**Table S2.Cormack-Jolly-Seber bootstrap goodness-of-fit results.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Model | AICc | δAIC*c* | *w*AIC*c* | *k* | p-value |  |
| (*t*)*p*(*.*) | 1176.537 | 0 | 0.5988 | 14 | 0.52 | 0.992 |
| (*.*)*p*(*.*) | 1177.355 | 0.8179 | 0.39781 | 2 | 0.56 | 0.985 |
| (*t*)*p*(*t*) | 1186.884 | 10.3461 | 0.00339 | 34 | 0.39 | 1.031 |
| (*.*)*p*(*t*) |  | no convergence reached | |  |  |  |

All models from the capture matrix with all individuals (1553 individuals) are shown. Models include probability of survival () and capture (*p*) with time (*t*). Shown are Akaike’s information criterion corrected for small samples (AIC*c*) difference between the top-ranked model AIC*c* and the current model δAIC*c*), AIC*c*weights (*w*AIC*c*) and the number of estimable parameters (*k*). From bootstrap goodness-of-fit tests the probability of a deviance less than or equal to the observed deviance from 100 bootstrap goodness-of-fit simulations of the model (p-value), and the quasi likelihood over (or under) dispersion factor ( area also presented.