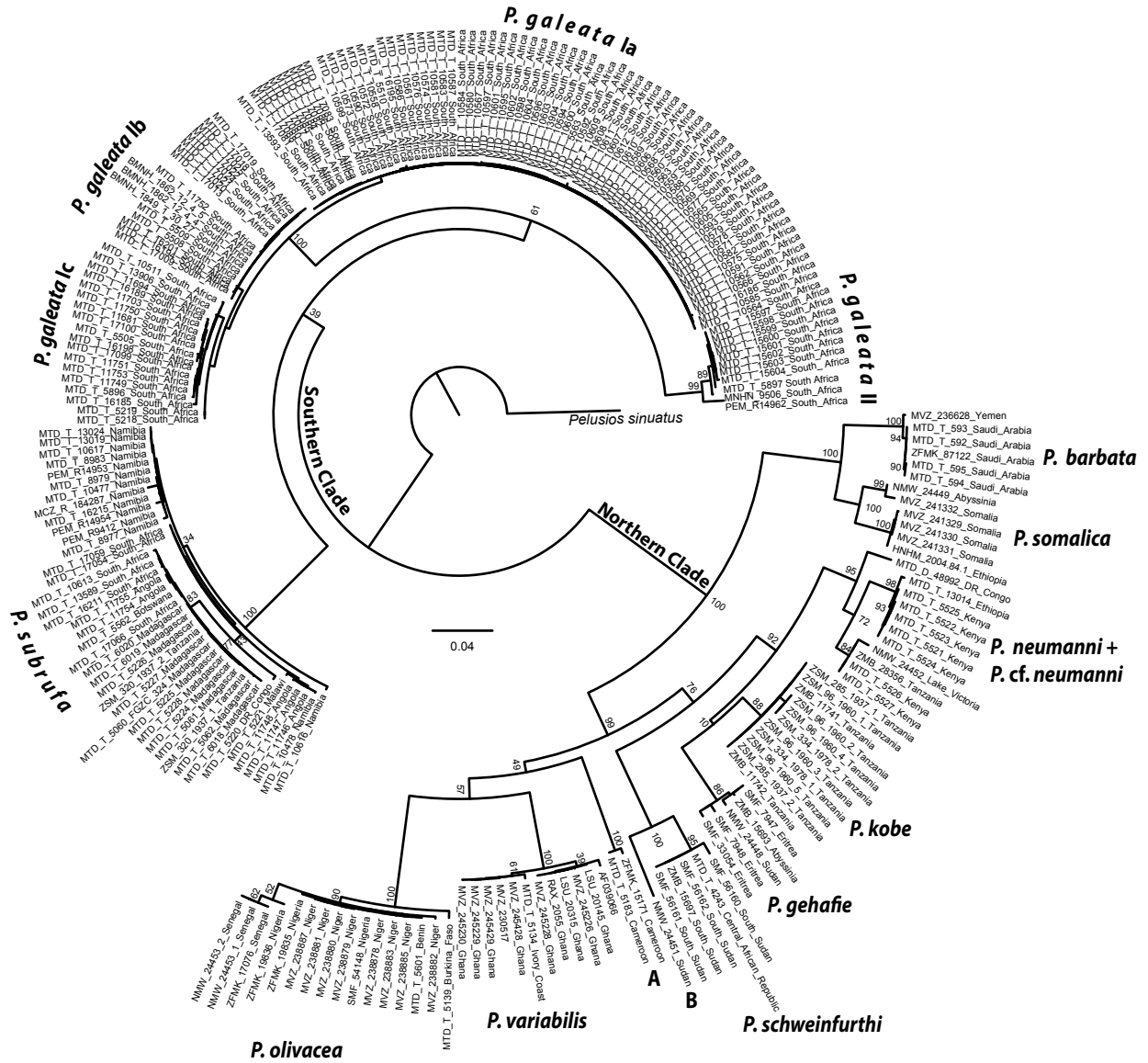


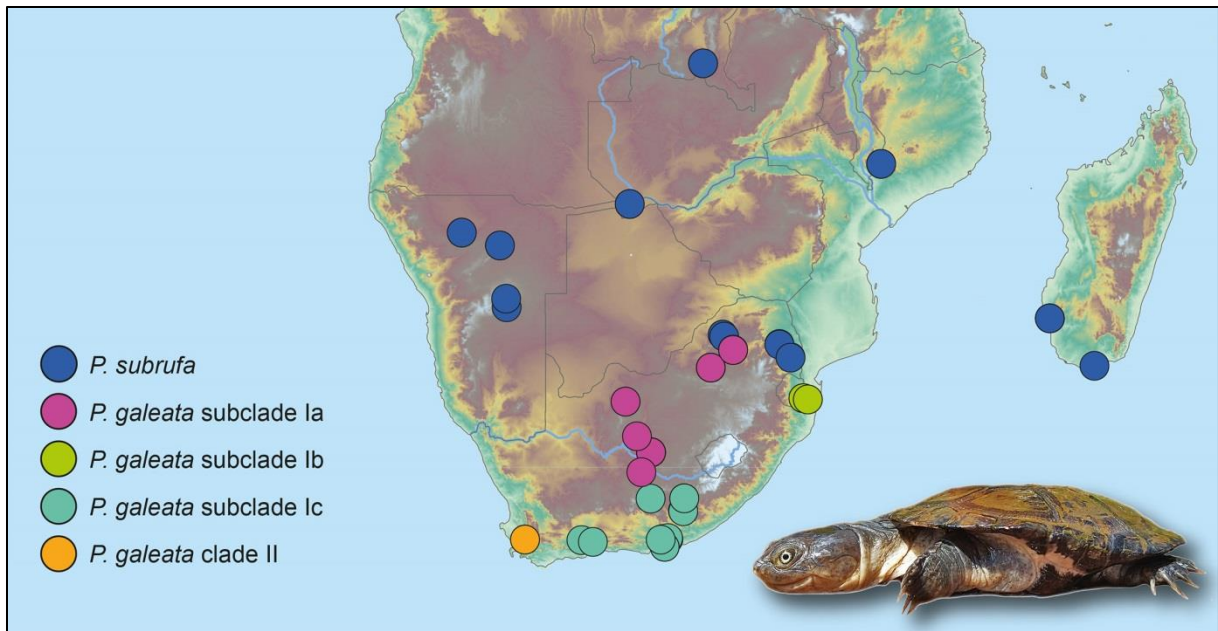
# In quest of contact: phylogeography of helmeted terrapins (*Pelomedusa galeata*, *P. subrufa* sensu stricto)

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