SUPPLEMENTARY TABLES AND FIGURES

	Hp	MPD	π ± SD	Average AI
Total (195)	10	12.9	0.032 ± 0.016	-
Females (114)	6	10.4	0.026 ± 0.013	-
Band 1 (26)	3	4.9	0.012 ± 0.007	0.60
Band 2 (54)	3	14.9	0.036 ± 0.018	0.54
Band 3 (34)	2	0.3	0.001 ± 0.001	0.83
Unit Males (46)	8	15.8	0.039 ± 0.019	-
Band 1 (4)	3	20.5	0.050 ± 0.034	0.60
Band 2 (23)	4	17.0	0.042 ± 0.021	0.54
Band 3 (19)	5	13.0	0.032 ± 0.017	0.83
Bachelors (35)	6	16.6	0.041 ± 0.021	-

Table S1. Within bands, females are more likely to share the same haplotype than males. Gelada mtDNA haplotype diversity. Sample size (N), number of haplotypes (Hp), mean pairwise differences among haplotypes (MPD) and nucleotide diversity (π). Average AI represents the average association index among units within each of the three bands.

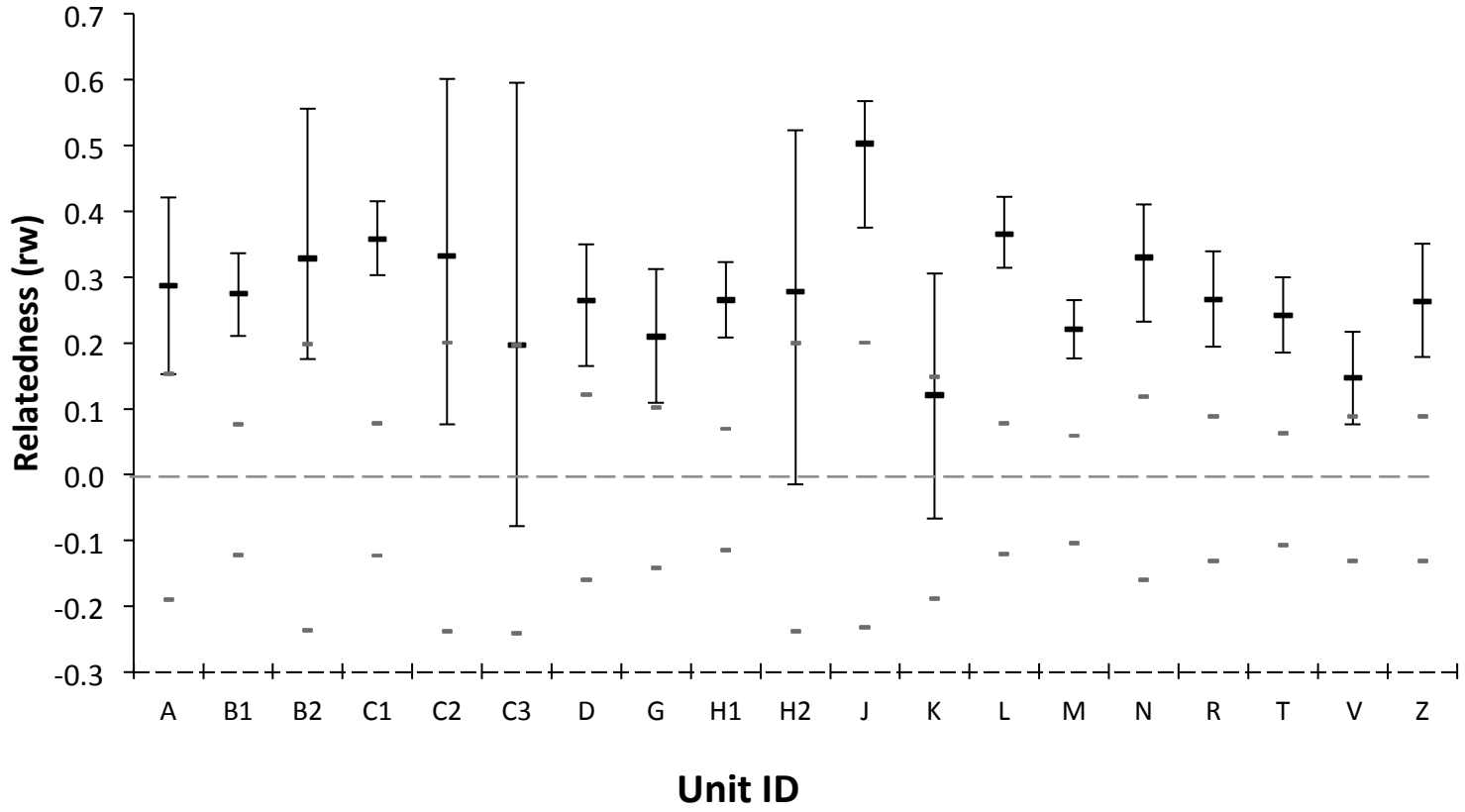

Figure S1: Average relatedness among dyads with 95% confidence intervals (CI). Grey dashes represent bootstrapped 95% CI assuming random mating and dispersal. Females within 18/19 study units are significantly more related than chance (right panel).

