

**Species limits and phylogeographic structure
in two genera of solitary African mole-rats
Georychus and *Heliophobius***

Supplementary file 3

Figure S.1: Species tree of *Georychus* inferred in BPP from ddRAD loci with values of the genealogical divergence index (*gdi*). The values were always calculated relative to the sister species. They are missing if either the species in question or its sister species are represented by just one allele per locus. Species delimitation, species tree and the color code are the same as in Figure 3 in the main text.

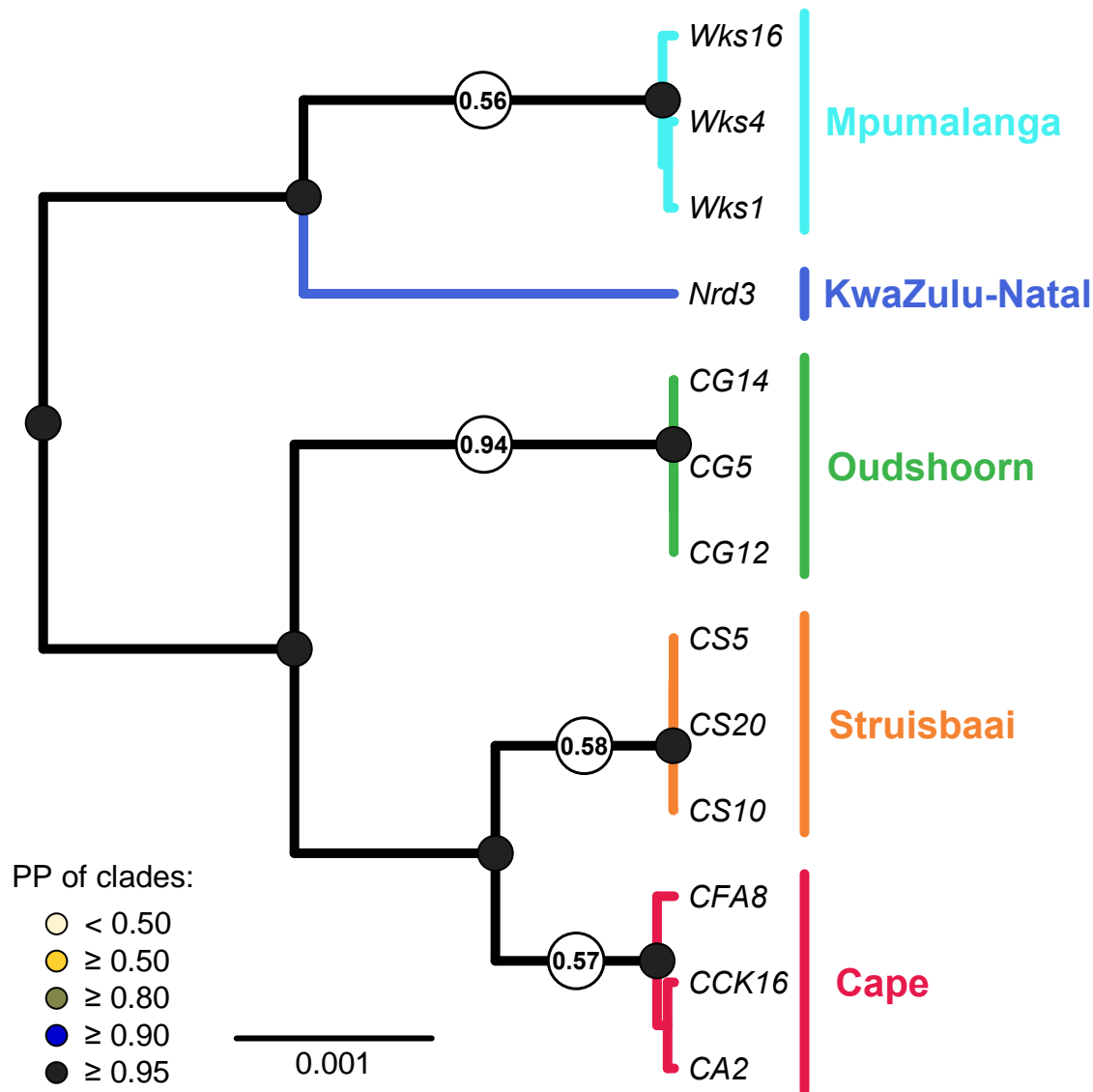


Figure S.2: Species tree of *Georychus* inferred in BPP from Sanger sequenced loci. The color code is the same as in Figure 3 in the main text.

