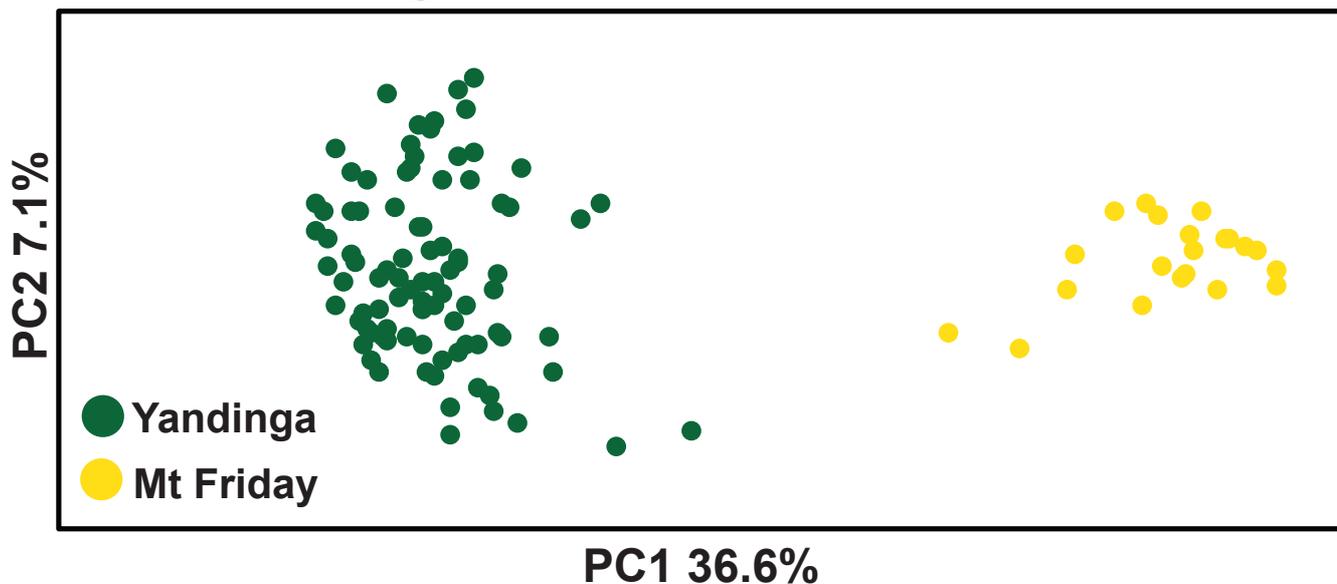