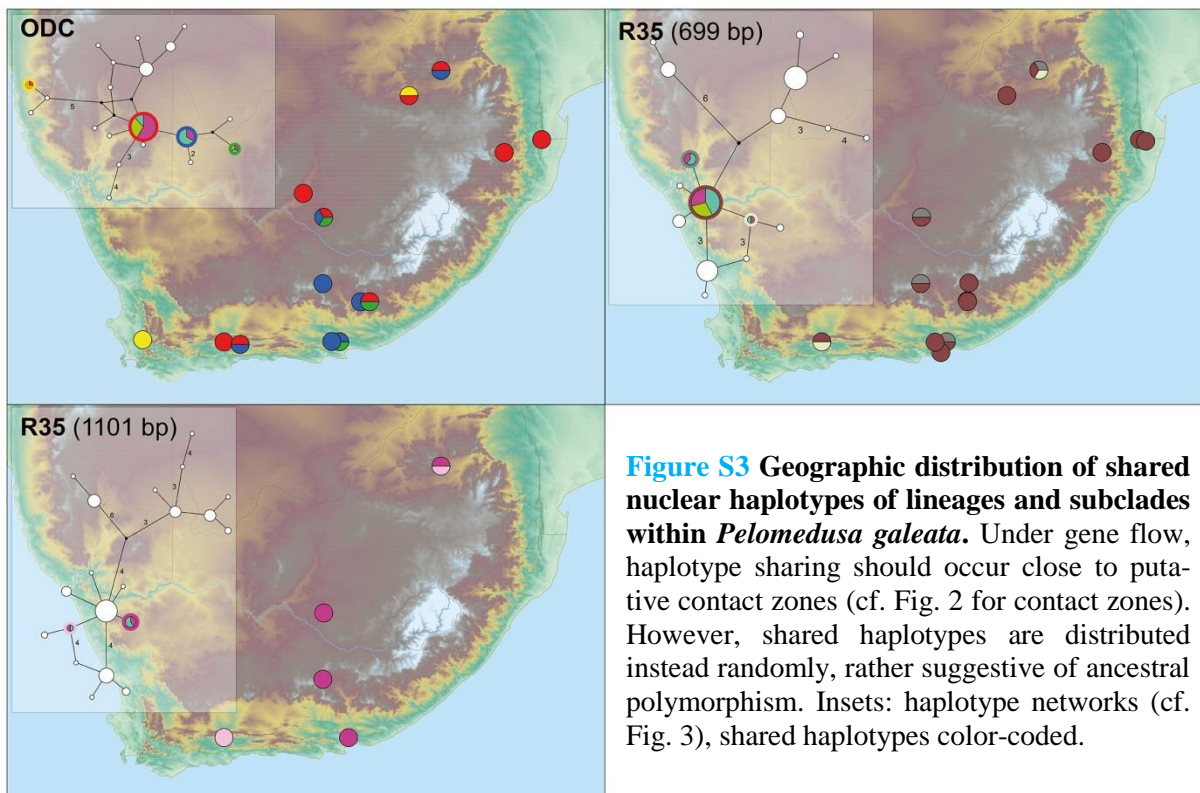
Supplemental Information – PeerJ



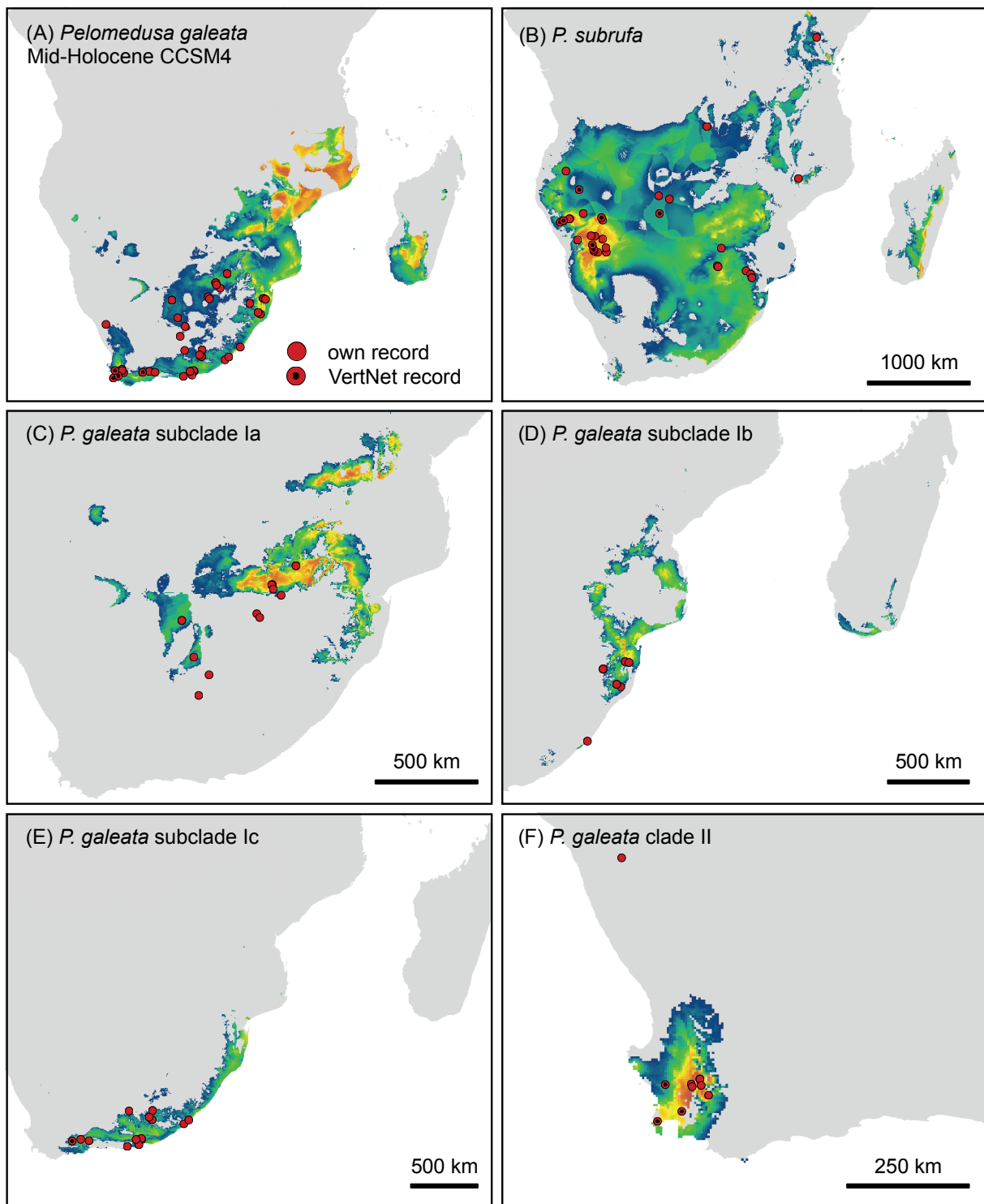
**Figure S1** Complete Maximum Likelihood tree, showing individual samples. For sample codes not explained