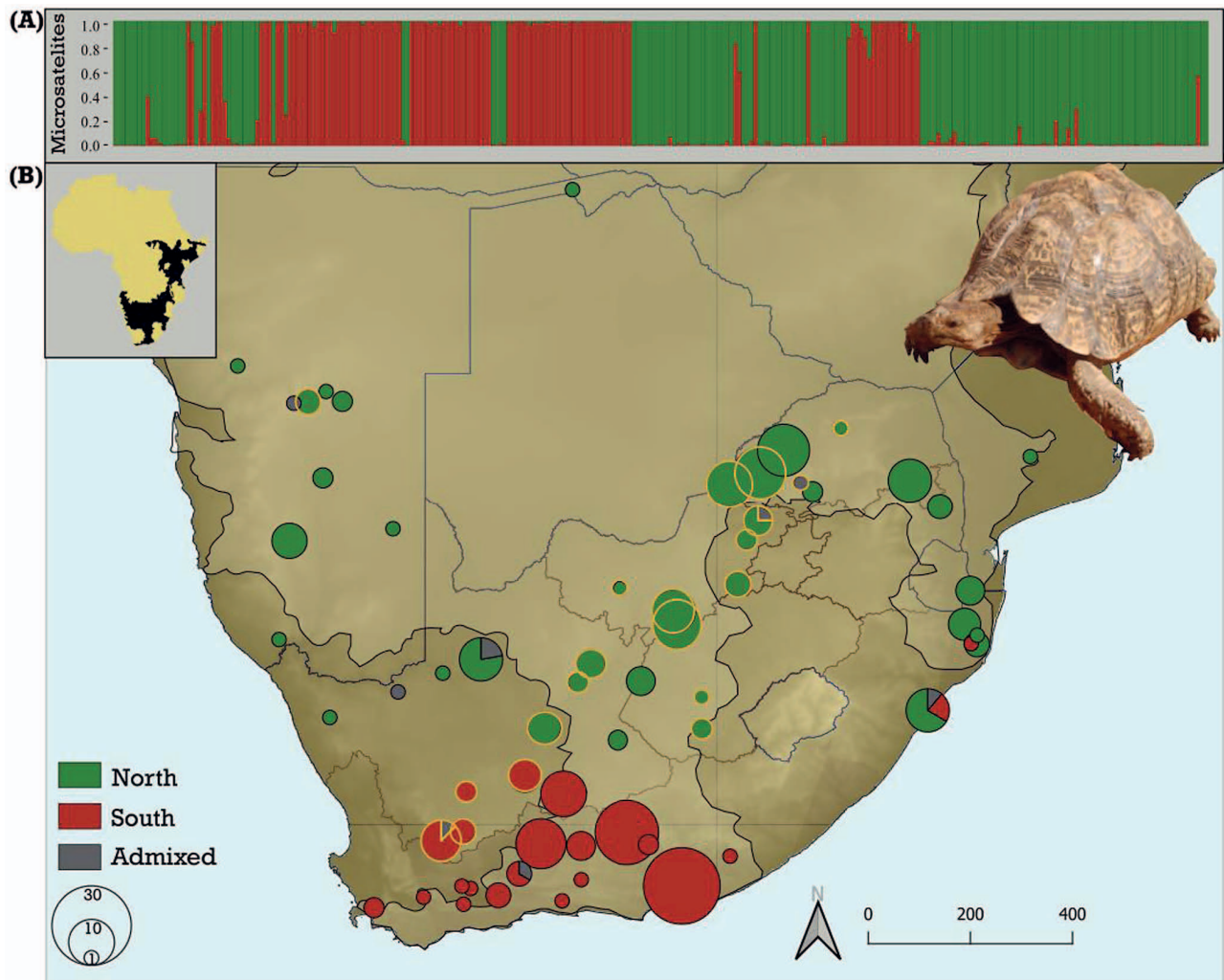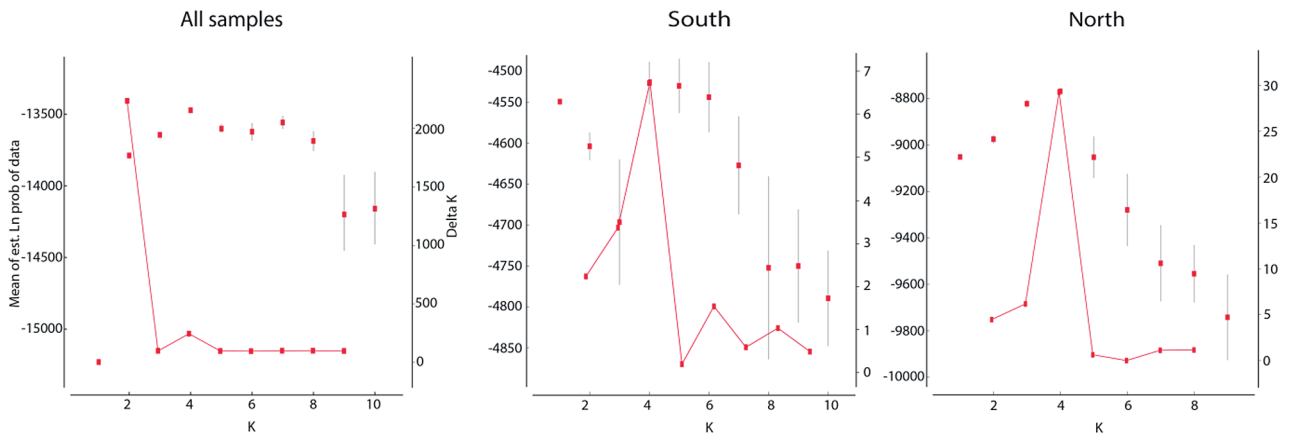**Supplementary document S1.** Samples of *Stigmochelys pardalis* used in the present study. Cells in the columns for STRUCTURE clusters are coloured according to the respective nuclear genomic identity. Values for STRUCTURE clusters show the respective inferred percentage of cluster assignment. CL – carapace length. See attached Excel Table.

