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 to re-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 |
|  |  | 63.7(38.7, 2359.4) | 212.6 (98.8, 477.6) | 202.6 (101.3, 239.7) | 181.5 (127.9, 358.6) |
|  |  |  |  |  |  |
|  |  |  |  |  |  |
|  | † |  |  |  |  |

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

Line 62-64 now reads: “We show that over the time period studied was stable (showed no detectable trend), and ranged between(SD±) and(SD±) per year using a combined estimate of from SNP loci.”

Line 340-342 now reads: “The final SNP dataset after filtering consisted of 4592 diallelic SNPs consisting of 233 EAP individuals with high quality SNP genotypes (Dataset-2)”.

Line 350 the text … “with the exception of the 2010 cohort” was removed

Line 353-Line 355 now reads:

Due to the error in the intermediate data file, we recompleted the analysis from the raw data. Because of this we used updated r-packages. We have made the following changes to line 189 which now reads: “Post-processing of SNPs was completed in R (R Core Team, 2018) using various R-packages (dartr (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).”

For our analysis, cohorts required a sample size of > 25. Where groups had less then the required 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 264 now states: “Where the sample size of a cohort was less than 25, results are reported in Supplementary Table S5.1.”

We had added a line of text at to acknowledge our colleagues who brought this error to our attentions. The lines 524-526 now read: “We acknowledge Dean Blower and Paul Butcher who identified an error in the original published version of this MS.”

All scripts and data used in this reanalysis are available online. Line 326 now reads “Data for this study are available at zendoo: [10.5281/zenodo.10172611](file:///C:\Users\DAVENPORTD\Downloads\10.5281\zenodo.10172611)”.

We apologize for this error.

Dani Davenport