in Table S1, see Petzold et al. (2014) and Nagy et al. (2015).



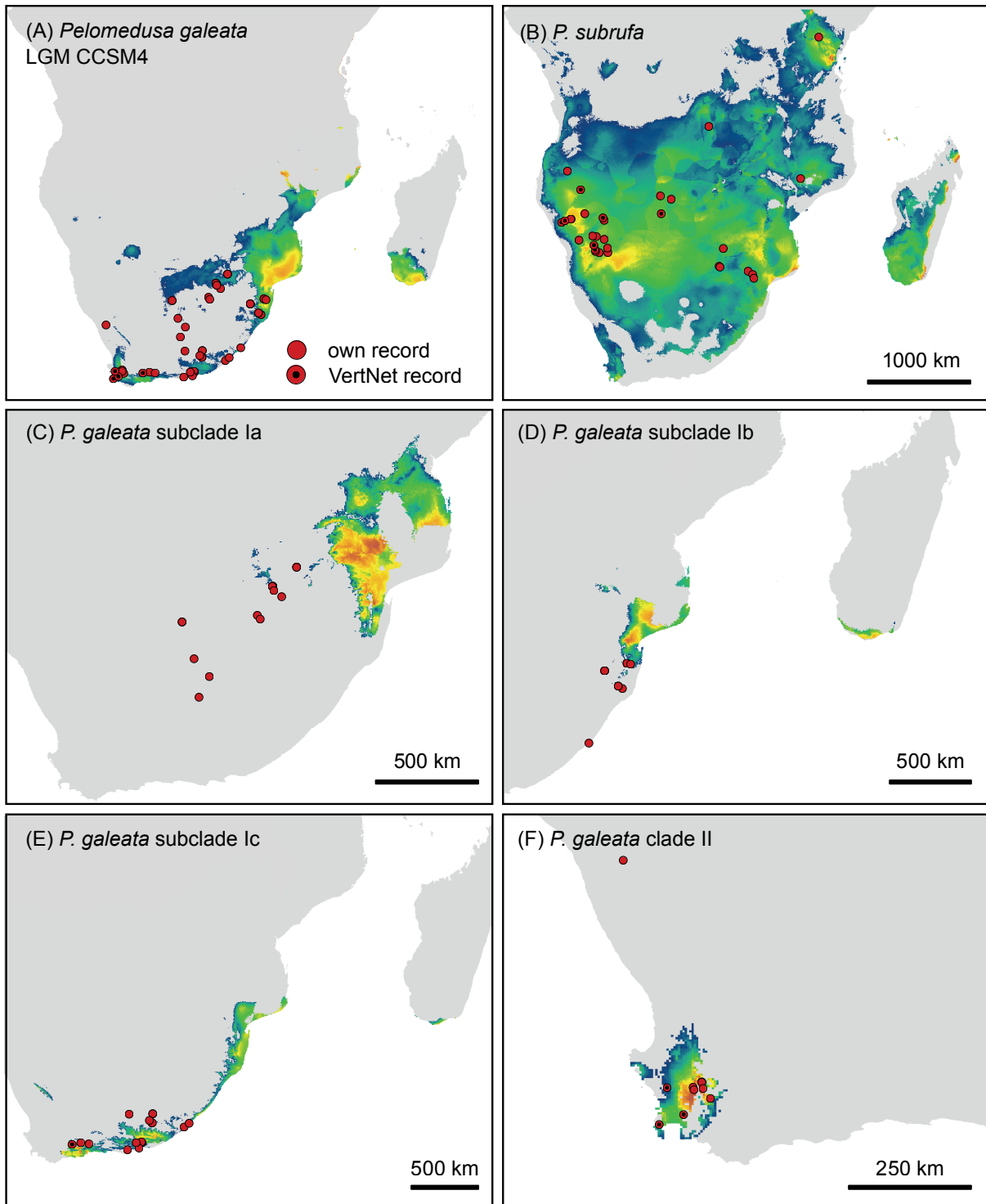
**Figure S2** Sampling sites with nuclear DNA information. Color-coding corresponds to mitochondrial lineages and subclades.