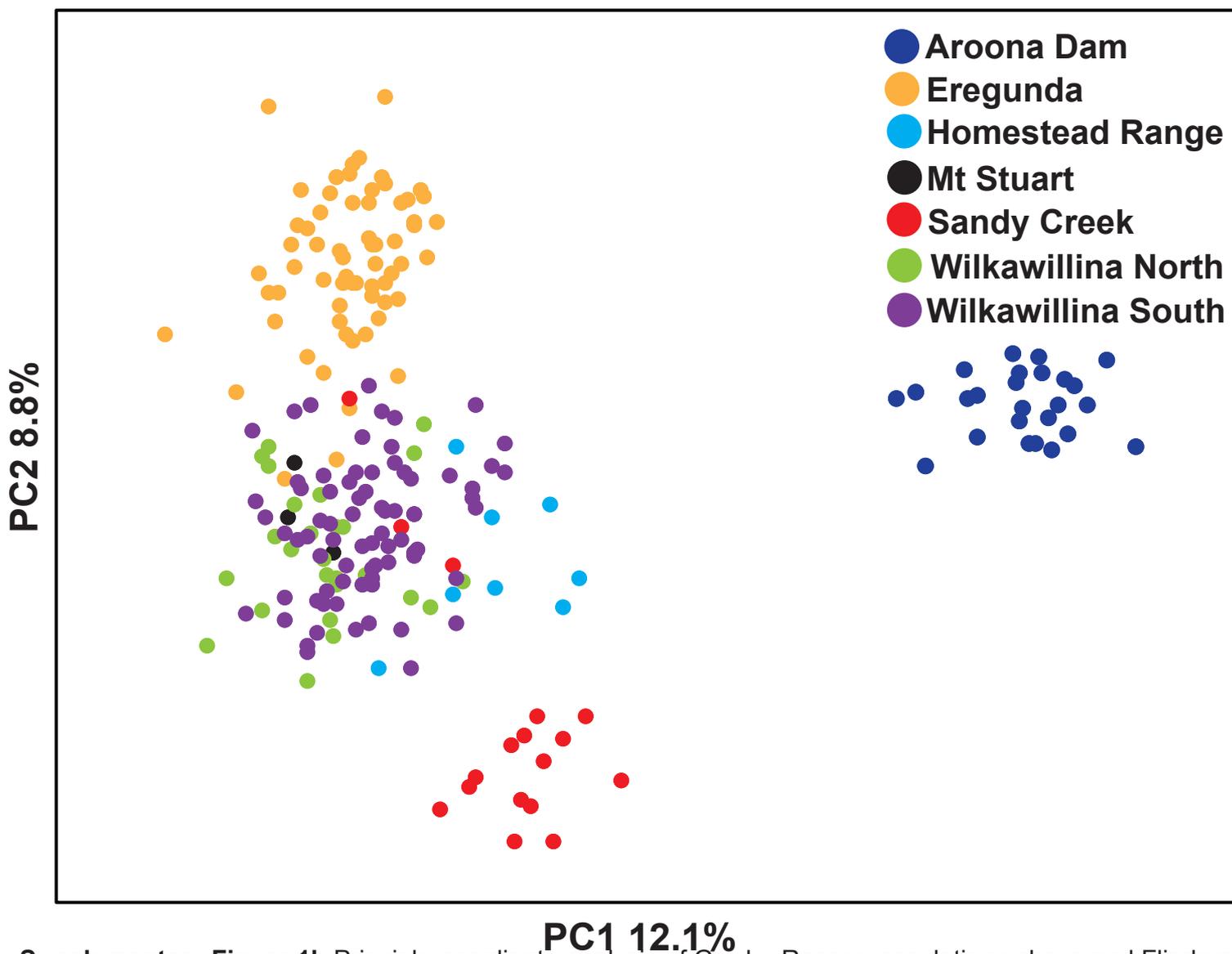


