

Figure S1: sampling strategy and central Coast Ranges sampling gap

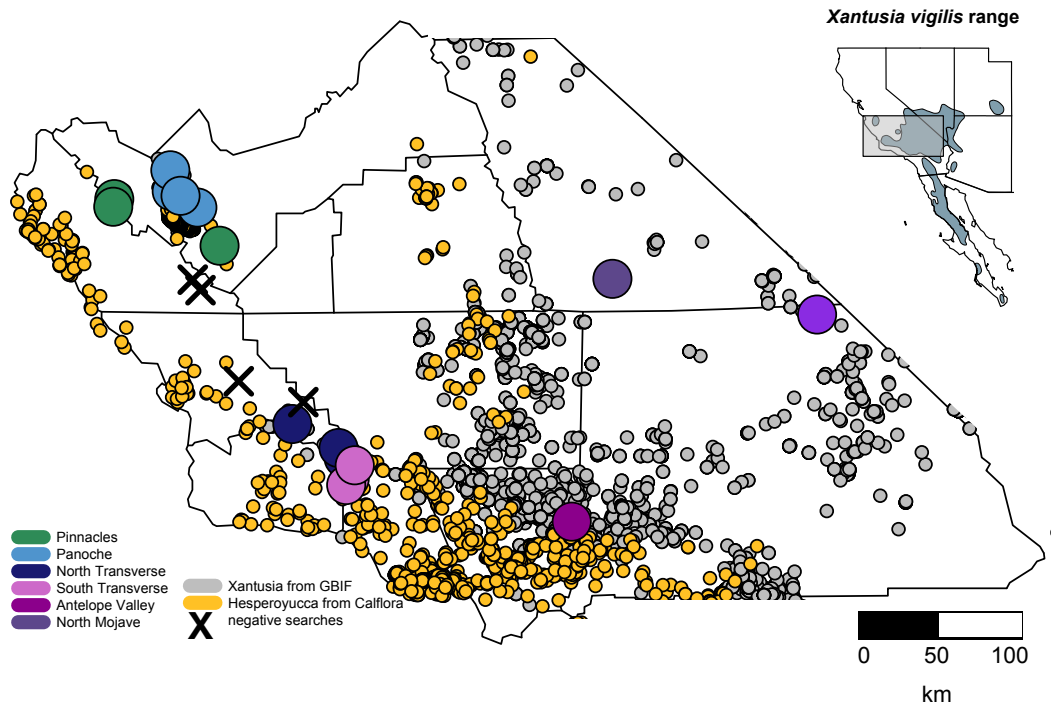


Figure S1: Our sampled populations in this paper (see Figure 2, Figure S2A for population and region labels), compared to GBIF records for *Xantusia vigilis* and CalFlora records of *Hesperoyucca whipplei*. Also noted are locations of searches by two authors that did not locate *X. vigilis* in the central Coast Ranges sampling gap. Further sampling may identify populations in this gap.

