

Supplemental Information for:

Gene flow connects key leopard (*Panthera pardus*) populations despite habitat fragmentation and persecution

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1. Discriminate Analysis of Principal Components (DAPC) Results

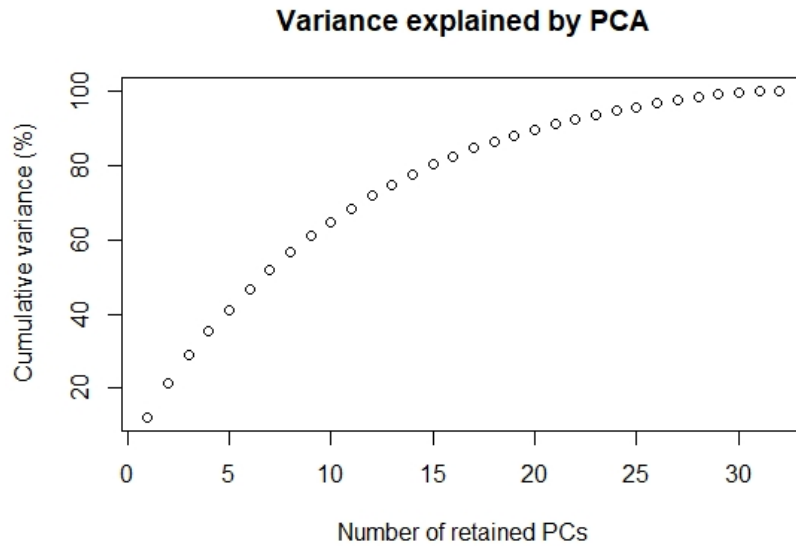


Fig. S1. Variance in the Mpumalanga leopard microsatellite data explained by Principal components. For DAPC analysis (Jombart, 2008; Jombart, Devillard, & Balloux, 2010), 25 PCs were retained which meant approximately 95% of the population structure data was included in the DAPC study.

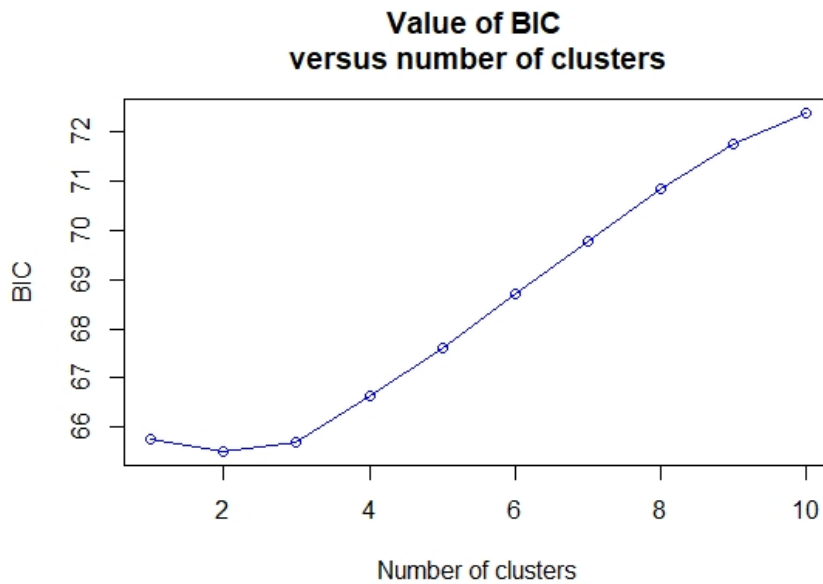


Fig. S2. DAPC Plot graph analysis of Mpumalanga leopard microsatellite data. The BIC with the lowest point is generally suggested as the most probable population structure. In this case, based on BIC calculations, the most probable population structure of Mpumalanga leopard samples was into two populations.

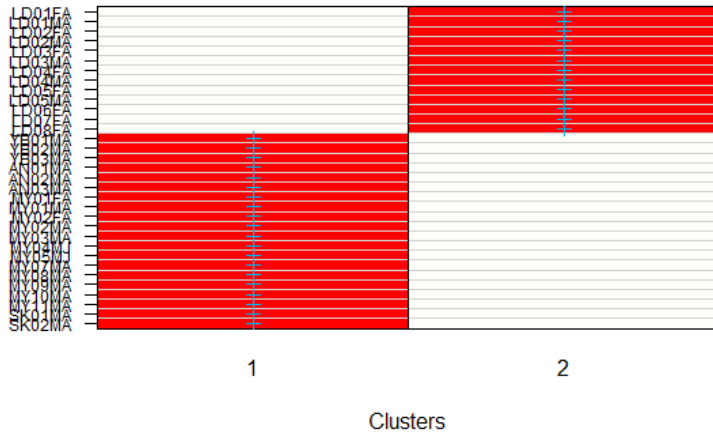


Fig. S3. Population breakdown of Mpumalanga leopards based on DAPC analysis. DAPC analysis of microsatellite data suggested that two subpopulations exist within the Mpumalanga leopard samples collected. This chart is the population breakdown into each prospective population. Cluster 1 ‘East Mpumalanga’ has samples from Andover Nature Reserve (AN), Manyeleti Game Reserve (MY), Lydenburg (LY) and two skin samples collected from confiscates leopard pelts (SK). Cluster 2 ‘West Mpumalanga’ comprised of all samples collected from Loskop Dam Nature Reserve (LD).