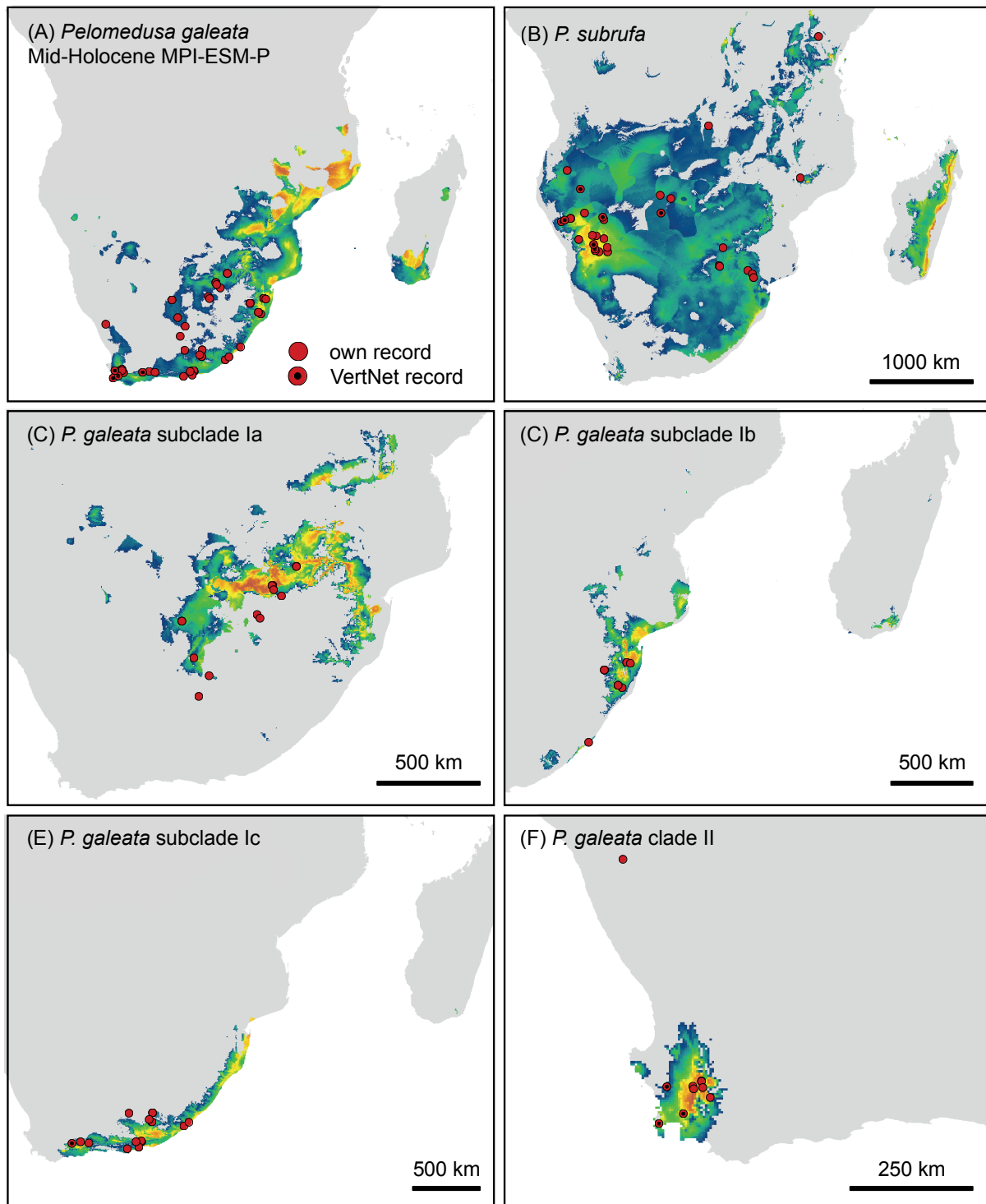
**Figure S3** Geographic distribution of shared nuclear haplotypes of lineages and subclades within *Pelomedusa galeata*. Under gene flow, haplotype sharing should occur close to putative contact zones (cf. Fig. 2 for contact zones). However, shared haplotypes are distributed instead randomly, rather suggestive of ancestral polymorphism. Insets: haplotype networks (cf. Fig. 3), shared haplotypes color-coded.



**Figure S4** Predicted climatic niches for *Pelomedusa galeata* (A), *P. subrufa* (B) and genetic clusters within *P. galeata* (C-F) during the mid-Holocene (CCSM4). Probabilities for habitat suitability range from low (blue) to high (orange).