Figure S2A: population codes on Figure 2 map

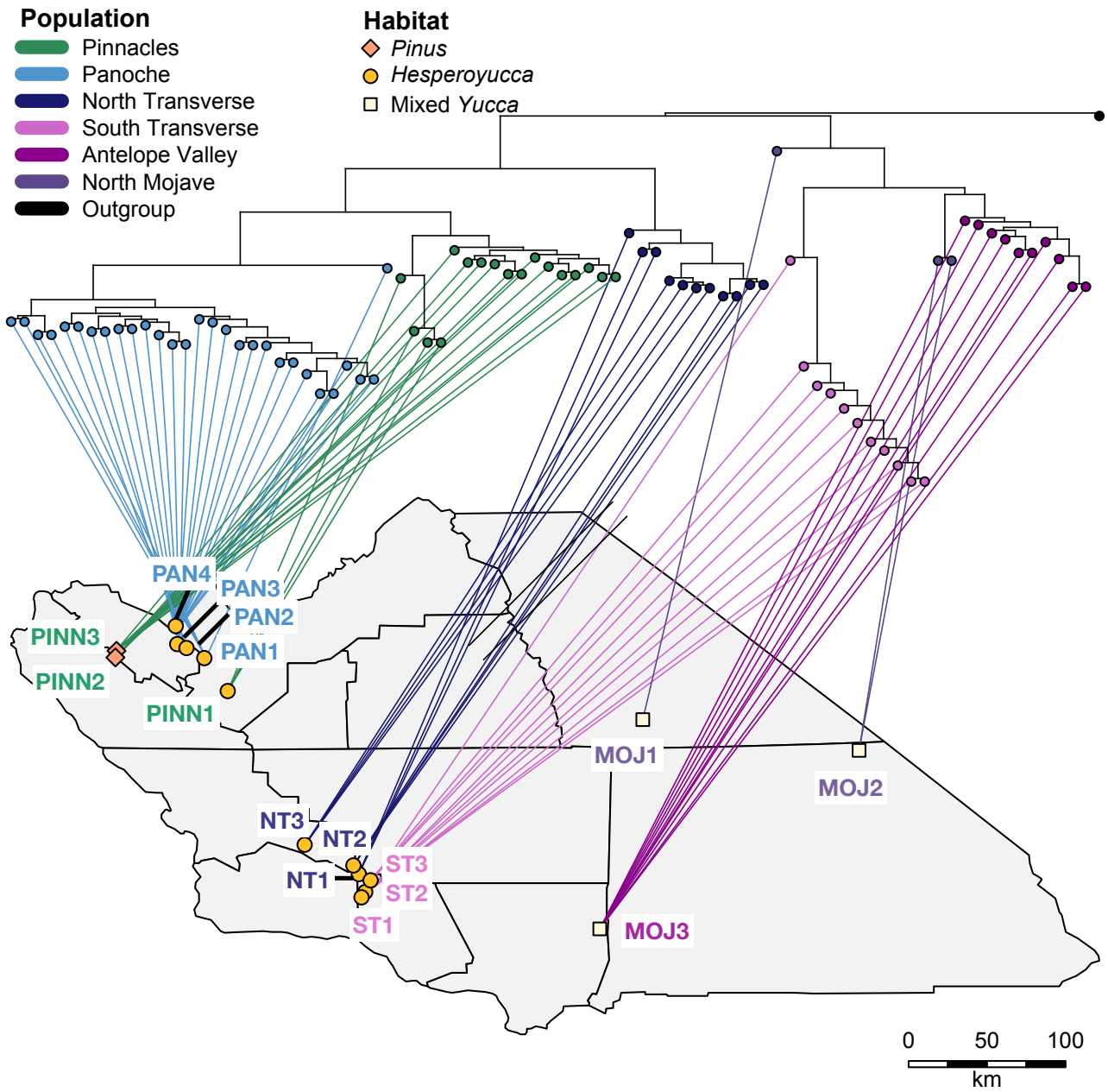


Figure S2: bootstrap support and gene concordance values for our RAD tree

Our Astral tree displaying bootstrap support for nodes (first number, range 0-1) and the percentage of fragments supporting the topology presented (second number, range 0-100).

While bootstrap supports are high for the region-level splits, gene concordance is low, reflecting the complexity of the demographic history of the landscape.

