Correction document for Davenport, D. *et al.* Effective number of white shark ( *Carcharodon carcharias,* Linnaeus) breeders is stable over four successive years in the population adjacent to eastern Australia and New Zealand. *Ecol. Evol.* **11**, 186–198 (2021).

Due to the error in an intermediate data file, we recompleted the analysis used in this study to estimate Nb from the from the raw SNP genotype data.

We wish to correct Table 1 to the following:

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  |  | **2010** | **2011** | **2012** | **2013** |
| **MSAT** | ***n*** | **21** | **33** | **39** | **54** |
|  |  | ∞  (82.5-∞) | 263.9  (51.4-∞) | 128.7  (43.1-∞) | 122.6  (49.3, 12934.9) |
|  |  | 33  (18,74)[7,56] | 49  (30,84)[3,95] | 51  (36,88)[5,97] | 62  (41,96)[17,137] |
| **SNP** | ***n*** | **29** | **39** | **52** | **63** |
|  |  | 62.1(32.7, 249.5 | 208.1 (110.1, 1135.9) | 201.9 (126.7, 449.0) | 179.8 (121.9, 320.8) |
|  |  | 96(56,198)  [7,3] | 247(148,567)[4,5] | 196(132,332)[8,15] | 174(123,252)[16,22] |
|  |  | 74.6(20.6) | 228.7 (57.8) | 197.21 (39.08) | 174.85 (29.3) |
|  | † | 0.10 | 0.30 | 0.26 | 0.23 |

Where values from this updated table appear in text, we have made changes. The following lines were affected:

Line 65 now reads: “…for example the 2013 age-cohort was 174 (123,252 95%CI) and ) was 179.8 (121.9, 320.8 95%CI). We show that over the time period studied was stable (showed no detectable trend), and ranged between74.6(20.6±SD) and228.7(57.8±SD) per year using a combined estimate of from SNP loci.”

Line 337-339 now reads: “The final SNP dataset after filtering consisted of 4256 diallelic SNPs consisting of 235 EAP individuals with high quality SNP genotypes (Dataset-2).”

Line 350 the text … “with the exception of the 2010 cohort” was removed as this is no longer reflected in the result.

Line 353-Line 355 “Although confidence intervals overlapped, estimates of Imagewere generally higher than those determined from Imageacross all cohorts. The 2011 cohort showed the largest difference between estimates; Image= 214.6 (95%CI 104.8-551.1), Image= 344 (95%CI 211-872).” was deleted as it no longer reflects the result.

We added a line, line 355 now reads: “Tests for a trend in Nb overtime using regression methods was not significant (OLS regression p-value = 0.345; GLS regression p-value = 0.861). “

Line 369 now reads “I For cohorts 2010 to 2013, ranged from the smallest estimated value in 2010, to the largest in 2011, (Table 1). The inferred ratio of ranged from = 0.10 to = 0.30, calculated using estimates of from Bruce et al., (2018).”

Line 423 now states “ estimated using SNPs differed between methods, although differences were not significant having overlapping CIs. ” which replaces text which previously read “ estimated using SNPs differed between methods, such that Imagewas lower compared toImage*.*

Due to the error in the intermediate data file, we re-completed the analysis from the raw data. Because of this, we used updated R-packages. We have made the following changes to line 192 which now reads: “Post-processing of SNPs was completed in R (R Core Team, 2018) using various R-packages (dartR v.2 (Mijangos et al., 2022), hieferstat (Goudet & Jombart, 2022))”, and line 230-231 was deleted, where it previously read : “Hardy-Weinberg equilibrium (HWE) was evaluated using an exact test based on 10,000 Monte Carlo permutations of alleles and implemented in *Genepop* (Rousset, 2008).”

Line 220 was added and it reads “We use the method of Luikart et al., (2020) (ordinary least squares regression), and Generalized least-squares (GLS regression) that incorporates an estimate of autocorrelation, to test the significance of a trend in Nb estimates across cohorts”

For our analysis, cohorts required a sample size of > 25. Where groups had less than the required number of samples, we have added an additional Supplementary Appendix (Supplementary Appendix 5, Table S5.1) where interested readers can find the results for cohorts not included in the main analysis. To direct readers to this resource, line 268 now states: “Where the sample size of a cohort was less than 25, results are reported in Supplementary Table S5.1.”

We have added a line of text at to acknowledge our colleagues who brought this error to our attention. The lines 523 now read: “We acknowledge Dean Blower and Paul Butcher who identified an error in the original published version of this MS. Dean Blower was added to the authorship list after publication to recognise his finding of the error.”

All scripts and data used in this reanalysis are available online. Line 326 now reads “Data for this study are available at zendoo <https://doi.org/10.5281/zenodo.10172611>”.

We apologize for this error.

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