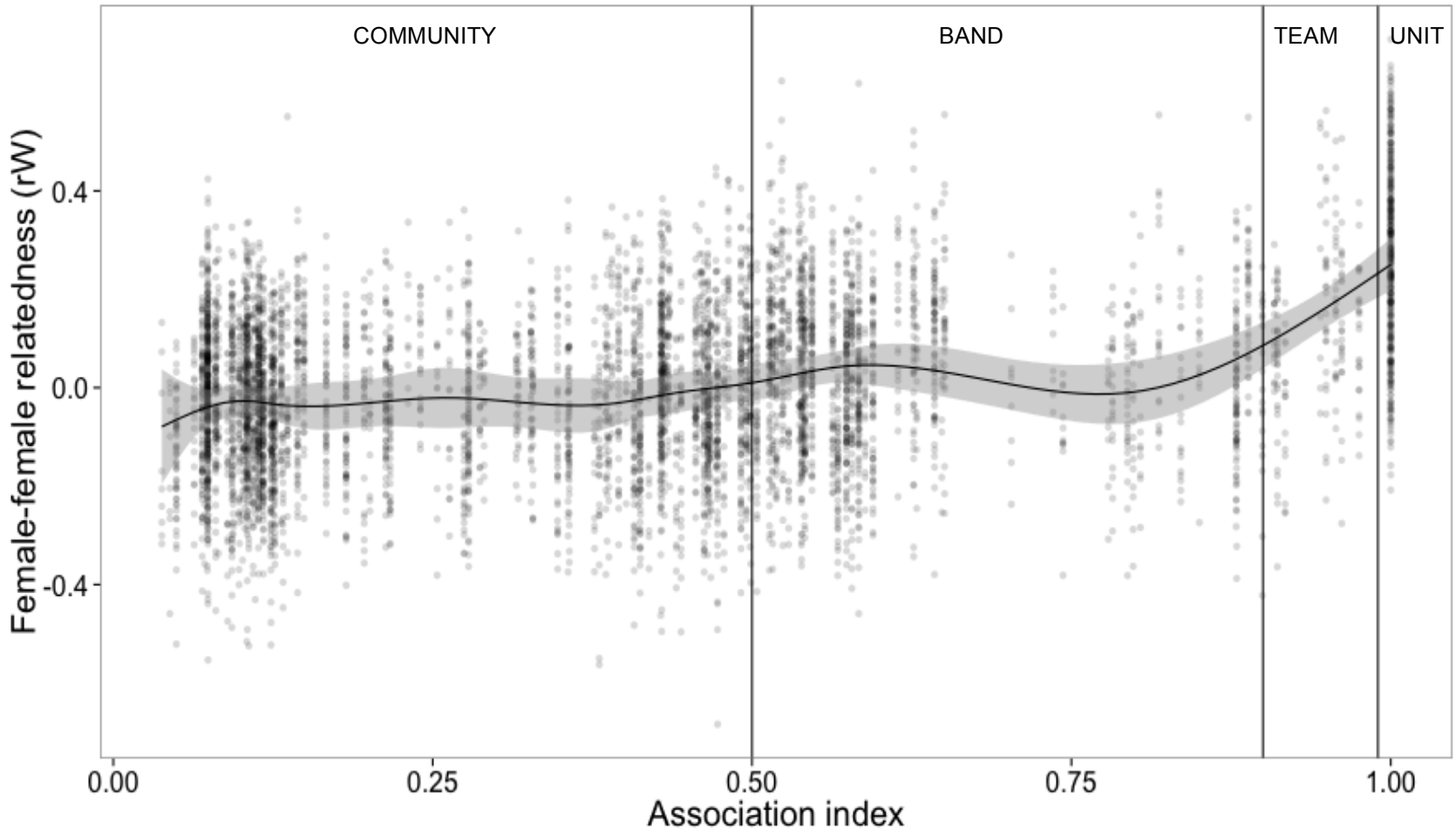

Figure S2: Female-female dyads that associated more closely had higher values of pairwise genetic relatedness. AIs were significantly correlated with relatedness for all female-female dyads. Each point represents pairwise relatedness for one female-female dyad (N=6441 dyads). The curve was fit using LOESS and the shaded area represents a 95% CI around the curve.