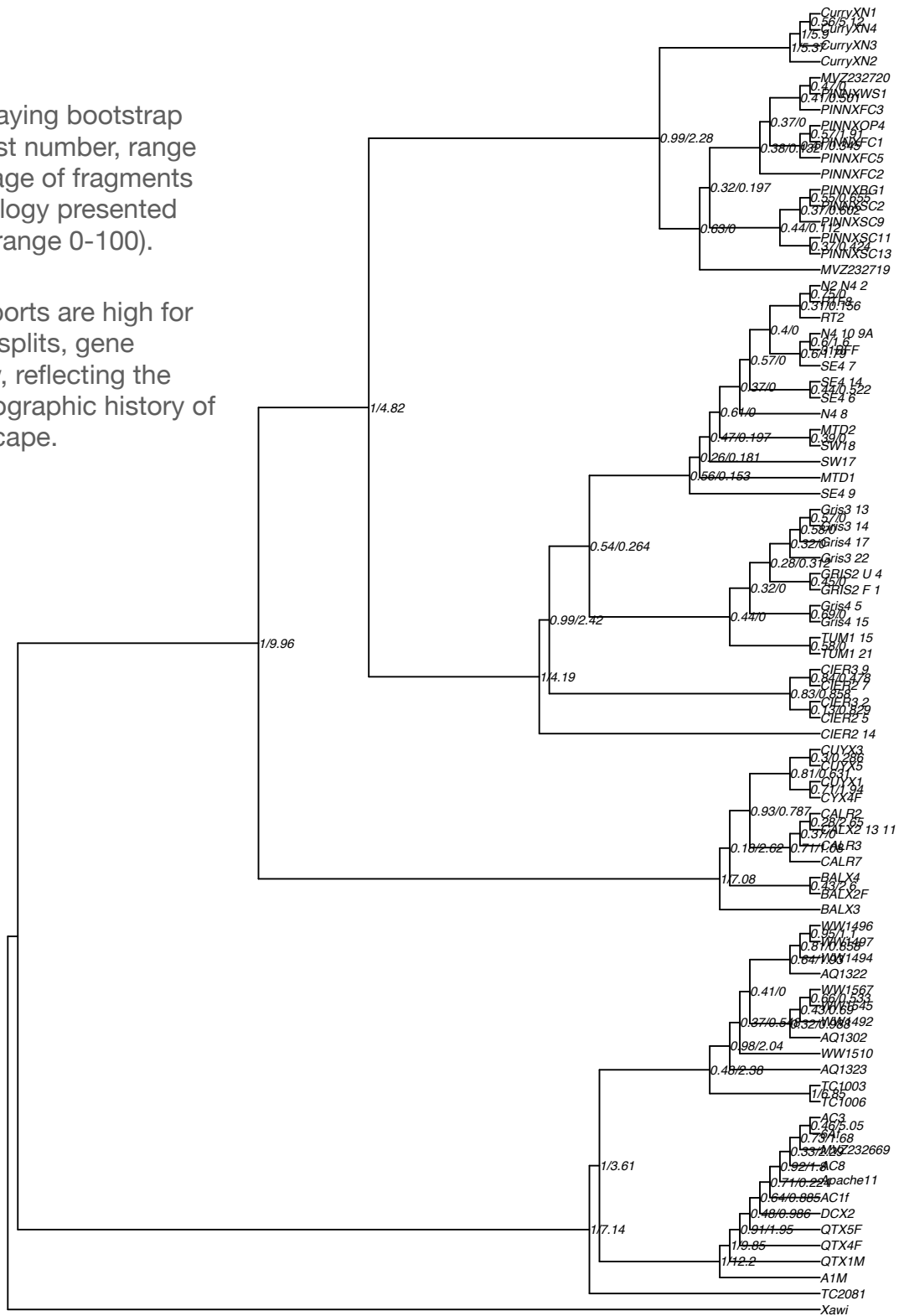
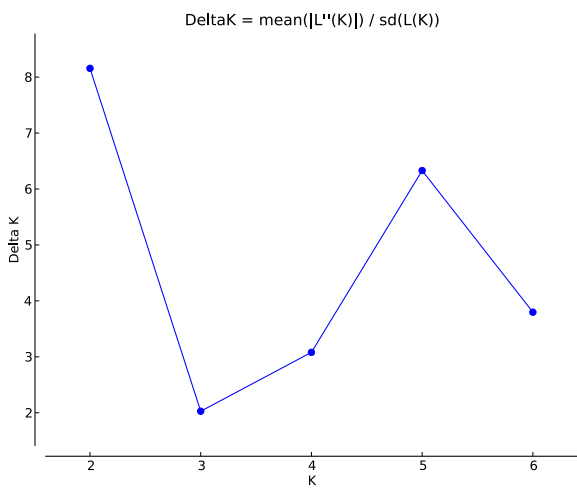