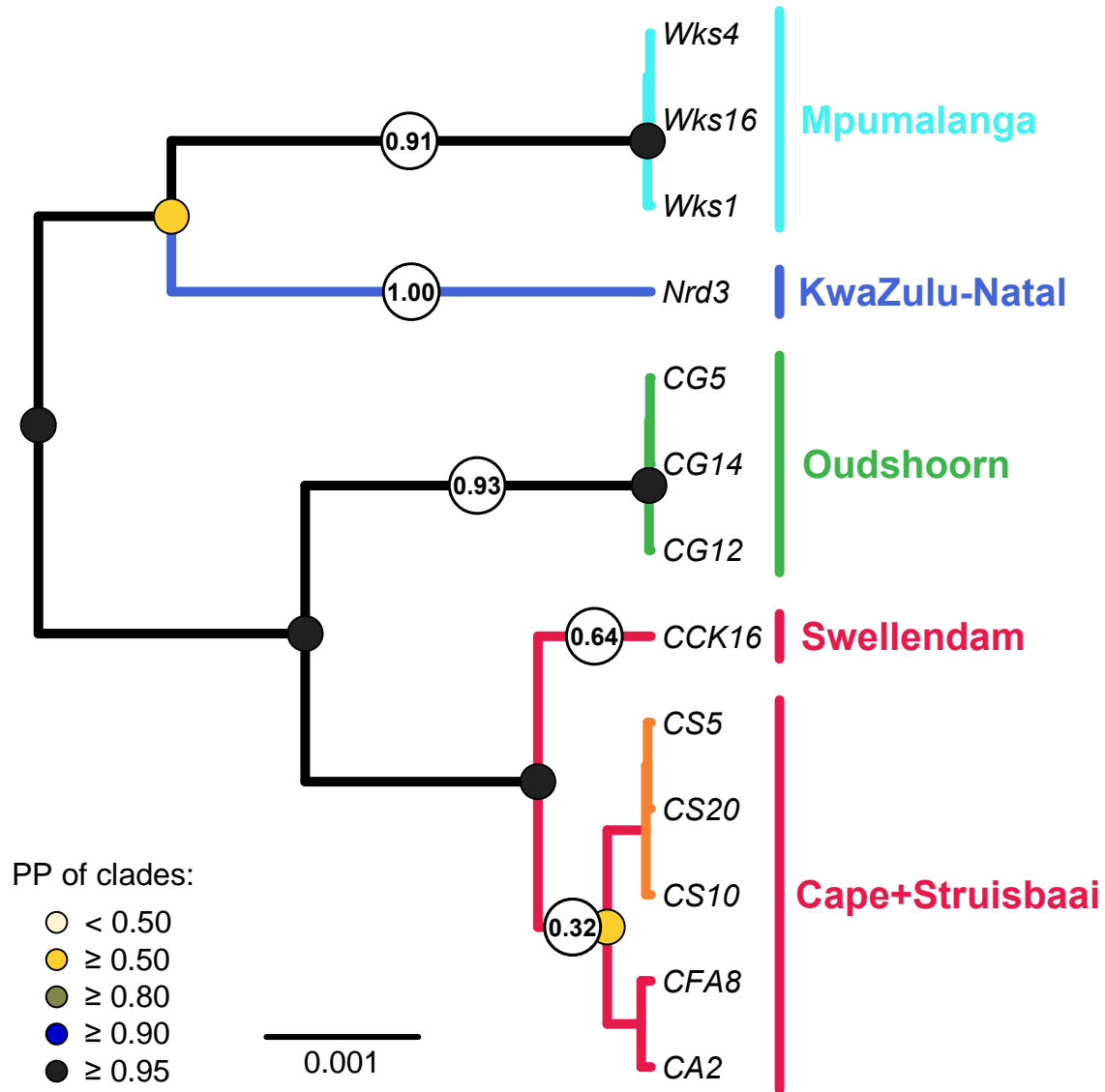


Figure S.3: Species tree of *Heliophobius* inferred in BPP from ddRAD loci with values of the genealogical divergence index (*gdi*). The values were always calculated relative to the sister species. They are missing if either the species in question or its sister species are represented by just one allele per locus. Species delimitation, species tree and the color code are the same as in Figure 4 in the main text.