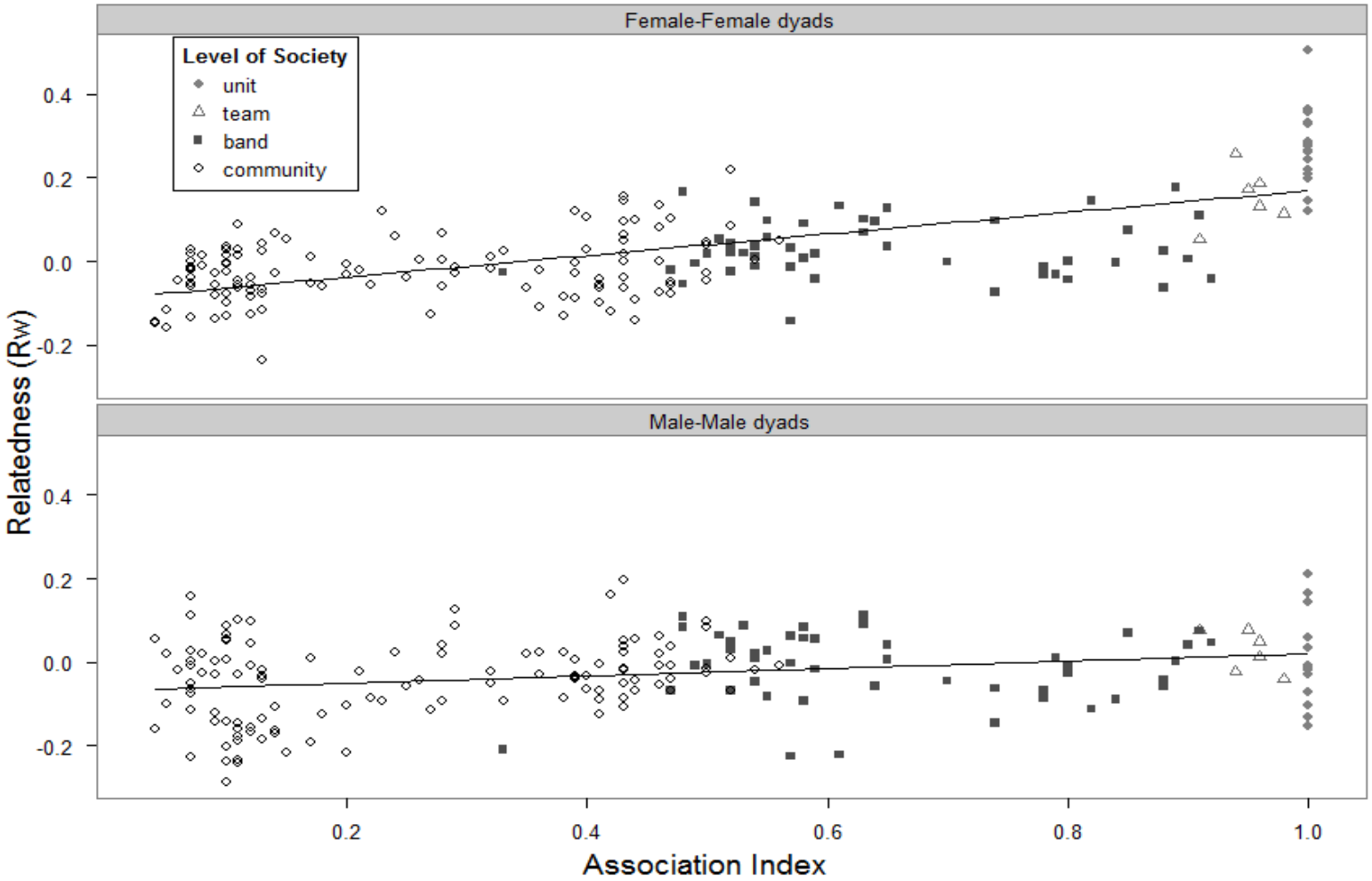

Figure S3: Correlation between association and relatedness (rw) in female-female dyads (top panel) and male-male dyads (bottom panel). There is a strong positive correlation between association and relatedness among females, but not among males. Within unit dyads (gray diamonds), within team dyads (open triangles), within band dyads (grey squares), within community dyads (open diamonds).