2. Geneland Results

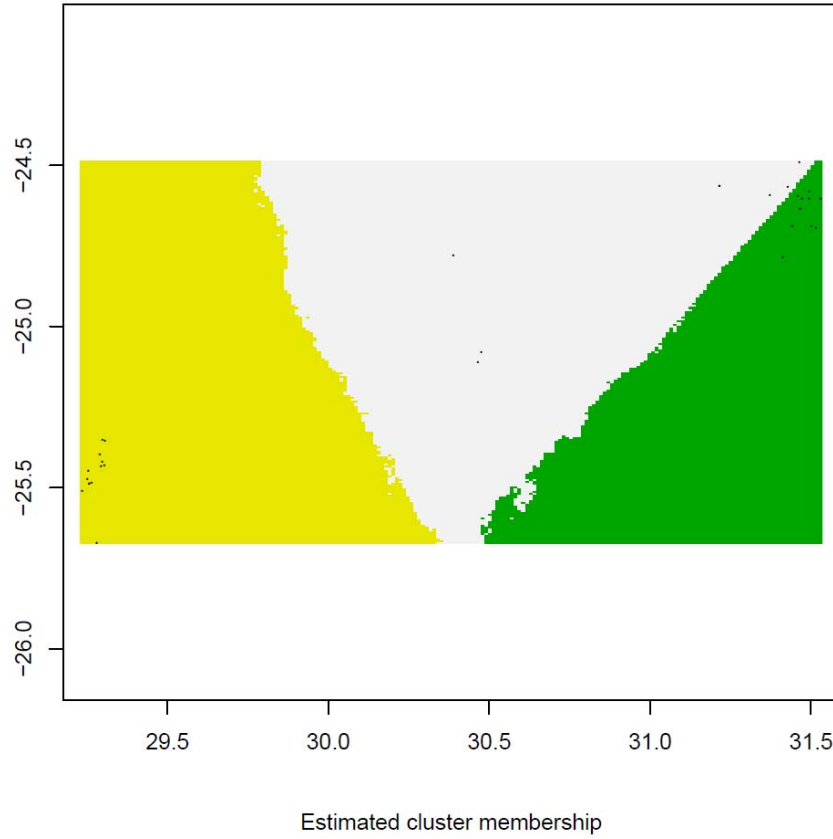


Fig. S4 Spatial structure of the sampled Mpumalanga leopard population into three subpopulations based on Geneland analysis (Guillot, Mortier, & Estoup, 2005).