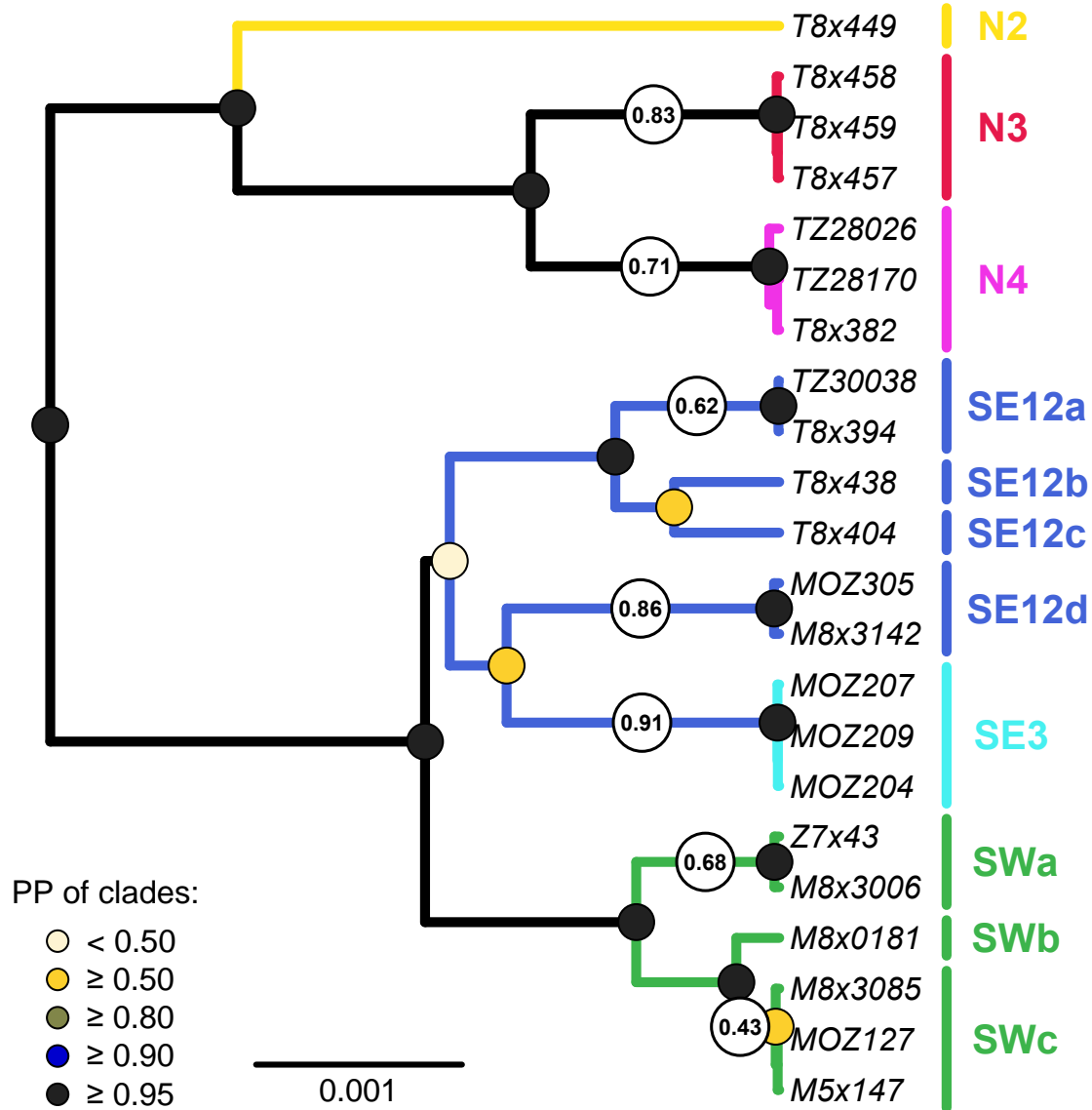


Figure S.4: Species tree of *Heliophobius* inferred in BPP from Sanger sequenced loci. The color code is the same as in Figure 4 in the main text.