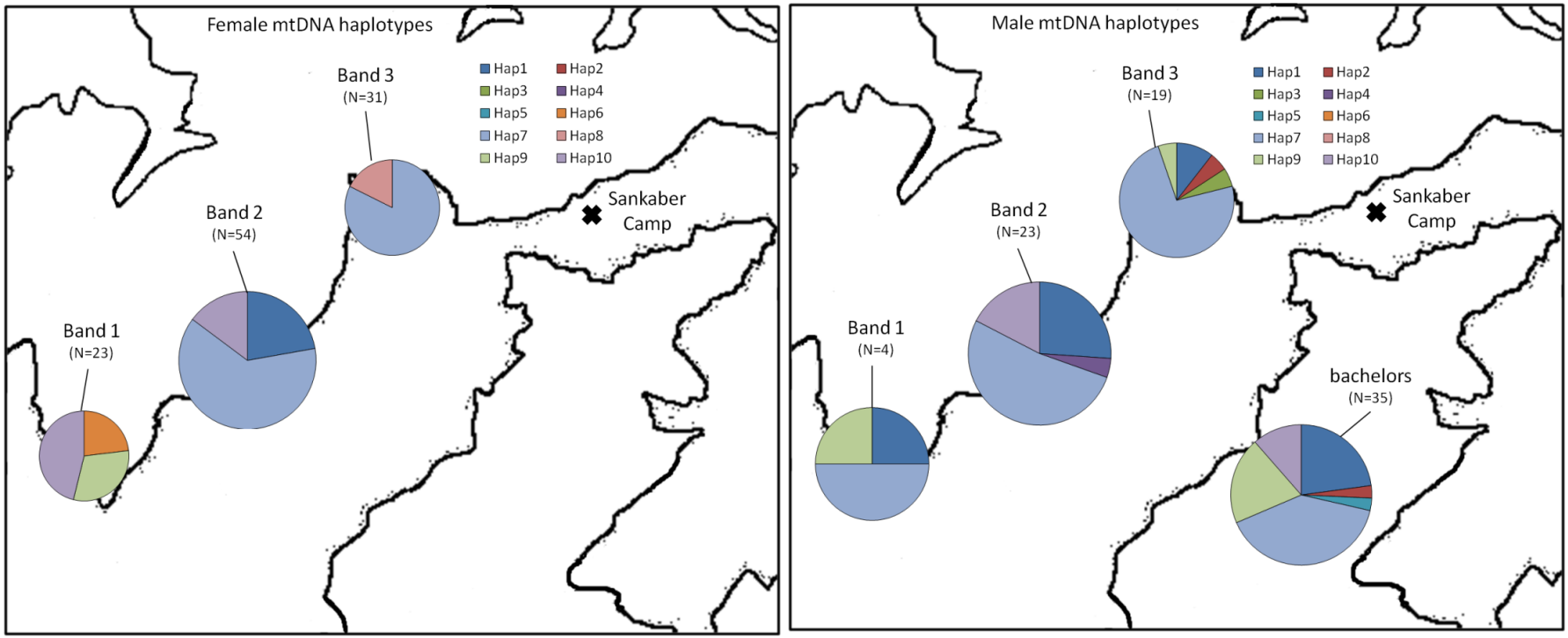

Figure S4: Distribution of mtDNA haplotypes in the three study bands. Female mtDNA haplotype distribution is strongly associated with association patterns and band membership (left panel), which is not the case in the distribution of mtDNA haplotypes in males (right panel). Each color represents a unique haplotype.

