

Figure S1. Genotypic clustering and admixture in *Ctenotus pantherinus* based on a ddRAD dataset assembled without a divergent Kimberly sample (see text). Bars depict the relative proportion of alleles in each individual corresponding to the inferred genotypic clusters (i.e., individuals' ancestry proportions). Pie charts on map indicate the average ancestry proportions corresponding to each cluster at each site (based on all individuals at that site). Multi-colored pies indicate admixture among clusters. This analysis yielded the same results as the one including all sampled individuals (Fig. 6), including the best-fit number of clusters (= 4), their sample composition, and patterns of admixture.