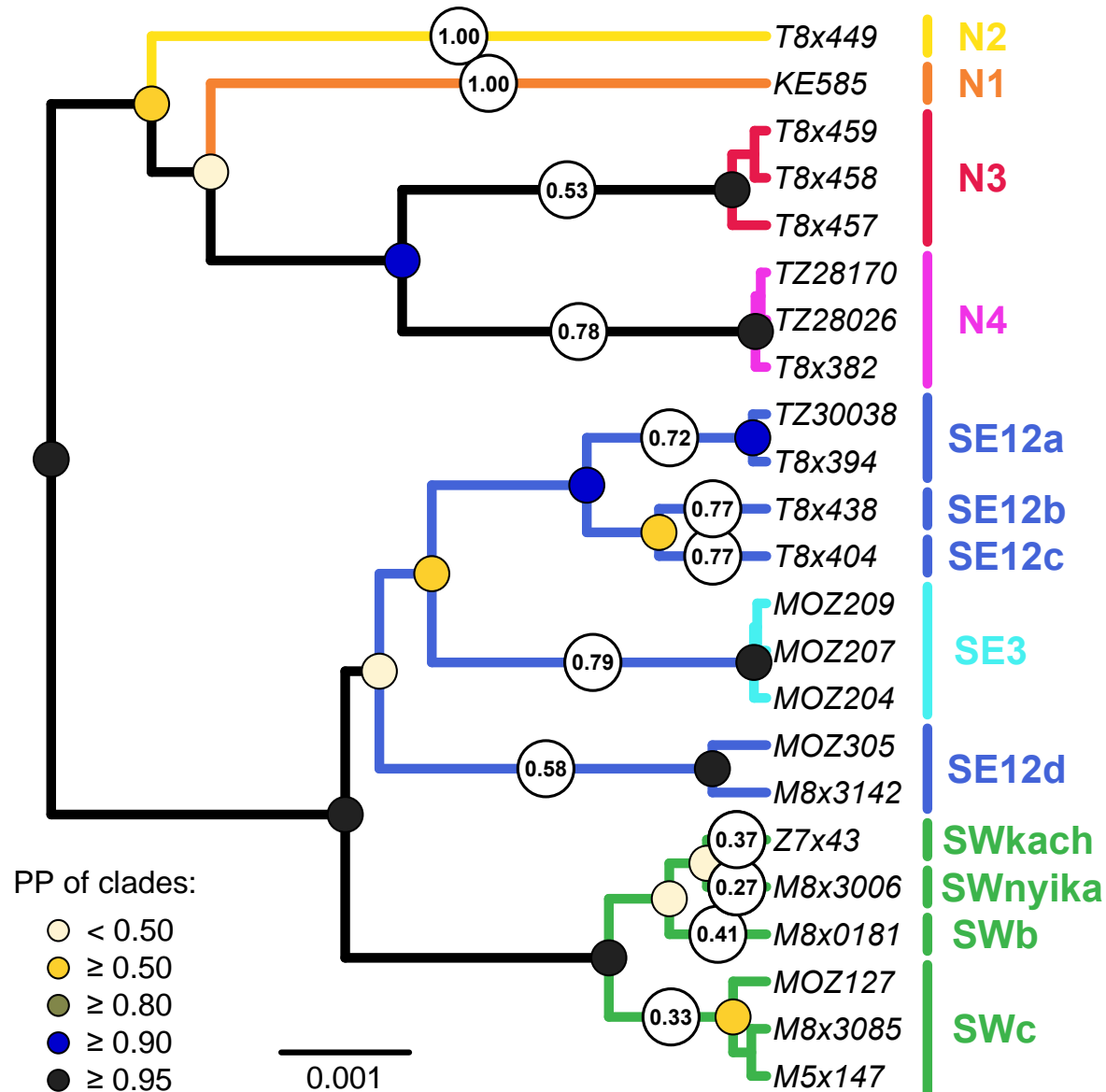


Figure S.5: Haplotype networks of six Sanger sequenced loci in *Georychus*. The colors indicate classification of the individuals into CYTB lineages.