Gawler Ranges

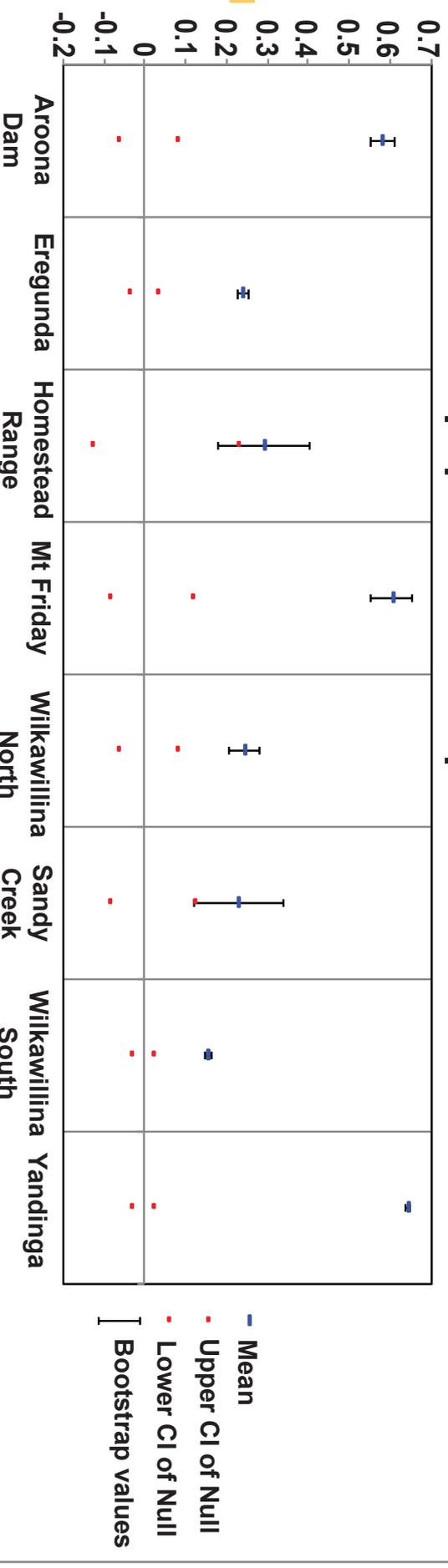


Flinders Ranges

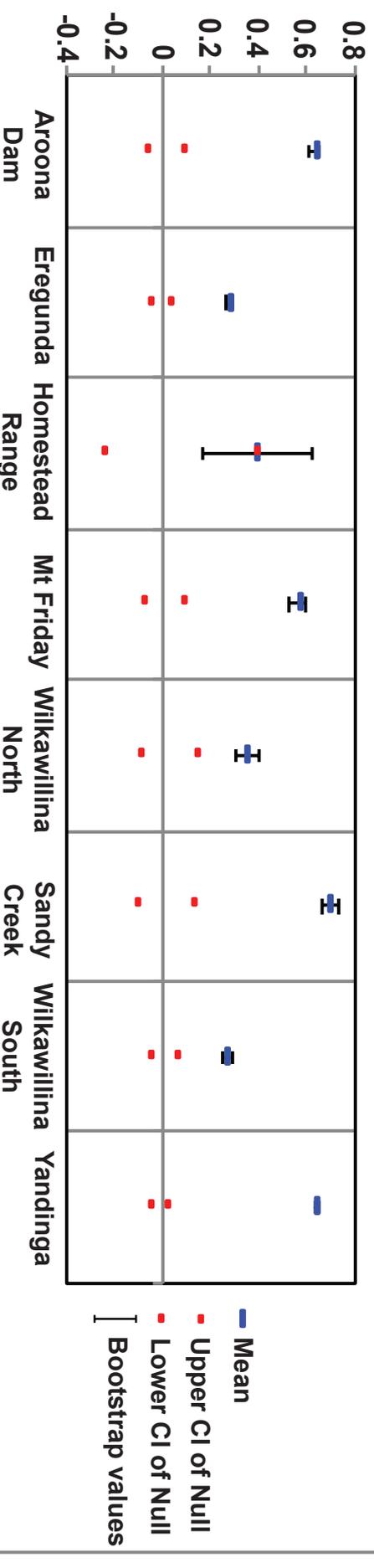


Supplementary Figure 1b Principle coordinate analysis of Gawler Ranges populations above and Flinders Ranges populations of *P. x. xanthopus* below based on microsatellite genotypes.

