S2 Table. Estimated *Ne gen* from ONeSAMP.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **N samples** | **N loci** | **Priors (min-max)** | ***Ne gen* (95% CI)** |
| **Whole study area** | 48 | 9 | 2-100 | 27.2 (21.8-37.9) |
| 48 | 6 | 2-100 | 30.1 (23.7-45.4) |
| 48 | 9 | 2-200 | 23.7 (18.8-36.1) |
| 48 | 6 | 2-200 | 26.9 (20.9-49.9) |
| 48 | 9 | 2-50 | 25.8 (20.9-36.1) |
| 48 | 6 | 2-50 | **32.8 (25.5-46.1)** |
| **Muniellos** | 15 | 9 | 2-50 | 12.9 (10.5-17.8) |
| 15 | 6 | 2-50 | 12.4 (9.7-17.5) |
| 15 | 9 | 2-20 | 13.1 (10.9-16.9) |
| 15 | 6 | 2-20 | **9.8 (8.1-12.3)** |

Genetic effective population size (*Ne gen*, 95% CI in parentheses), estimated for the whole study area (48 samples) and for the subset of Muniellos reserve (15 samples). We explored the variability in the mean estimate and range using different priors (minimum and maximum values estimated a priori for the effective population size). We also show the estimates when including all microsatellite loci used in our study (9 loci), and excluding those that were not in Hardy-Weinberg equilibrium. In all cases, we used samples with only one missing value. Bold font indicates estimates used in the text.