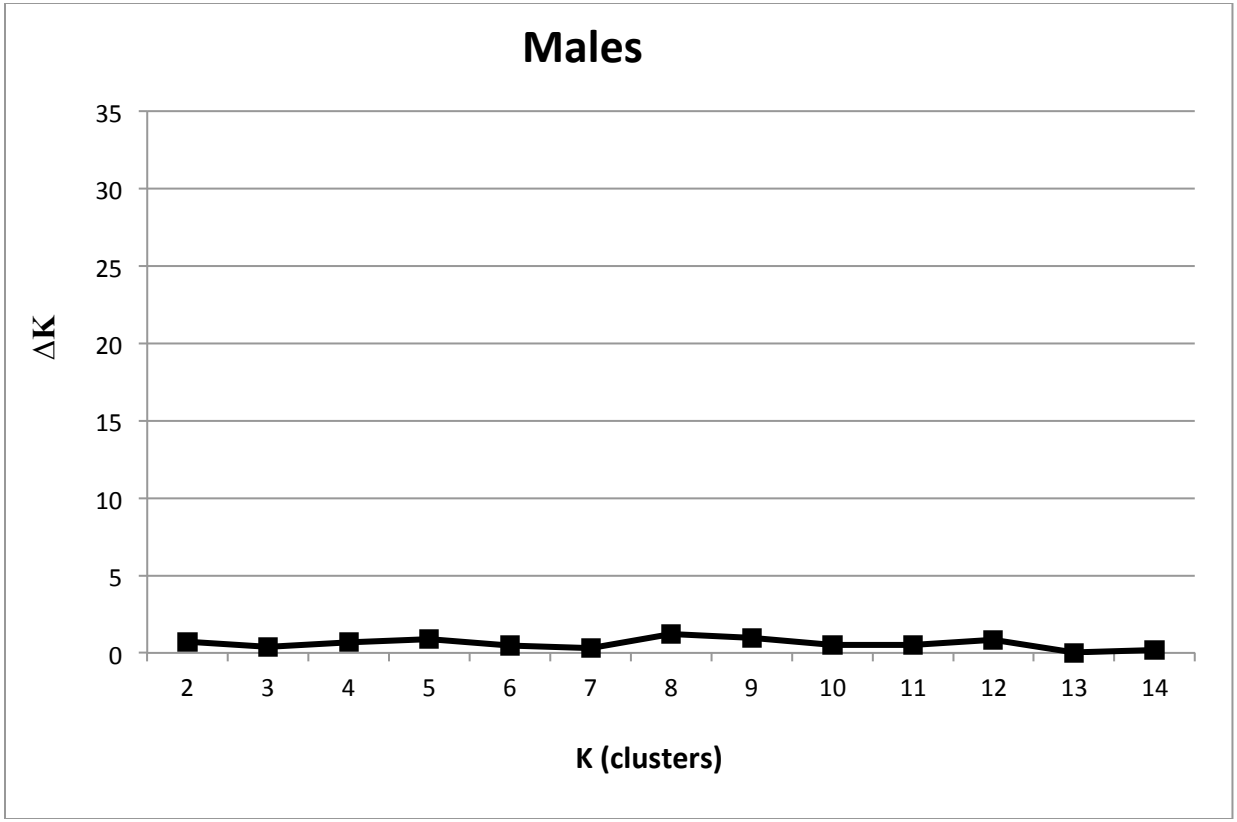

Figure S5: Delta K for STRUCTURE output using only male microsatellite genotypes. There is no apparent subgrouping among males.