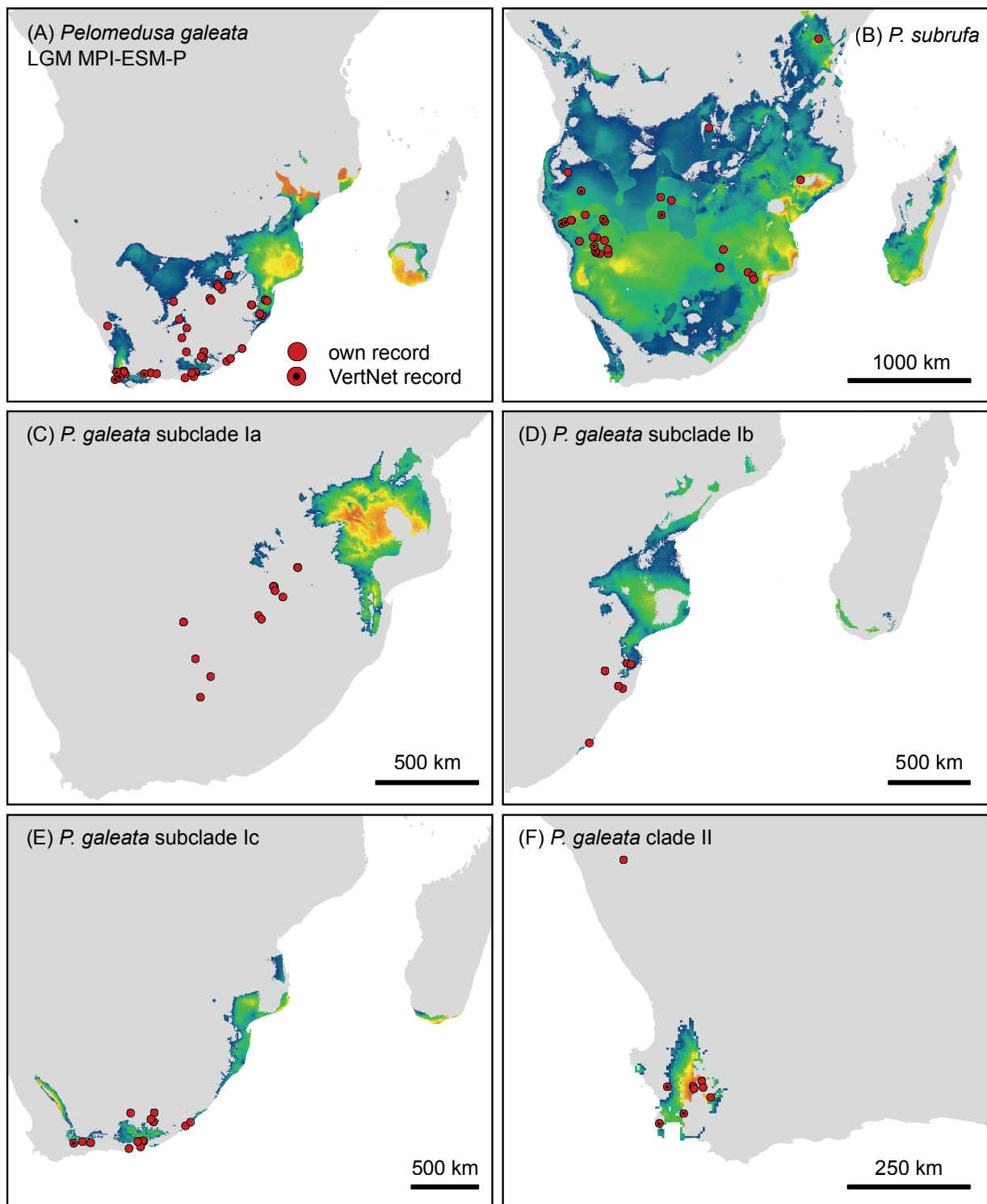


**Figure S5** Predicted climatic niches for *Pelomedusa galeata* (A), *P. subrufa* (B) and genetic clusters within *P. galeata* (C-F) during the Last Glacial Maximum (CCSM4). Probabilities for habitat suitability range from low (blue) to high (orange).



**Figure S6** Predicted climatic niches for *Pelomedusa galeata* (A), *P. subrufa* (B) and genetic clusters within *P. galeata* (C-F) during the mid-Holocene (MPI-ESM-P). Probabilities for habitat suitability range from low (blue) to high (orange).





**Figure S7** Predicted climatic niches for *Pelomedusa galeata* (A), *P. subrufa* (B) and genetic clusters within *P. galeata* (C-F) during the Last Glacial Maximum (MPI-ESM-P). Probabilities for habitat suitability range from low (blue) to high (orange).