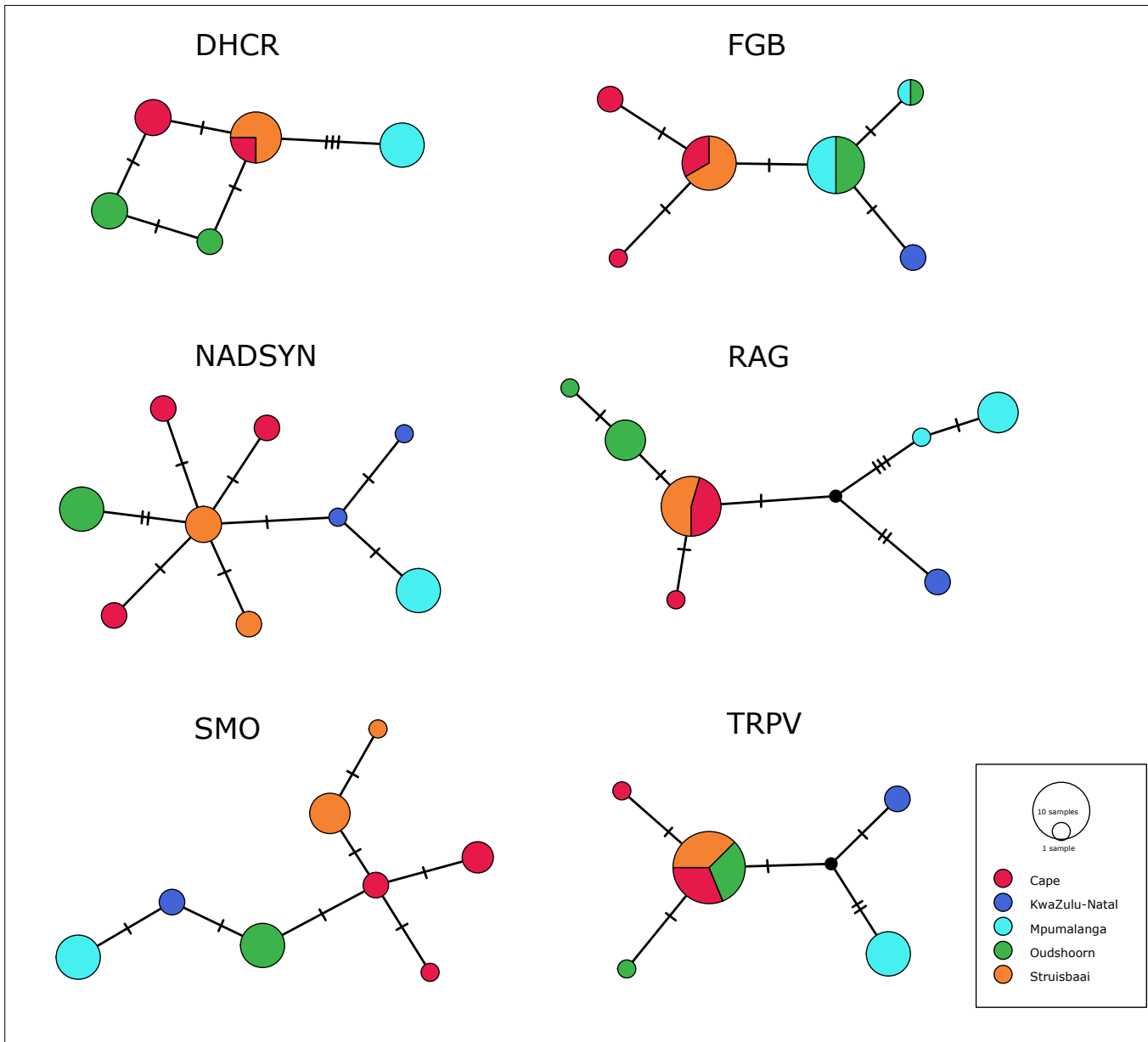


Figure S.6: Haplotype networks of six Sanger sequenced loci in *Heliophobius*. The colors indicate classification of the individuals into CYTB lineages.