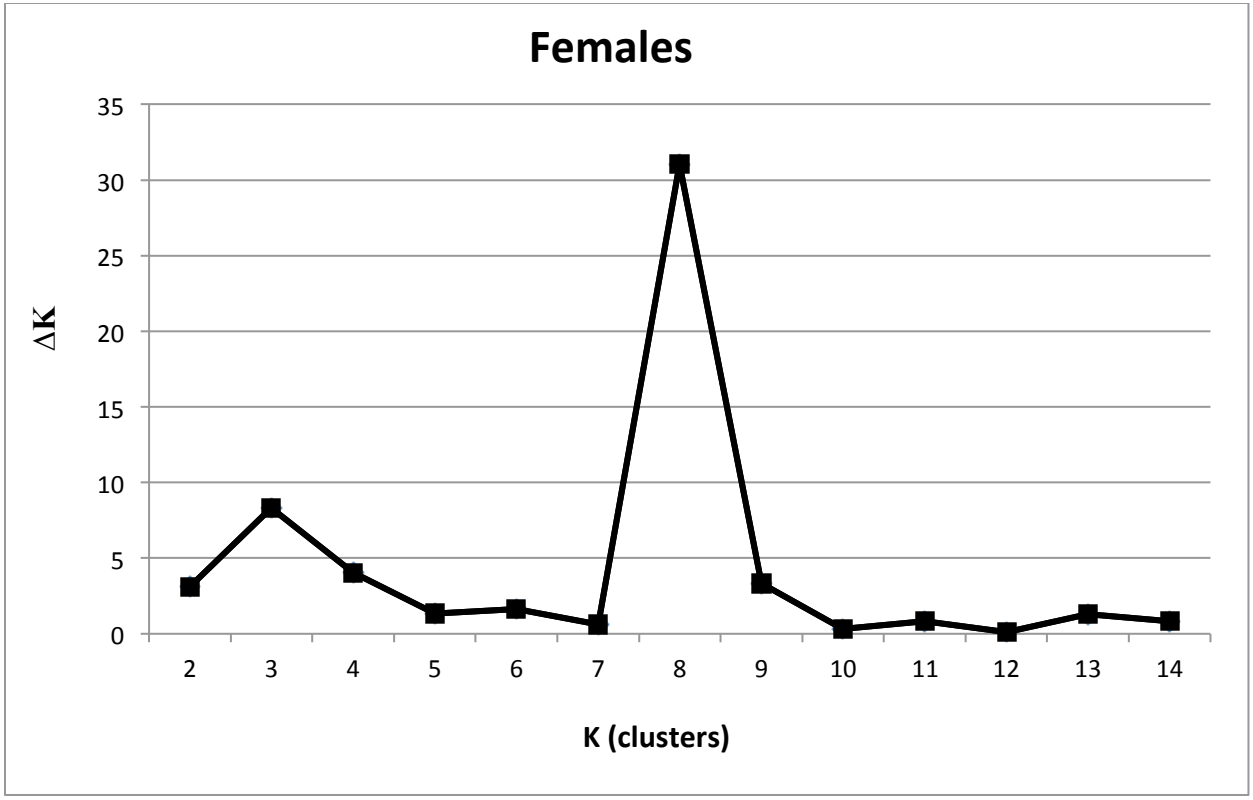

Figure S6: Delta K for STRUCTURE output using only female microsatellite genotypes. It is likely that we have 8 subgroups with a more subtle substructure of 3 groups.