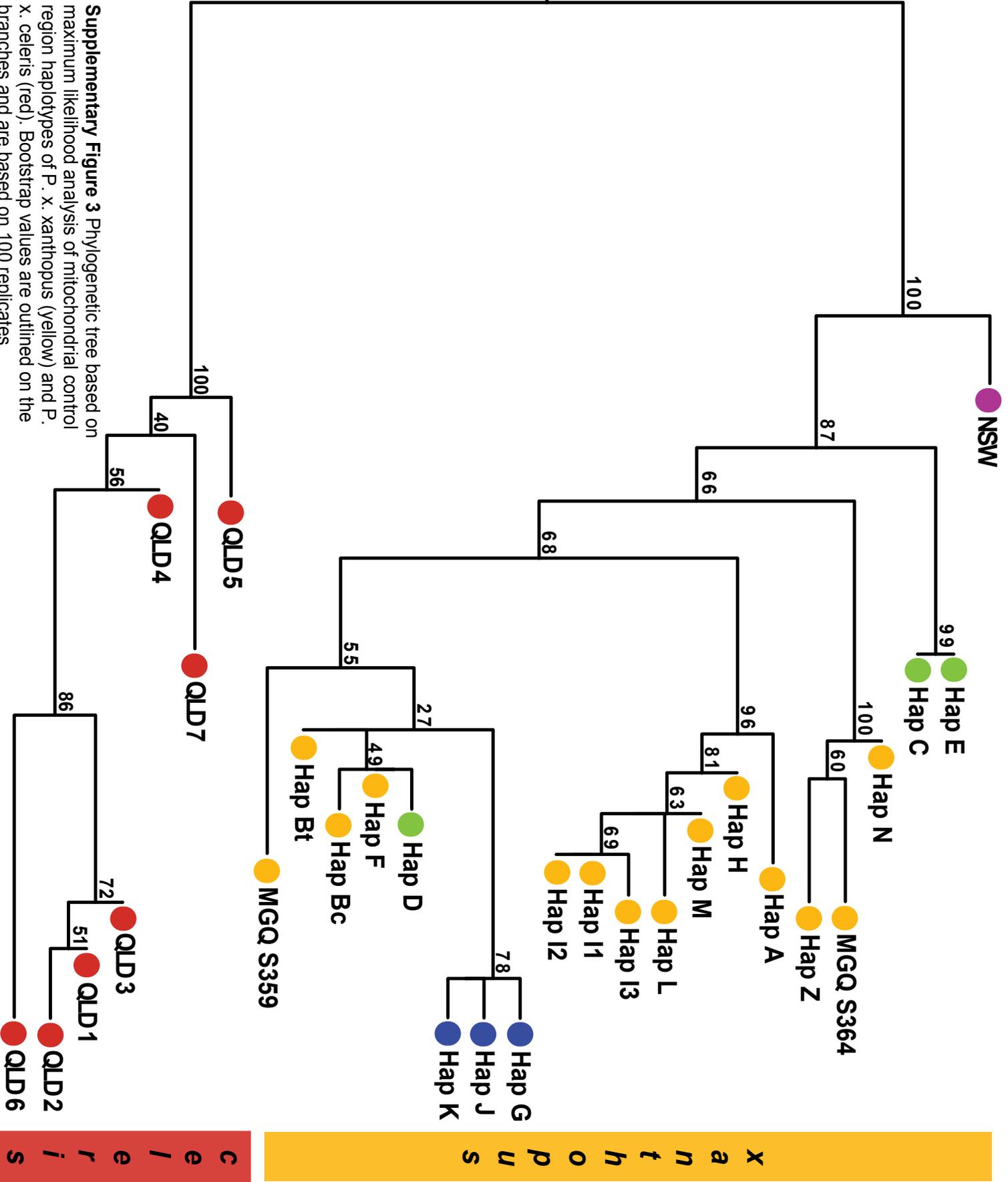
Mean within population male pairwise relatedness



Mean within population female pairwise relatedness



Supplementary Figure 2 Mean pairwise relatedness for individual male (above) and female (below) *P. x. xanthopus* from populations in South Australia. Error bars surround the mean pairwise relatedness value (blue line) based on bootstrap analysis; and red lines represent the 95% upper and lower confidence bounds around the null hypothesis of no difference across populations.

