**Table S5: *Χ*2-test for differences in frequency distribution of single-locus genotypes between LBC and HBC individuals from southern Kruger (homozygotes with a majority allele vs. heterozygotes without a majority allele; baseline PL-*H*e < 0.56)**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Class of single-locus genotype | LBC observed | HBC observed | LBC expected | HBC expected | Fraction HBC  observed | Fraction HBC expected |
| Homozygotes, with majority allele | 1011 | 345 | 1001.42 | 354.58 | 0.25 | 0.26 |
| Heterozygotes, no majority allele | 82 | 42 | 91.58 | 32.42 | 0.34 | 0.26 |

χ2-value = 4.18, *P*randomization = 0.032. Null hypothesis: identical frequency distribution of the different classes of single-locus genotypes among LBC and among HBC individuals. Probability was estimated by randomization (100,000X) of complete multilocus genotypes between the two body condition classes (LBC and HBC). *P*-value is the fraction of randomized data sets showing a χ2-value equal to or larger than the observed data. Total number of observed single-locus genotypes: number of microsatellites X number of individuals.

Abbreviations: HBC: high body condition, LBC: low body condition.