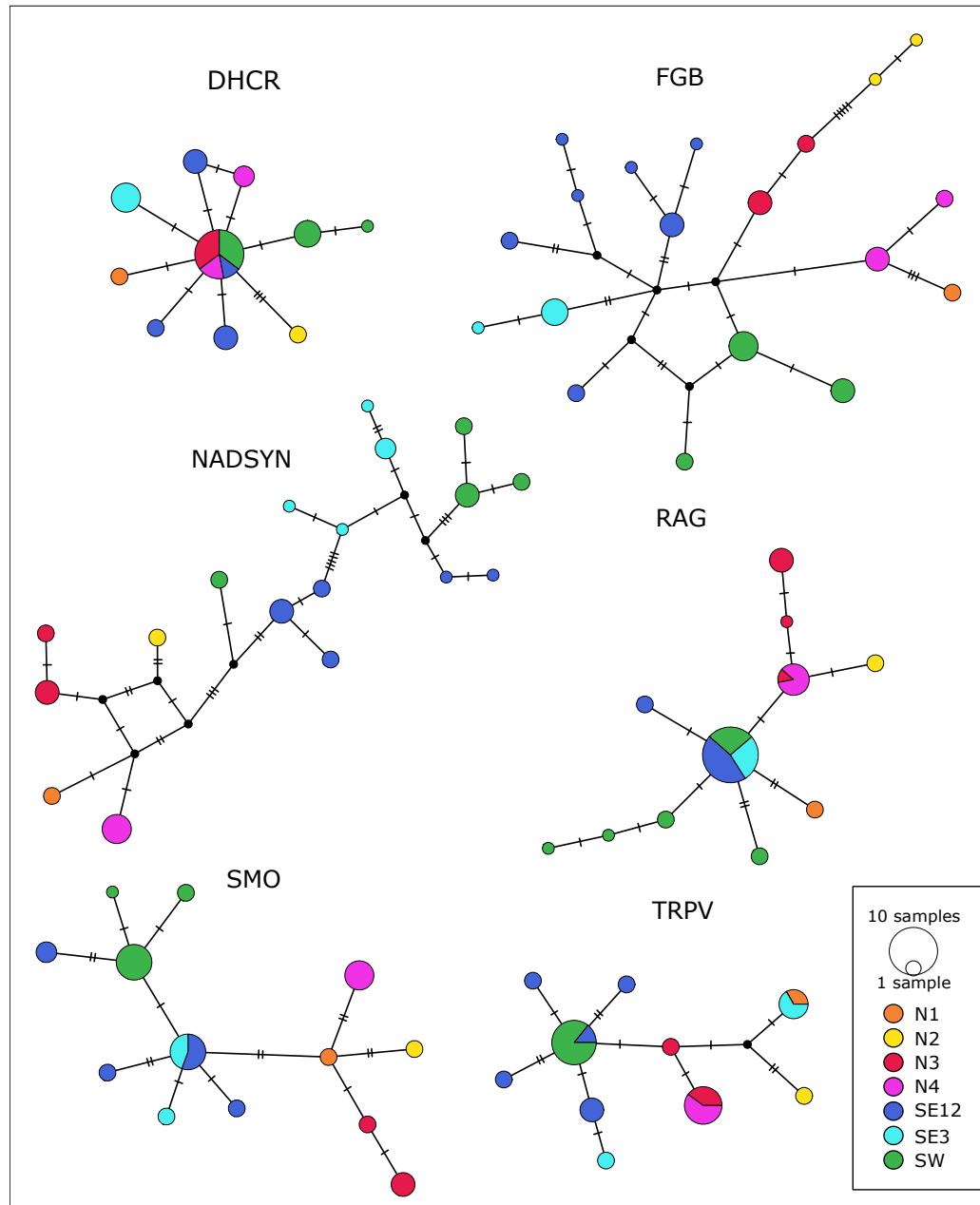


Figure S.7: Co-ancestry matrix of *Georychus* (middle panel) and the corresponding matrix of missingness (right panel). The left panel shows the fineSTRUCTURE dendrogram with branches colored according to assignment of the individuals into CYTB lineages. The assignment was based on CYTB sequences or, when missing, on the sampling site.

