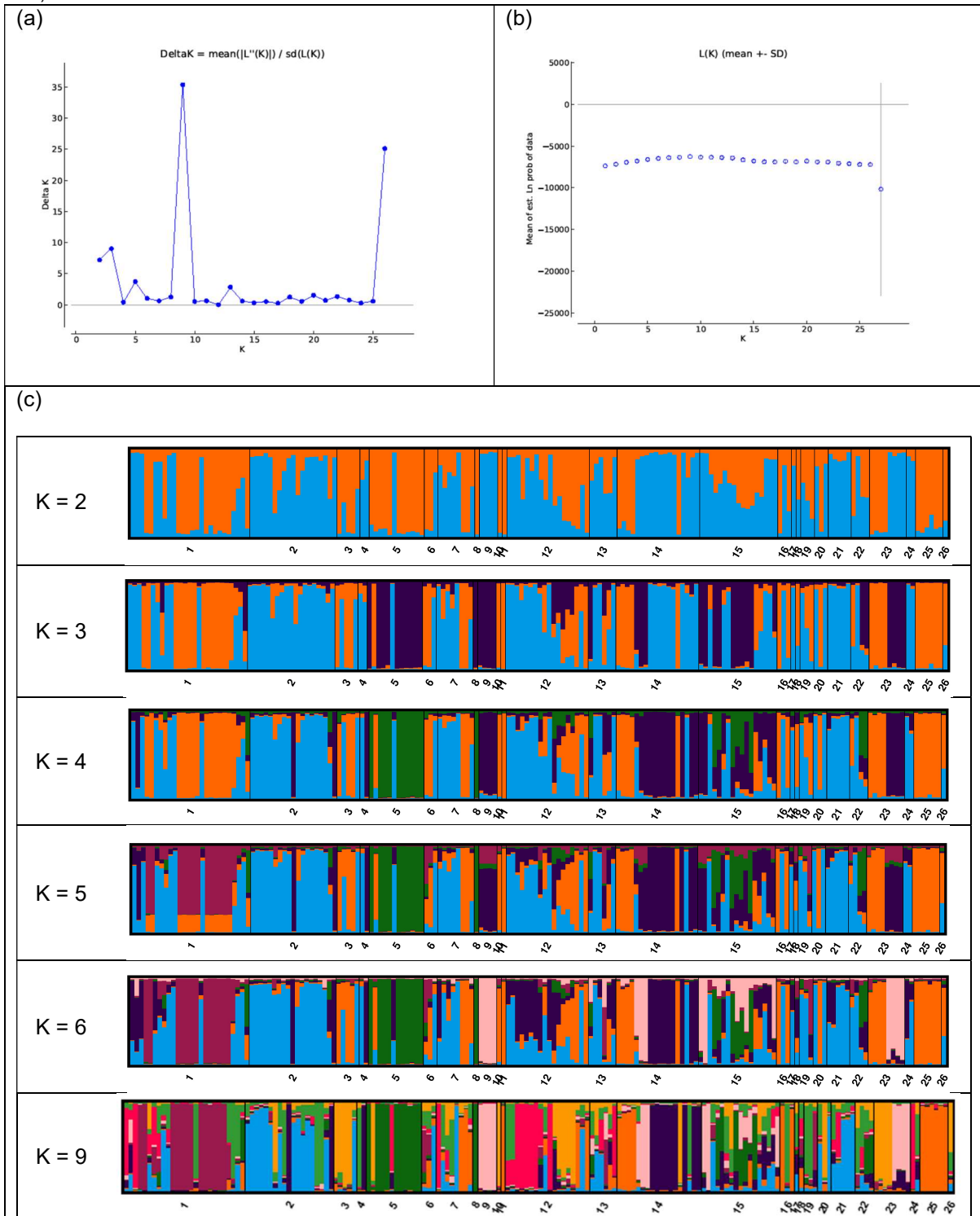
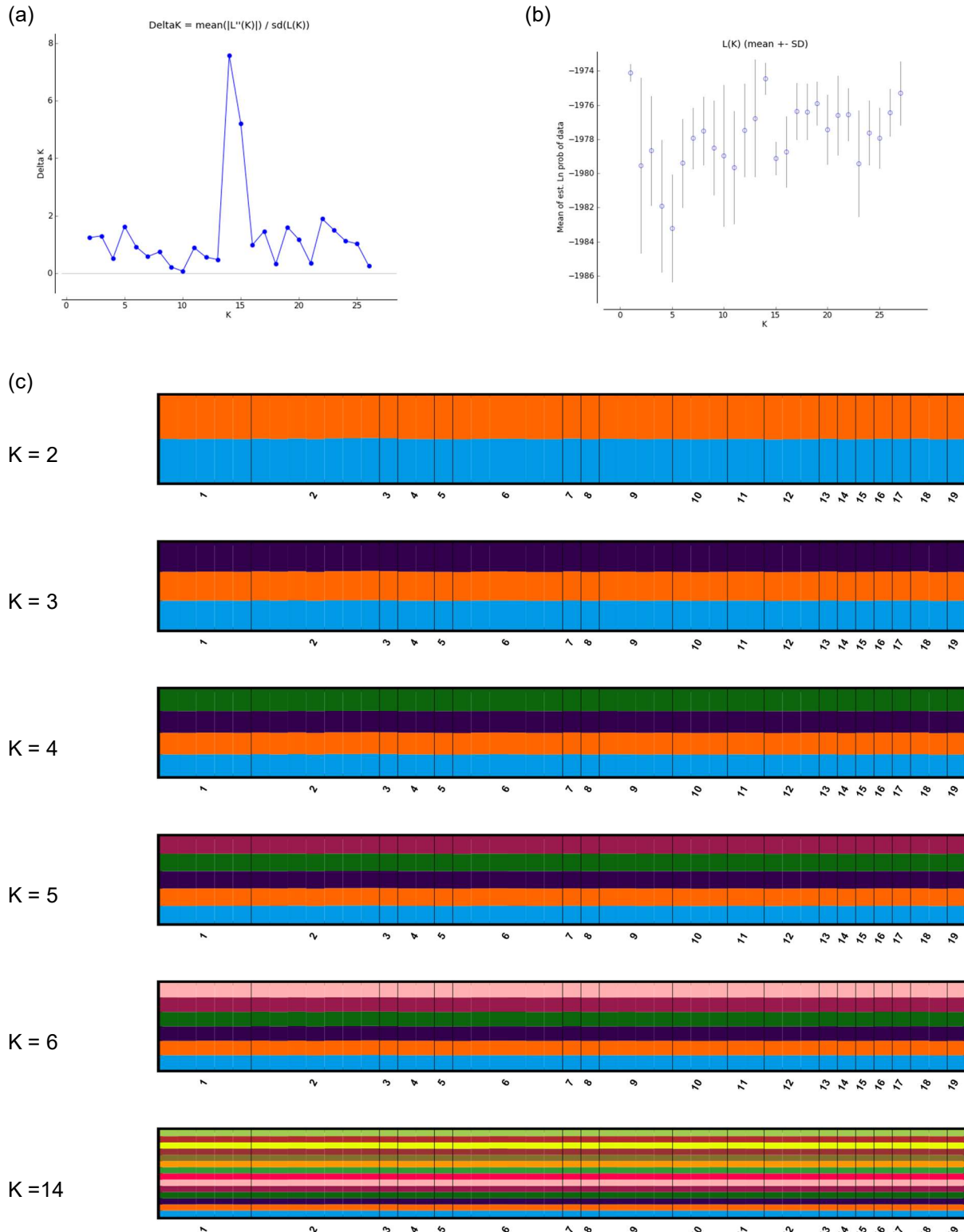


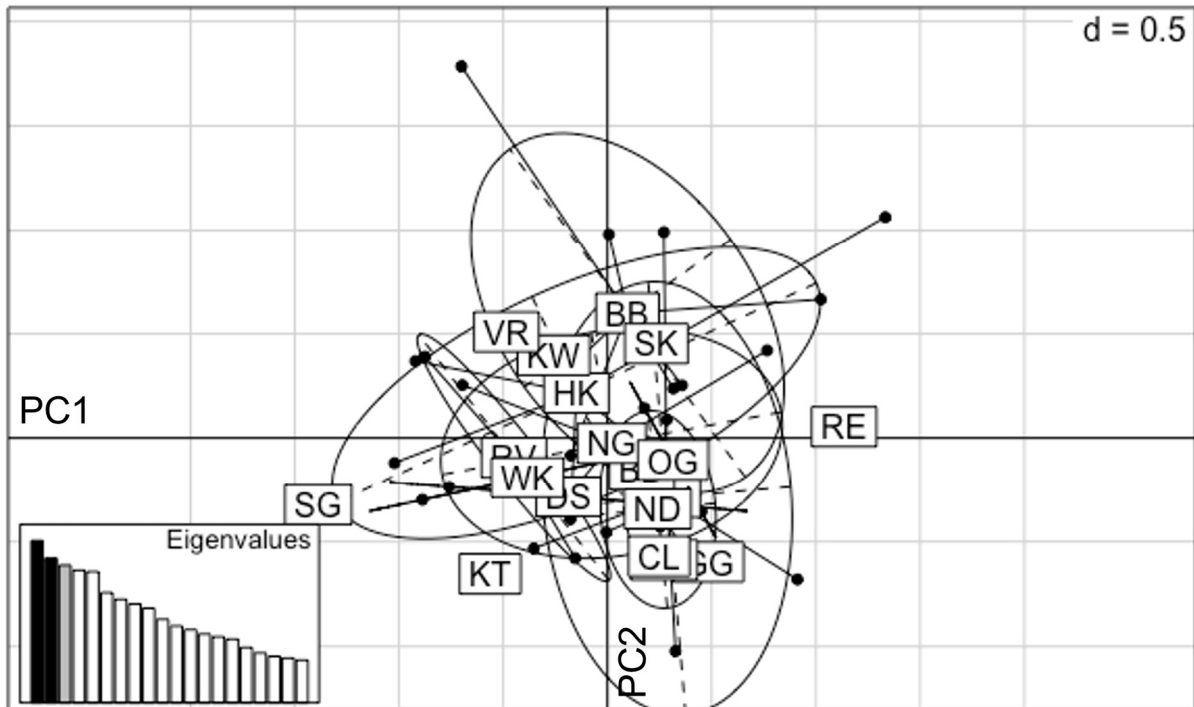
**Supplementary Figure 1: STRUCTURE HARVESTER results for (a) Delta K values and (b) probability (-LnPr) of K = 1 – 27 averaged over 20 runs and (c) genetic differentiation between the jackal sample locations (farms) based on STRUCTURE analysis (performed with K = 2 – 6) of 1 = GV, 2 = BB, 3 = BR, 4 = BD, 5 = DS, 6 = GG, 7 = HK, 8 = KD, 9 = KW, 10 = KK, 11 = KT, 12 = NG, 13 = ND, 14 = OG, 15 = RV, 16 = RE, 17 = RT, 18 = RD, 19 = SG, 20 = SK, 21 = VR, 22 = WK, 23 = CL, 24 = KR, 25 = WB, 26 = TD**



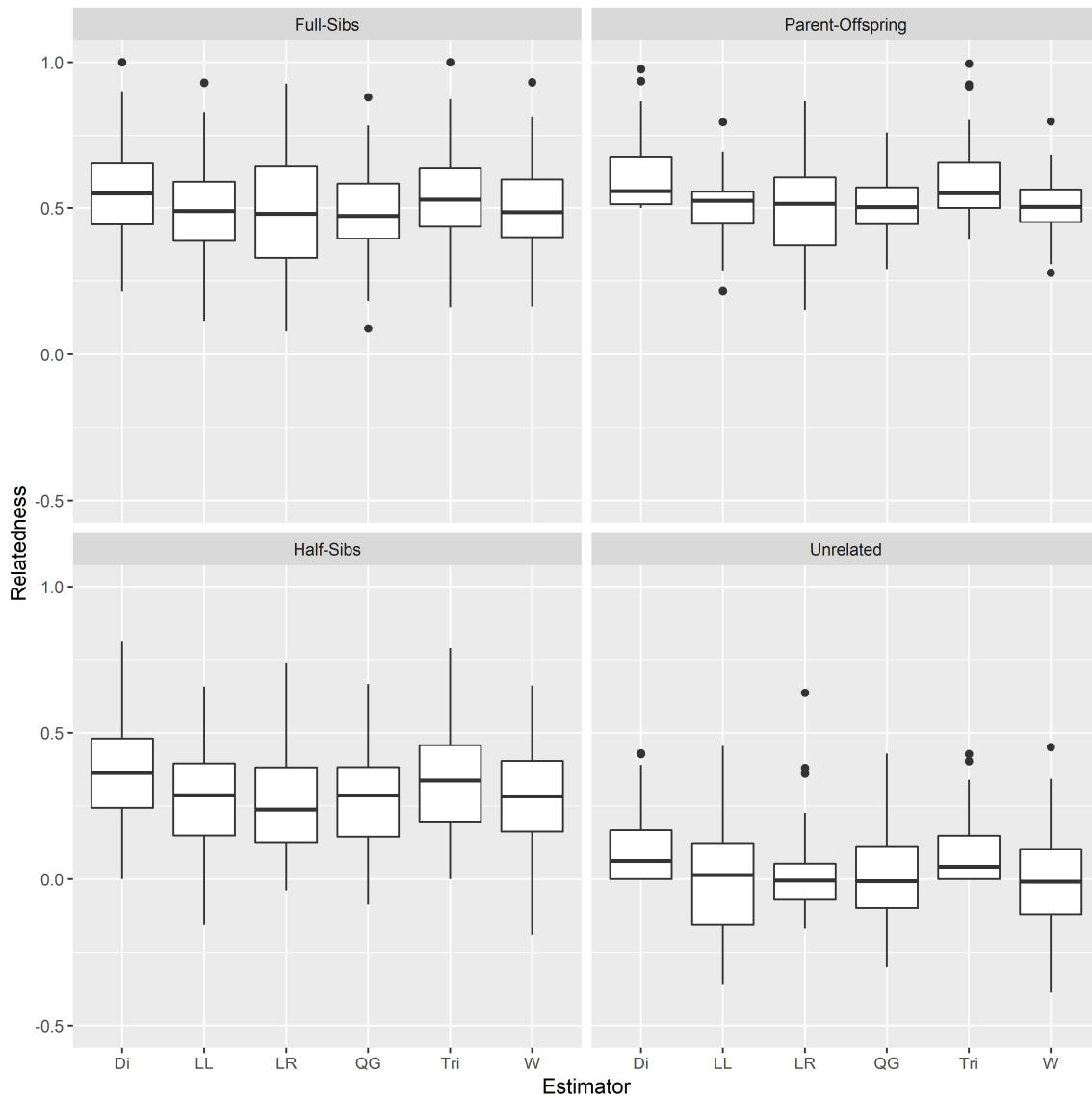