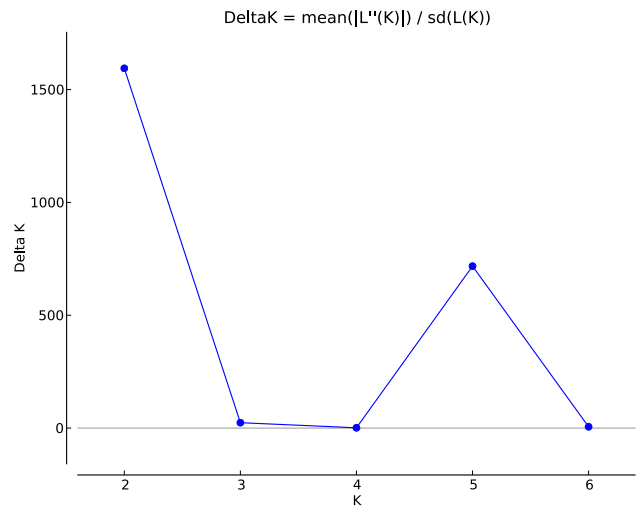
Figure S3: structure analyses

S3 A: Evanno delta K results support K=2 as the best division of populations with the full dataset

Microsatellites

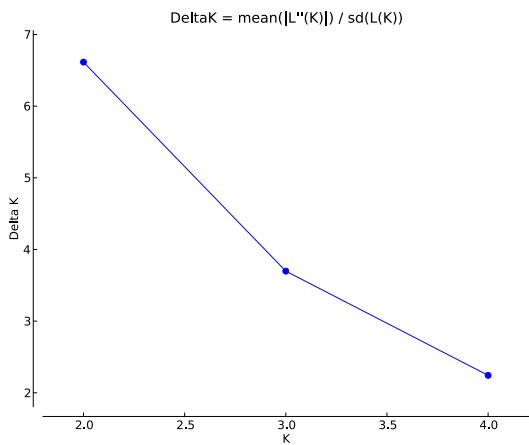


RADseq

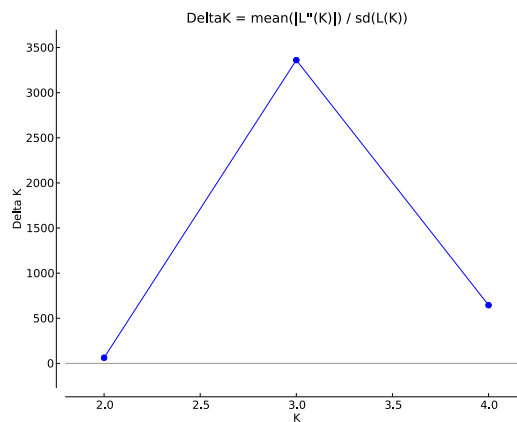


S3 B: Evanno delta K results for northern and southern populations

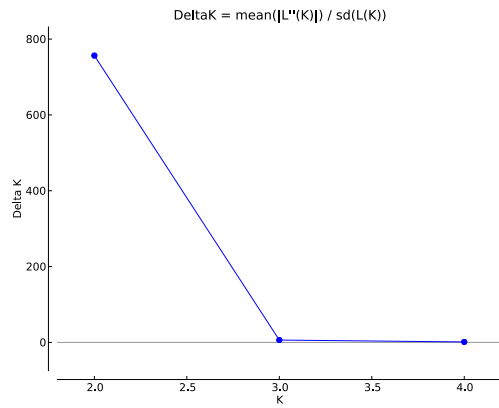