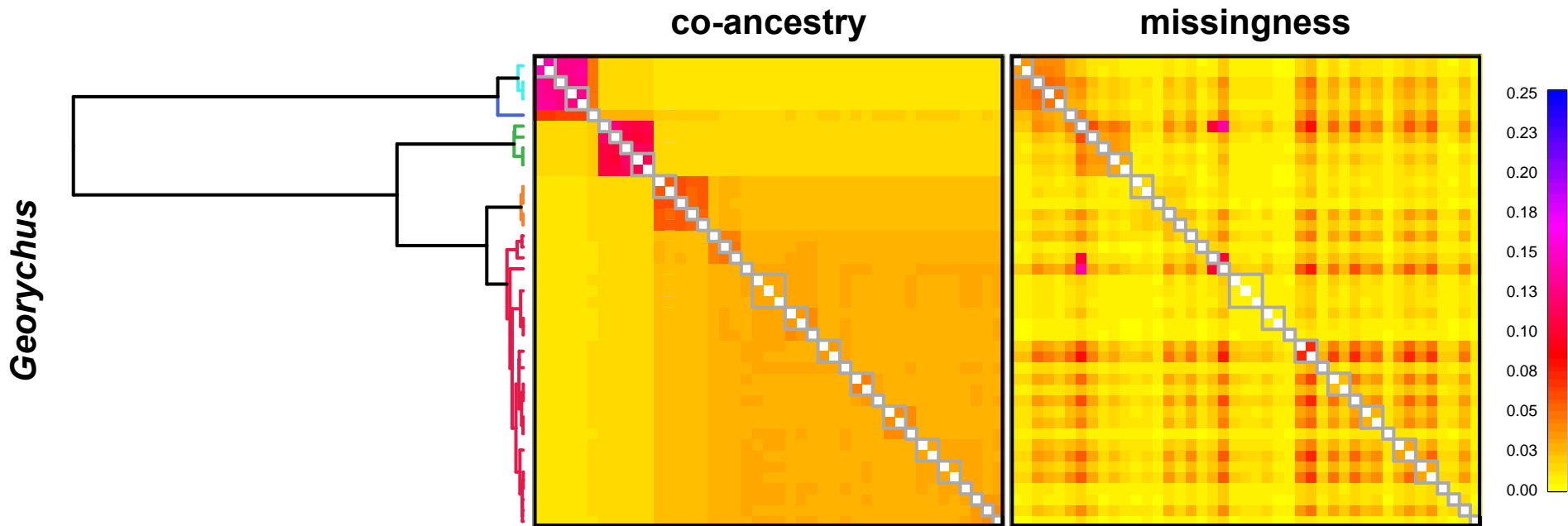


Figure S.8: Co-ancestry matrix of *Heliophobius* (middle panel) and the corresponding matrix of missingness (right panel). The left panel shows the fineSTRUCTURE dendrogram with branches colored according to assignment of the individuals into CYTB lineages. The assignment was based on CYTB sequences or, when missing, on the sampling site.

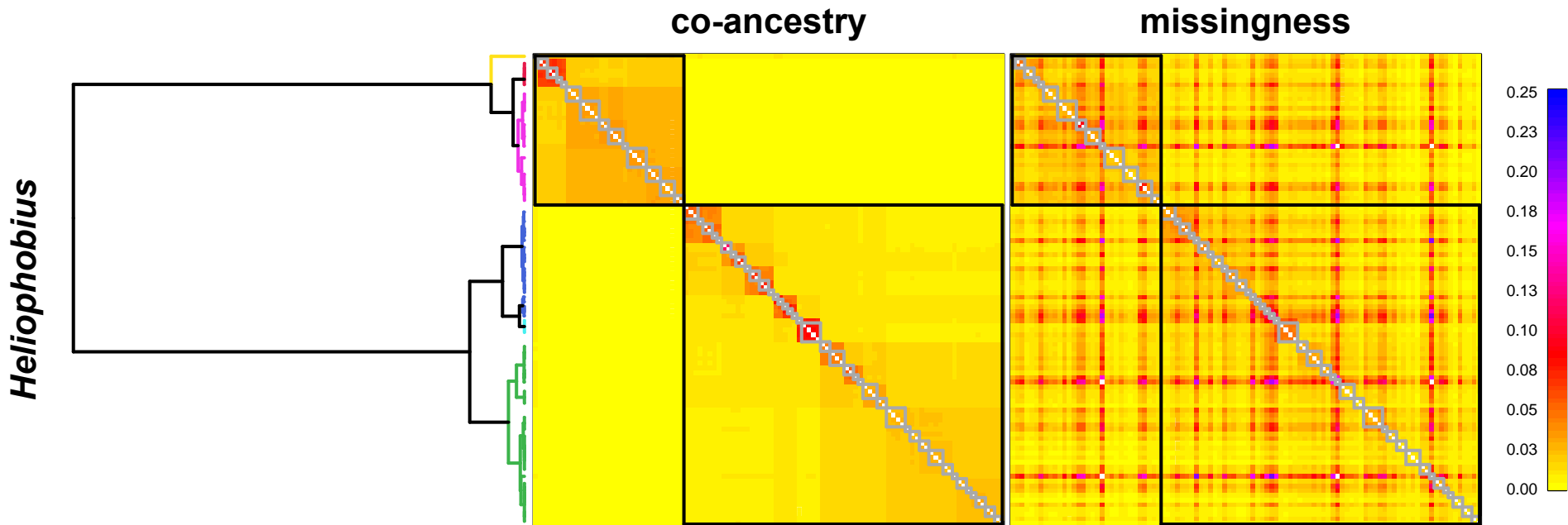


Figure S.9: Geographic distribution of sites with shifted climatic curves (=distinct climatic regimes). It shows only sites from regimes shown in Figure 9 (as green curves) and only those of them, whose predicted ROR was higher than prior. The color indicates the most common month of maximum precipitation among the sites of particular regime.