**Supplementary Figure 2: STRUCTURE HARVESTER results for (a) Delta K values and (b) probability (-LnPr) of K = 1 – 27 averaged over 20 runs and (c) genetic differentiation between the jackal sample locations (farms) based on STRUCTURE analysis (performed with K = 2 – 6 and K = 14) of 1 = GV, 2 = BB, 3 = BD, 4 = DS, 5 = GG, 6 = HK, 7 = KW, 8 = KT, 9 = NG, 10 = ND, 11 = OG, 12 = RV, 13 = RE, 14 = RD, 15 = SG, 16 = SK, 17 = VR, 18 = WK, 19 = CL. After removing relatives, some localities had no samples, hence fewer sampling localities as compared to the full data set. Note: The Evanno method (DeltaK) does not evaluate K = 1.**



**Supplementary Figure 3:** Principal Component Analysis (PCA) of the different jackal sampling locations (farms) with related individuals removed.



**Supplementary Figure 4:** Plot comparing the relatedness estimates using six estimators and simulated individuals of known relatedness. Di: Dyadic likelihood estimator “DyadML”, LL: Lynch-Li estimator, LR: Lynch and Ritland estimator, QG: Queller and Goodnight estimator, Tri: Triadic likelihood estimator “TrioML”, W: Wang estimator. Plot produced with ggplot2 3.3.0 (Wickham 2016).



**Supplementary Figure 5:** Results of the spatial autocorrelation analysis for **A** females and **B** males. The blue line indicates the autocorrelation coefficient of the data, with the 95% confidence interval at each distance class indicated by the black error bars, as determined by 1000 bootstrap resampling replicates. The red dashed lines indicate the 95% confidence interval around the null hypothesis (no spatial structure, i.e.  $r_{\text{auto}} = 0$ ), as determined by permutation (999 steps). Thus, if the error bars around the blue line do not overlap with the red dashed lines in a distance class, then genotypes were more (positive  $r_{\text{auto}}$ ), or less (negative  $r_{\text{auto}}$ ) similar than expected under the null hypothesis in that distance class. Such cases are indicated with an asterisk (\*).