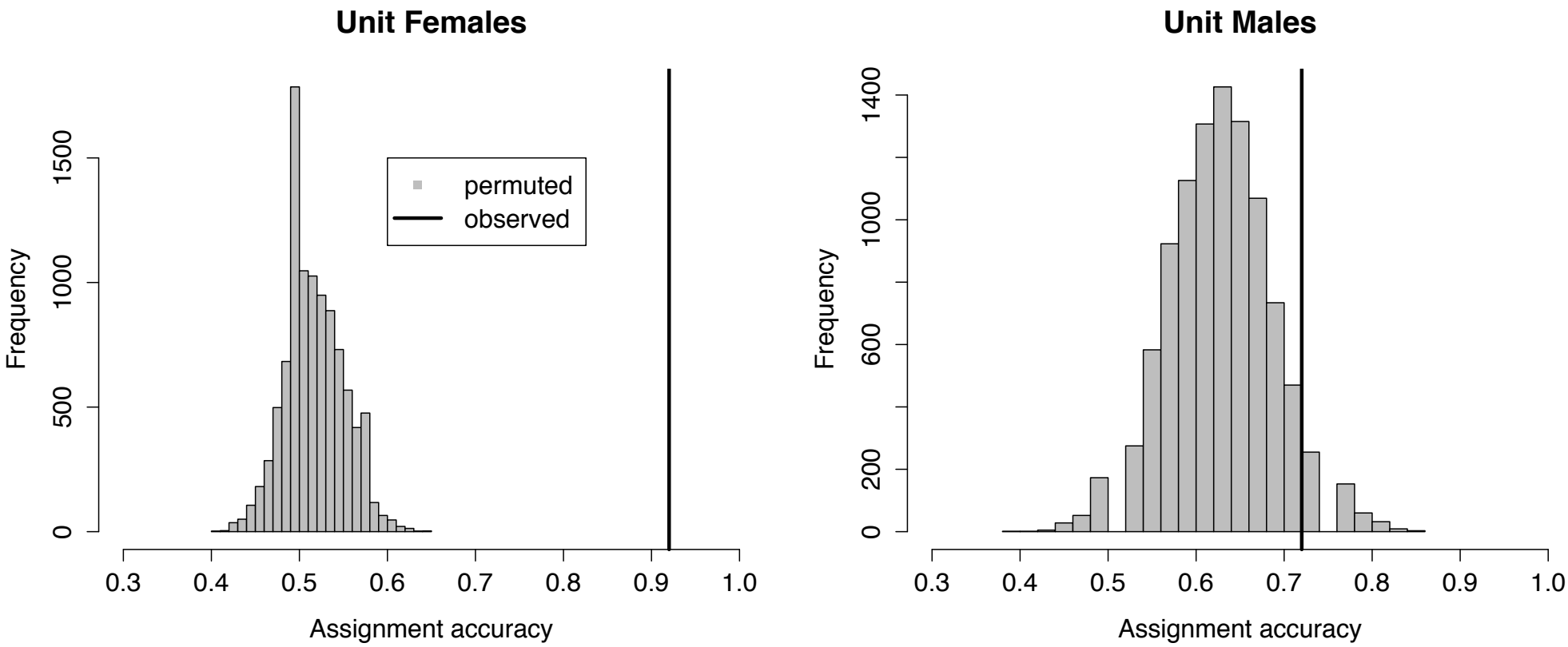

Figure S7: **Bands are genetically distinct for females, but not males. Proportion of females (left panel) and males (right panel) accurately assigned ("assignment accuracy") to their band using discriminant analysis of principal components (DAPC) of their genotypes. This was calculated using the R function "dapc" in the package *adegenet*. Grey bars represent the assignment accuracy of 10,000 permutations, in which individuals were randomly assigned to one of the three bands. Vertical black bar represents the observed assignment accuracy. Females were significantly more likely to be assigned to the correct deme than random ($p<0.0001$), but this was not the case for males ($p=0.0512$).**