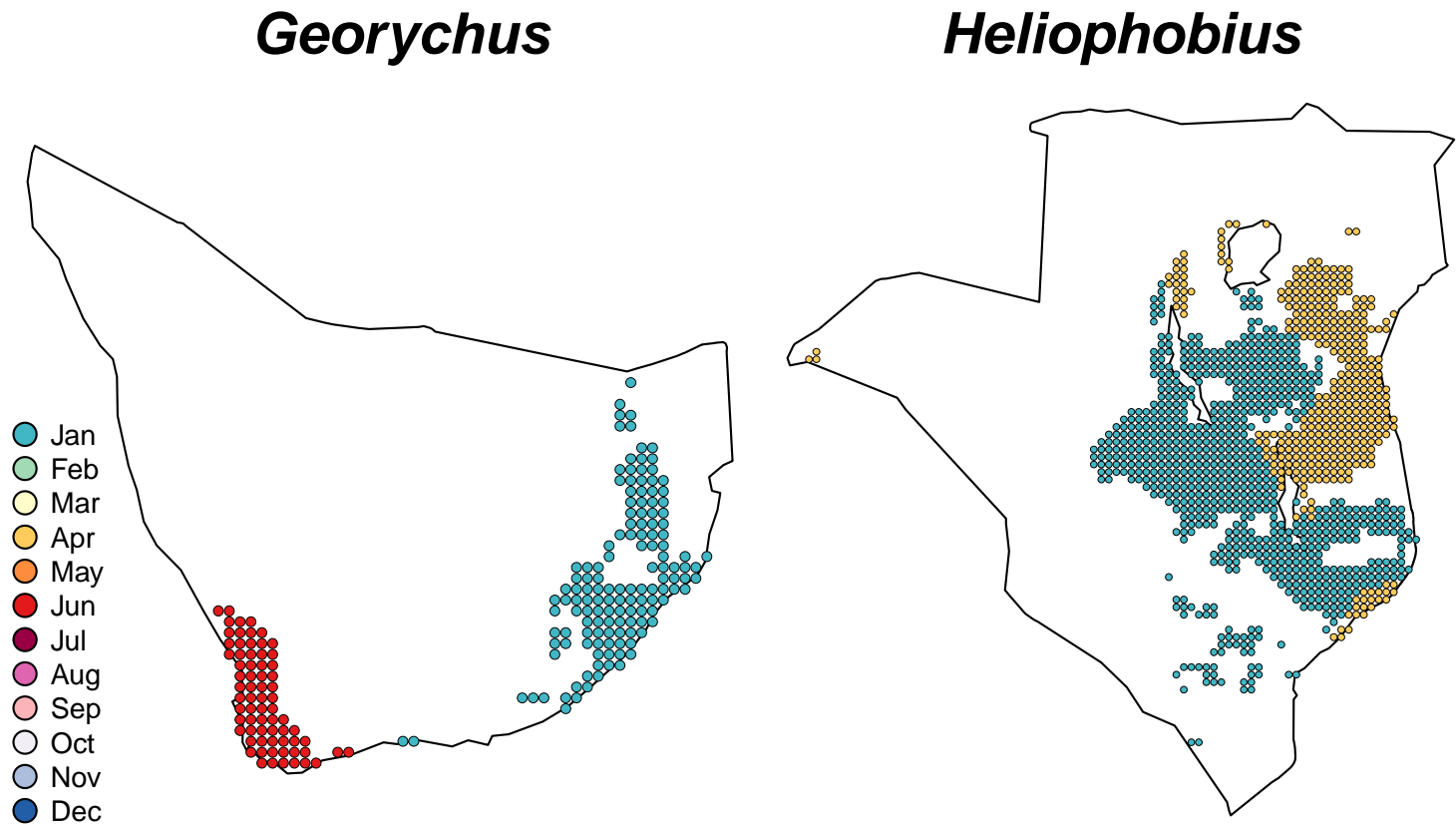


Figure S.10: Distribution of *Georychus* fossil sites on the background of the current distribution as estimated in Bennett and Faulkes (2000).