Supplementary document S2. A) Genotypic clustering of 270 leopard tortoises (*Stigmochelys pardalis*) from 66 sites as inferred by STRUCTURE using 14 microsatellite loci (run with best probability value shown). Distinct clusters are color coded according to STRUCTURE inferred clusters. Within each cluster an individual is represented by a vertical bar that reflects its ancestry. Mixed ancestry is indicated by differently coloured segments corresponding to inferred genetic percentages of the respective cluster. B) The distribution range of *S. pardalis* is displayed as shaded area according to Baker et al. 2015 and Spitzweg et al. 2019. Individual sampling sites were lumped for clarity. Yellow circles mark newly sampled individuals. Symbol sizes refer to the respective sample size. Slices represent percentages of individuals with mixed ancestries or conflicting cluster assignments. For original sites see Supplementary document S1. Inset shows the whole putative distributional range (black) of *Stigmochelys pardalis* according to TTWG (2017).

Supplementary document S3. Delta K (red squares connected with a red line) and Ln P(D) values (red squares) for STRUCTURE runs for the complete data set (all samples) and for each of the two clusters, South and North, separately.
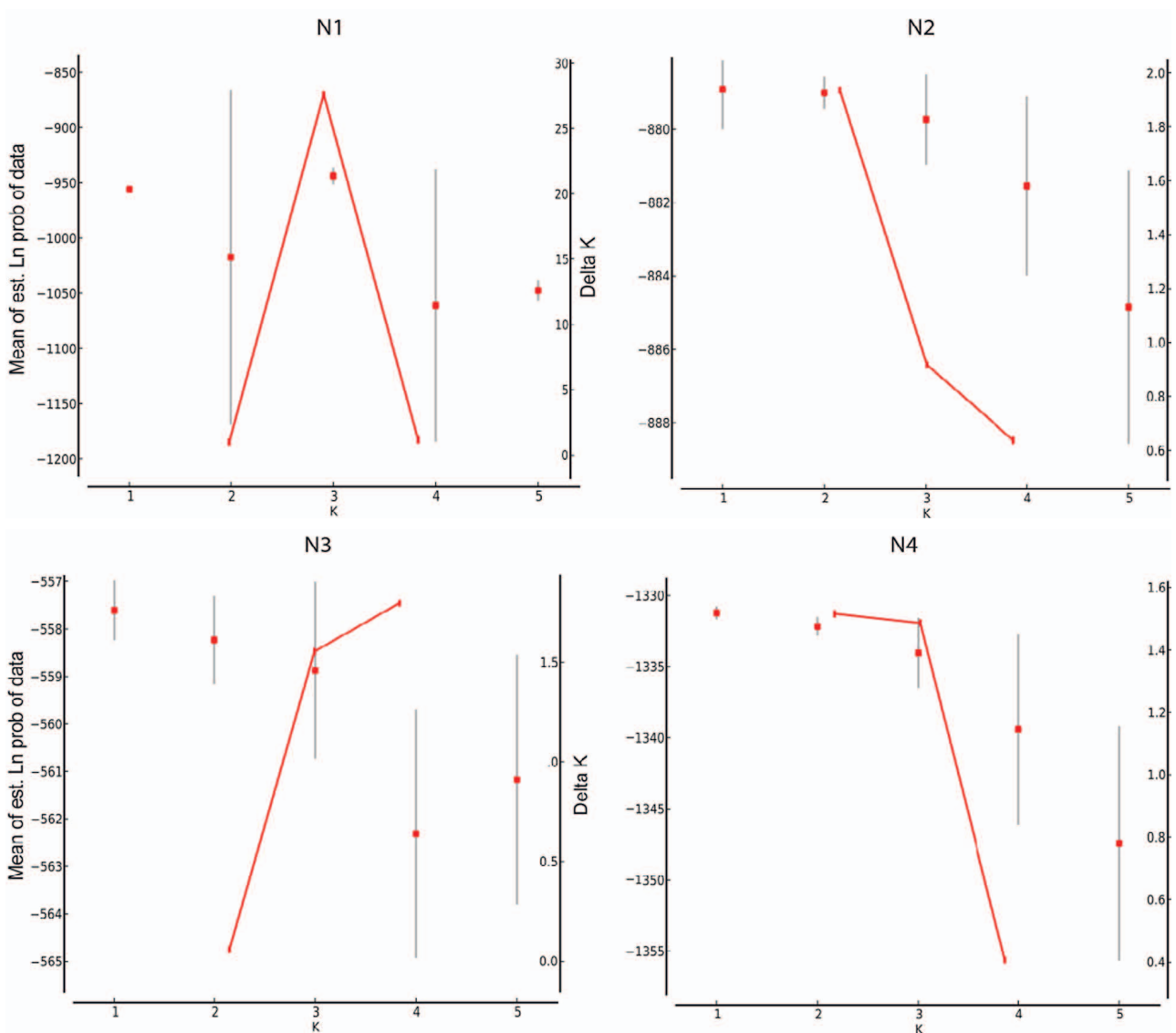
Supplementary document S4. Delta K (red line) and Ln P(D) values (red squares) for STRUCTURE runs for each northern subcluster (N1–N4) separately.