**Table S7: *Χ*2-test for differences in frequency distribution of single-locus genotypes between LBC and HBC individuals from southern Kruger (all genotype classes, excluding homozygotes with a majority allele; baseline PL-*H*e < 0.56)**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Class of single-locus genotype | LBC observed | HBC observed | LBC expected | HBC expected | Fraction HBCobserved | Fraction HBC expected |
| Heterozygotes, no majority allele | 82 | 42 | 85.28 | 38.72 | 0.34 | 0.31 |
| Homozygotes, no majority allele | 82 | 46 | 88.03 | 39.97 | 0.36 | 0.31 |
| Heterozygotes, with majority allele | 631 | 273 | 621.70 | 282.30 | 0.30 | 0.31 |

χ2-value = 2.17, *P*randomization = 0.34. 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.