Microsatellites, northern population



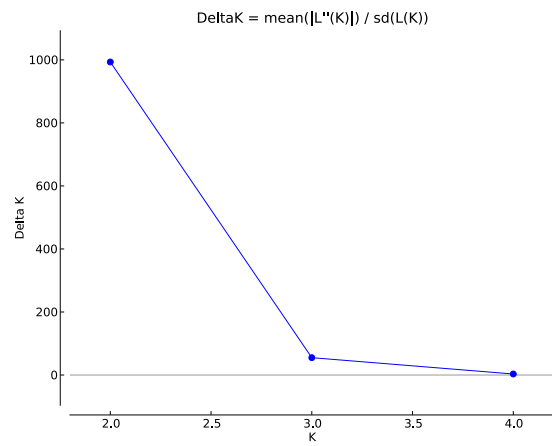
RADseq, northern population



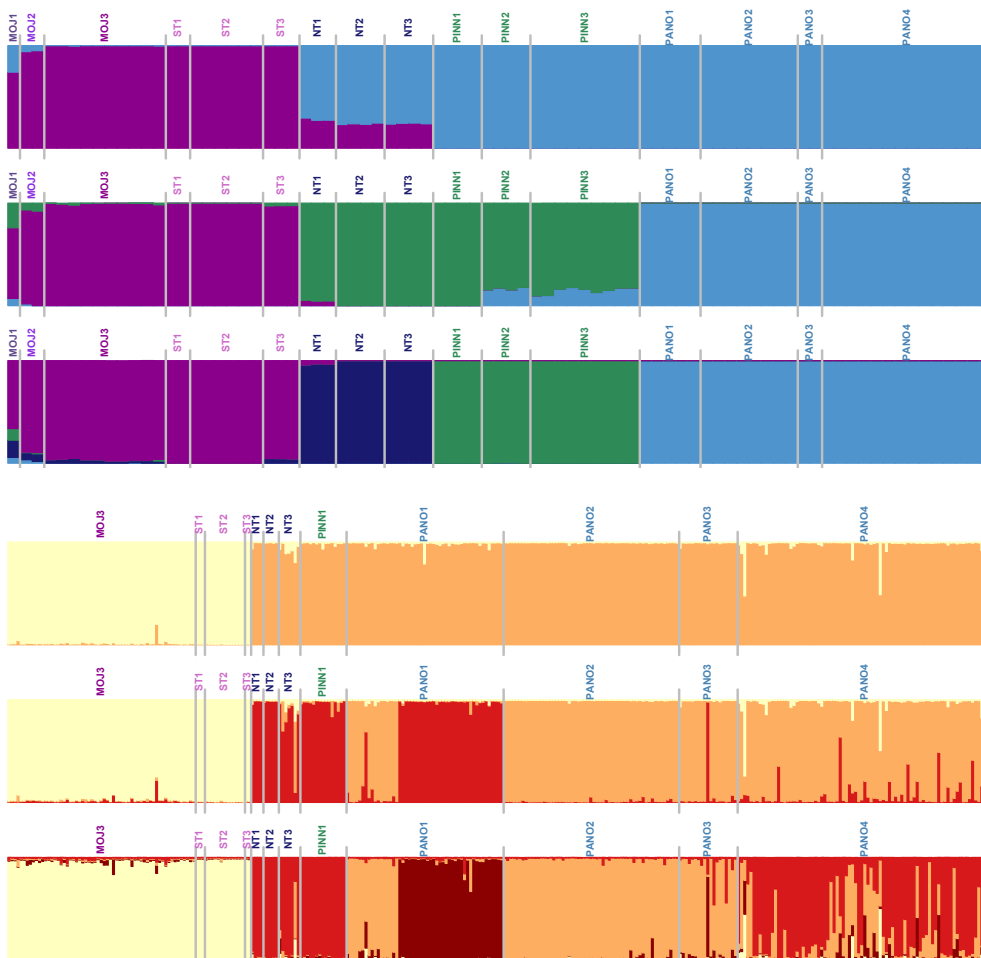
Microsatellites, southern population



RADseq, southern population



S3 C: Full dataset Structure results: RADseq (top) and micro satellite (bottom) From K=2 to K-4



S3 D: equal sample size microsatellite results