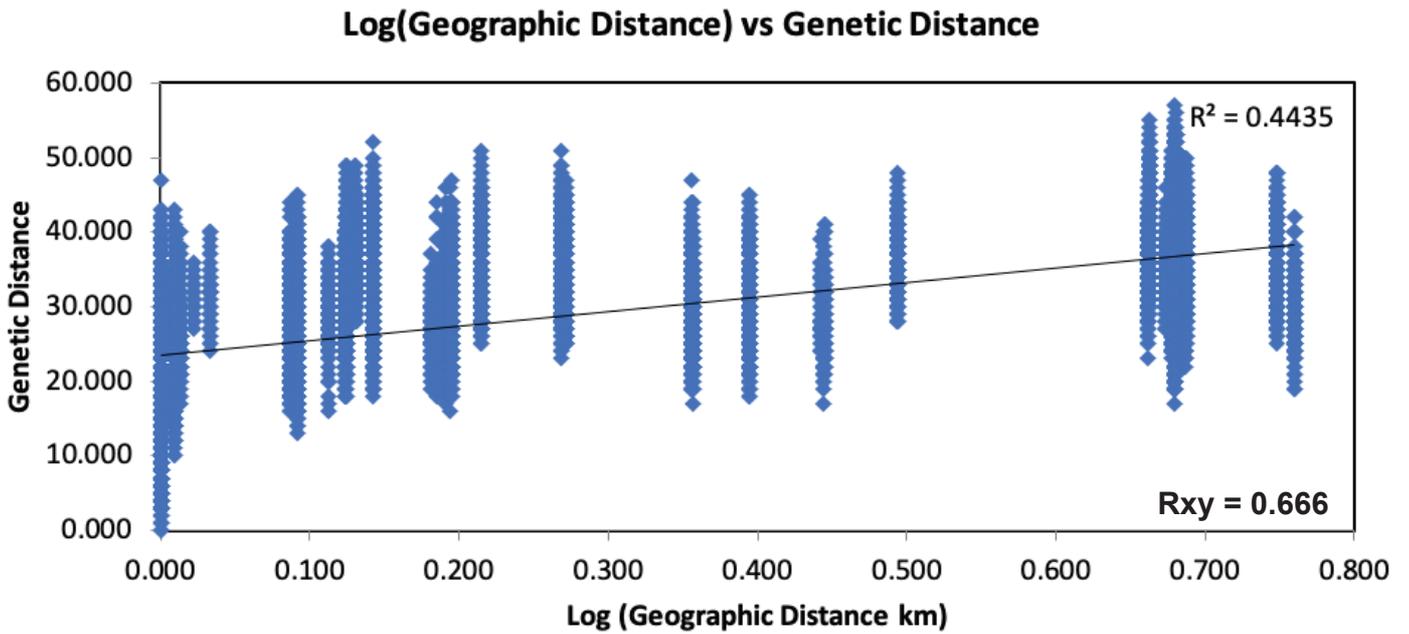


x a n t h o p u s

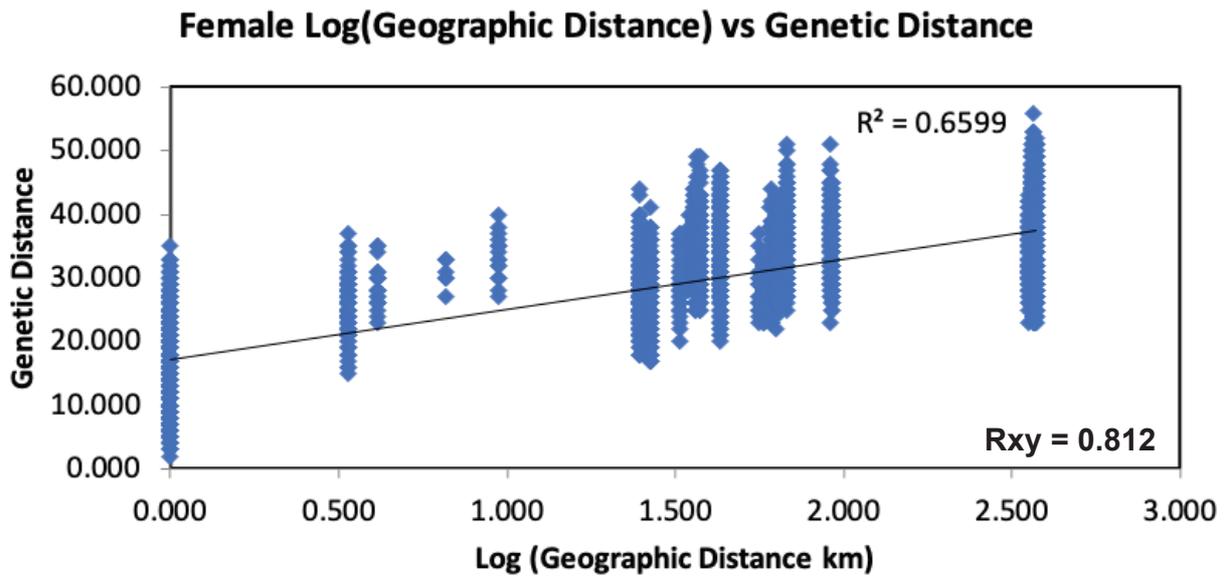
c e l e r i s

Supplementary Figure 3 Phylogenetic tree based on maximum likelihood analysis of mitochondrial control region haplotypes of *P. x. xanthopus* (yellow) and *P. x. celeris* (red). Bootstrap values are outlined on the branches and are based on 100 replicates.

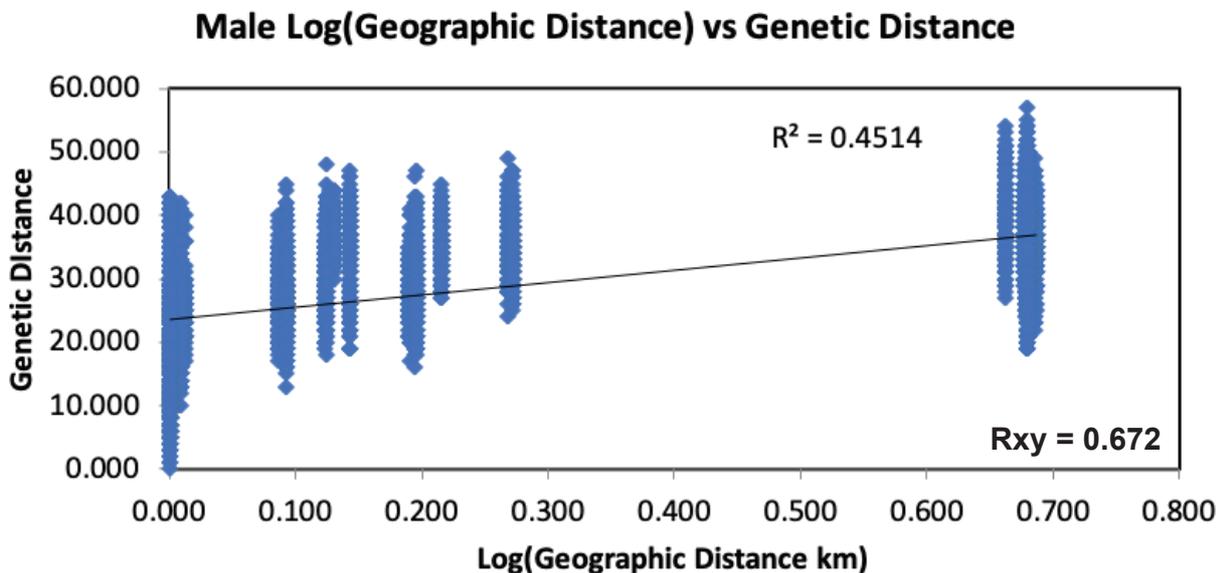
(a)



(b)



(c)



Supplementary Figure 4 Mantel tests for isolation-by-distance of log geographic distance against genetic distance for (a) all individuals, (b) males only, and (c) females only. All were significantly correlated.

Supplementary Figure 5 Decision framework from Frankham et al. (2011) highlighting the evaluation process for management based on genetic data.