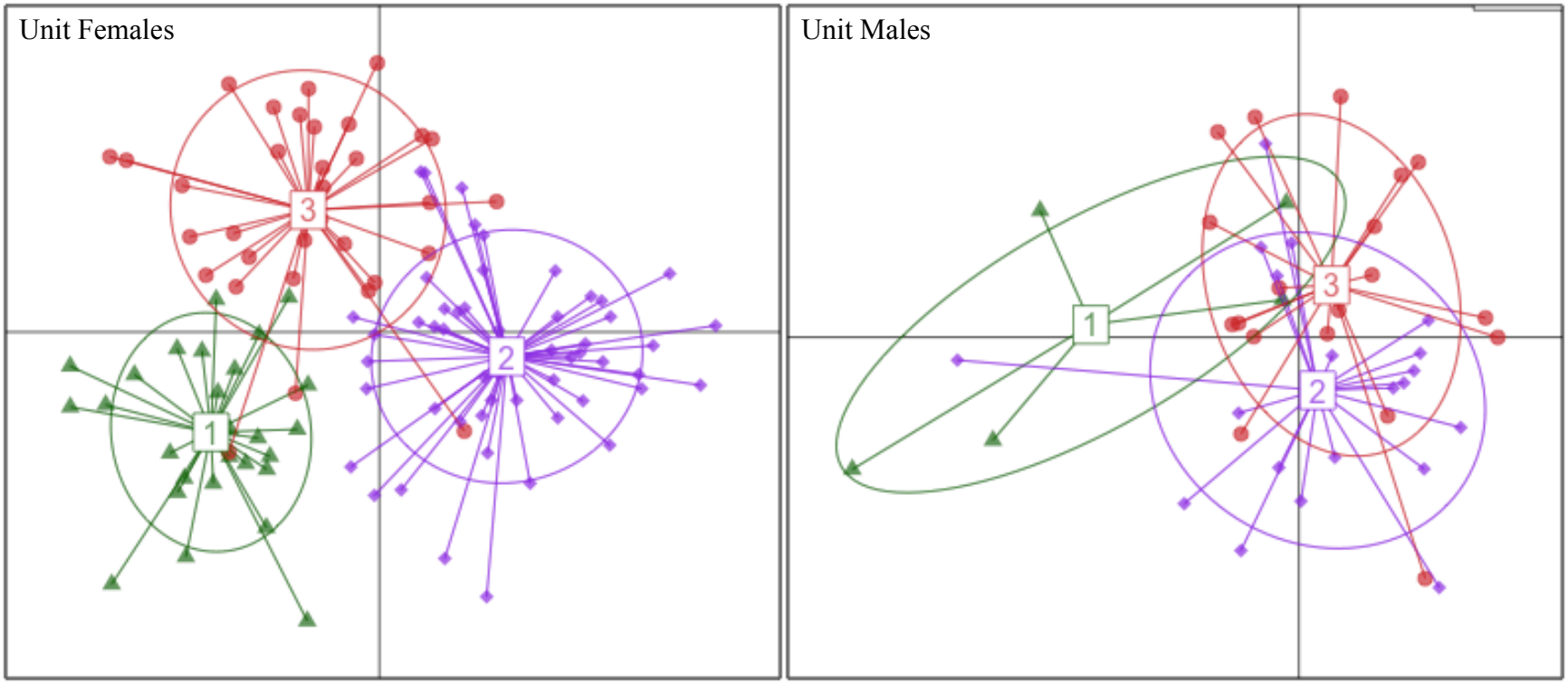

Figure S8: Scatterplot of the first two discriminant functions of the DAPC analysis. We observed more genetic structuring among unit females within bands (left panel) than in unit males within bands (right panel). Plots were created using the function “scatter” in the R package *adegenet*.