

1 Supplementary material: Detail of the options used for Ne calculation for each software. LD: estimation of Ne with the single sample method of
 2 linkage disequilibrium method (Waples & Do, 2008); Het_ex: heterozygote excess method (Zhdanova & Pudovkin, 2008); Coancestry: coancestry
 3 method (Nomura, 2008); Sibship: parentage method (Wang, 2009); Pollack: Estimation of Ne with the temporal method of Pollack (1983), then
 4 transformed in yearly Nb with Waples *et al.* (2007) method; Nei & Tajima: *idem* with Nei & Tajima (1981) method; Jorde & Ryman: *idem* with Jorde &
 5 Ryman (2007) method

Software	Usage	Options used	Comments
NeEstimator v2.01 (Do et al. 2014)	Single-sample Ne estimates (LD; Het_ex; Coancestry) Temporal Ne estimates (Pollack; Nei&Tajima; Jorde & Ryman)	Assuming random mating Lowest allelic frequency (p_{crit}): 0.02 Generation 0: 2007 Generation 1: 2009 Generation 2.5: 2012 Lowest allelic frequency (p_{crit}): 0.02	P_{crit} chosen by following Waples & Do 2008 recommendations Assuming generation time of 2 years. P_{crit} chosen by following Waples & Do 2008 recommendations
Colony v2.01.1 (Jones & Wang 2010)	Single sample Ne estimate (Sibship)	Medium length run, full likelihood method, assuming no allelic dropout and proportion of genotyping errors at 0.01 RNG seed set at 1234	Medium run used to reduce computational time.
SalmonNb v1.1 (Waples <i>et al.</i> 2007)	Temporal Ne estimates decomposition into yearly Nb	B coefficients: 2007-2009: 1.9 2009-2012: 2.19 2007-2012: 1.43 Number of independent alleles: 2007: 81 2009: 80 2012: 77	B coefficient taken from SalmonNb user guide and Waples <i>et al.</i> 2007