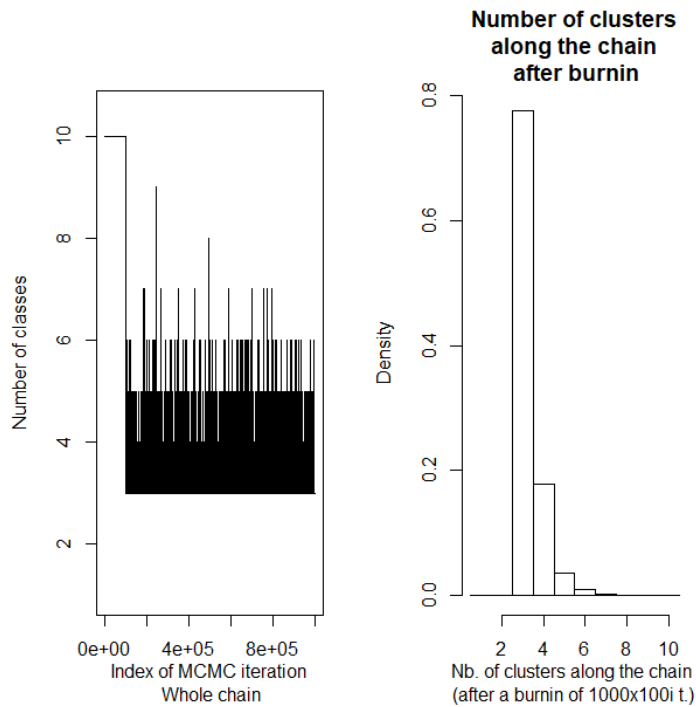


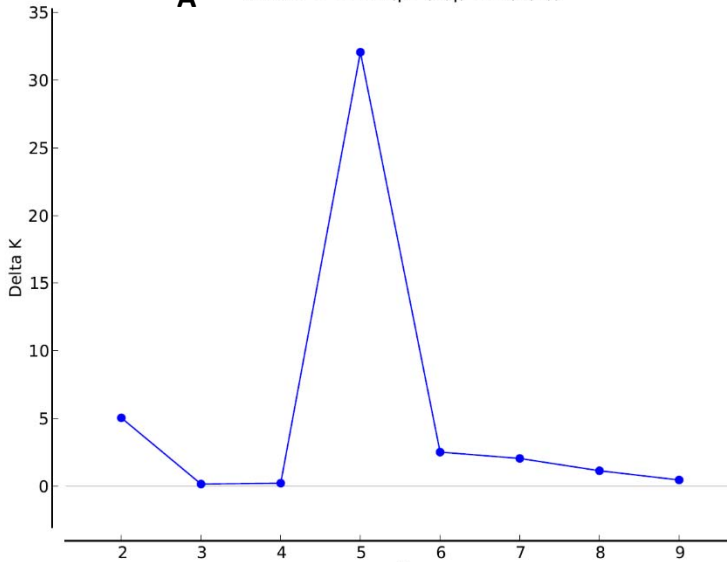
Fig. S5. Number of likely populations based on Geneland analysis. Markov Chain Montecarlo (MCMC) simulations for K1-10 and probability density of the most likely number of population clusters based on Geneland analysis (Guillot et al., 2005). 3 populations was the most highly supported population breakdown.

Table S1. Population assignment into three populations as estimated by Geneland (Guillot et al., 2005).

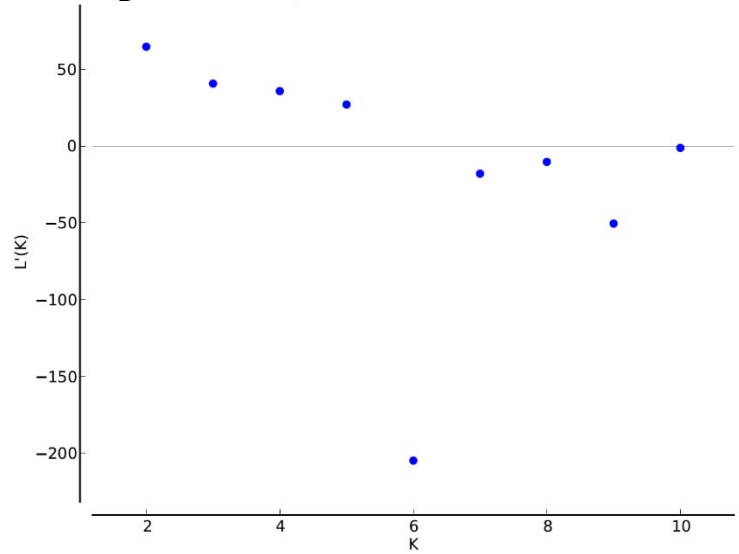
Pop1	Pop2	Pop3
LD01FA	YB01MA	AN02MA
LD01MA	YB02MA	MY01FA
LD02FA	YB03MA	MY01MA
LD02MA	AN01MA	MY02FA
LD03FA	AN03MA	MY02MA
LD03MA	MY03MA	MY04MA
LD04FA	MY09MA	MY05MA
LD04MA	SK01MA	MY07MA
LD05FA		MY08MA
LD05MA		MY10MA
LD06FA		MY11MA
LD07FA		SK02MA
LD08FA		

3. Structure Results

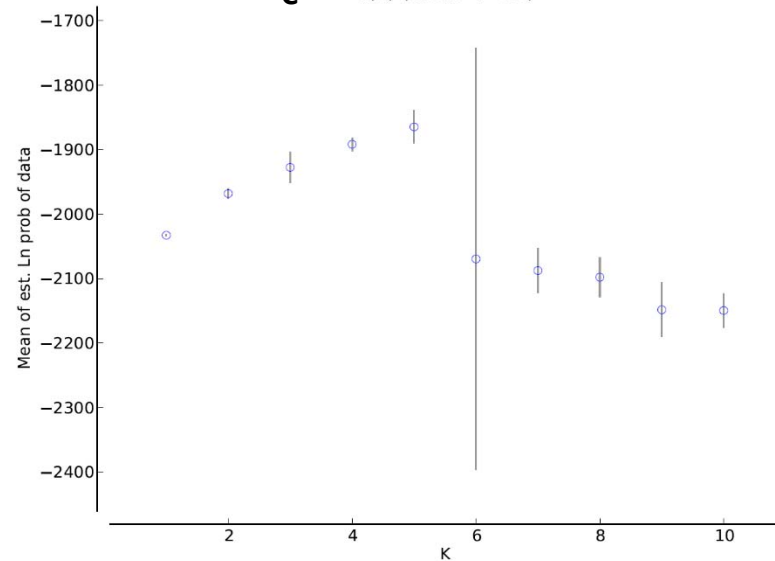
A $\Delta K = \text{mean}(|L''(K)|) / \text{sd}(L(K))$



B Rate of change of the likelihood distribution (mean)



C L(K) (mean +/- SD)



D

K	Reps	Mean LnP(K)	Stdev LnP(K)	Ln'(K)	Ln''(K)	Delta K
1	10	-2032.910000	0.659040	—	—	—
2	10	-1968.270000	6.789706	64.640000	24.010000	3.536235
3	10	-1927.640000	22.769580	40.630000	4.890000	0.214760
4	10	-1891.900000	9.526688	35.740000	8.740000	0.917423
5	10	-1864.900000	24.445677	27.000000	231.730000	9.479386
6	10	-2069.630000	325.595212	-204.730000	186.760000	0.573596
7	10	-2087.600000	33.428863	-17.970000	7.650000	0.228844
8	10	-2097.920000	29.464661	-10.320000	40.140000	1.362310
9	10	-2148.380000	41.352651	-50.460000	49.250000	1.190976
10	10	-2149.590000	25.805230	-1.210000	—	—

Fig. S6. Results from Structure (Pritchard, Stephens, & Donnelly, 2000) and Structure Harvester (Earl & Vonholdt, 2012) analysis of the leopard population structure across Mpumalanga province, South Africa. A) Graph representing the maximum number of populations (K) that could be present in the samples analysed **B)** Rate of change of the likelihood distribution (mean) **C)** Likelihood distribution (mean \pm standard deviation) **D)** Numerical representation of graph A.

4. Mantel Test

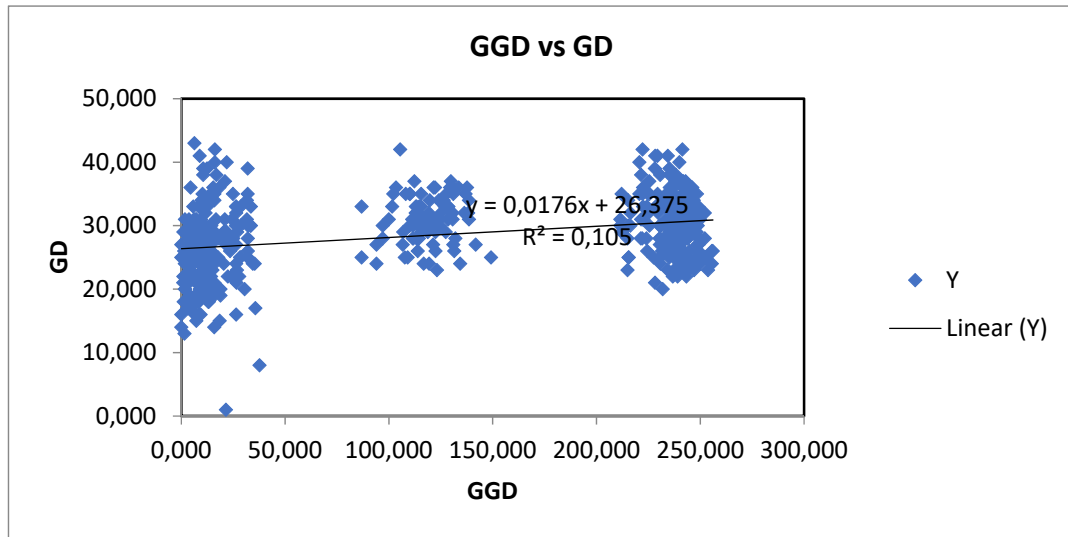


Fig. S7. Results of a Mantel test regressing pairwise geographic with pairwise genetic distances for leopards across Mpumalanga using GENEALX (Peakall & Smouse, 2012). Here, 10% of the microsatellite genetic variation can be explained by geographic distance.

5. BIMr Geneflow Results

Table S2. Results of 5 independent runs to determine gene flow between East Mpumalanga and West Mpumalanga

MCMC Run	Flow from East to West	Flow from West to East
1	0.104	0.033
2	0.096	0.033
3	0.096	0.034
4	0.095	0.033
5	0.095	0.033
Average	0.0972	0.0332

leopard populations calculated using the program BIMr (Faubet & Gaggiotti, 2008). A final gene flow was calculated by taking an average of each of the runs.

6. References

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