Appendix S3. Stabilization of the genetic parameters - allelic richness AR, observed heterozygosity H_o, expected heterozygosity H_s, within population heterozygote deficit F_{IS} and genetic differentiation F_{ST} - value after 100,000 generations and effect of the sampling design on the estimation of allele frequencies and genetic parameters. The simulations were run for such a large number of generations to reach parameter stabilization.

All the parameters reached stabilization; their values fluctuating around a stable mean (Figure S3.1.). The number of generations at which this was reached varied from 300 (F_{ST}) to 5000 (e.g. H_o). Sample size affected nonlinearly the estimation of allele frequencies, with greater precision associated with higher numbers of samples. Sex ratio and timing of sampling influenced the estimation of allele frequencies (visible in all populations to various extents, represented in Appendix S6). The effects were consistent across populations. Sample size affected nonlinearly the estimation of local genetic parameters. In 2 populations out of 5, trends were observed in the deviation from reference value for H_o, H_s and F_{IS} with biased sex ratio (Appendices S10, S12 and S14). We detected no clear effect of the timing of sampling on the estimation of AR, H_o and H_s, but F_{IS} was affected in 3 cases out of 4 (Appendix S13). Complete results of the effect of sampling design on the estimation of local genetic parameters can be found in Appendices S8, S10, S12 and S14. Sample size affected nonlinearly on the estimation of intergroup genetic parameters (Appendix S16). The estimation of genetic differentiation was slightly biased by the sex ratio of the subsamples. The estimation of genetic differentiation was biased by the timing of sampling (Appendix S16).

Although we did not introduce *a priori* differences between sexes, SR clearly affected the estimation of allele frequencies. This translated in slightly visible effects on observed and expected heterozygosity (H_o and H_s). These trends were similar between the two factors and going in the same direction, leading to no observable effect on the within population heterozygote deficit (F_{IS}). Sex ratio slightly affected the estimation of genetic differentiation. This effect, although tenuous, was directional. The fact that this effect was tenuous is probably due to a large extent to a high homogenization within population.

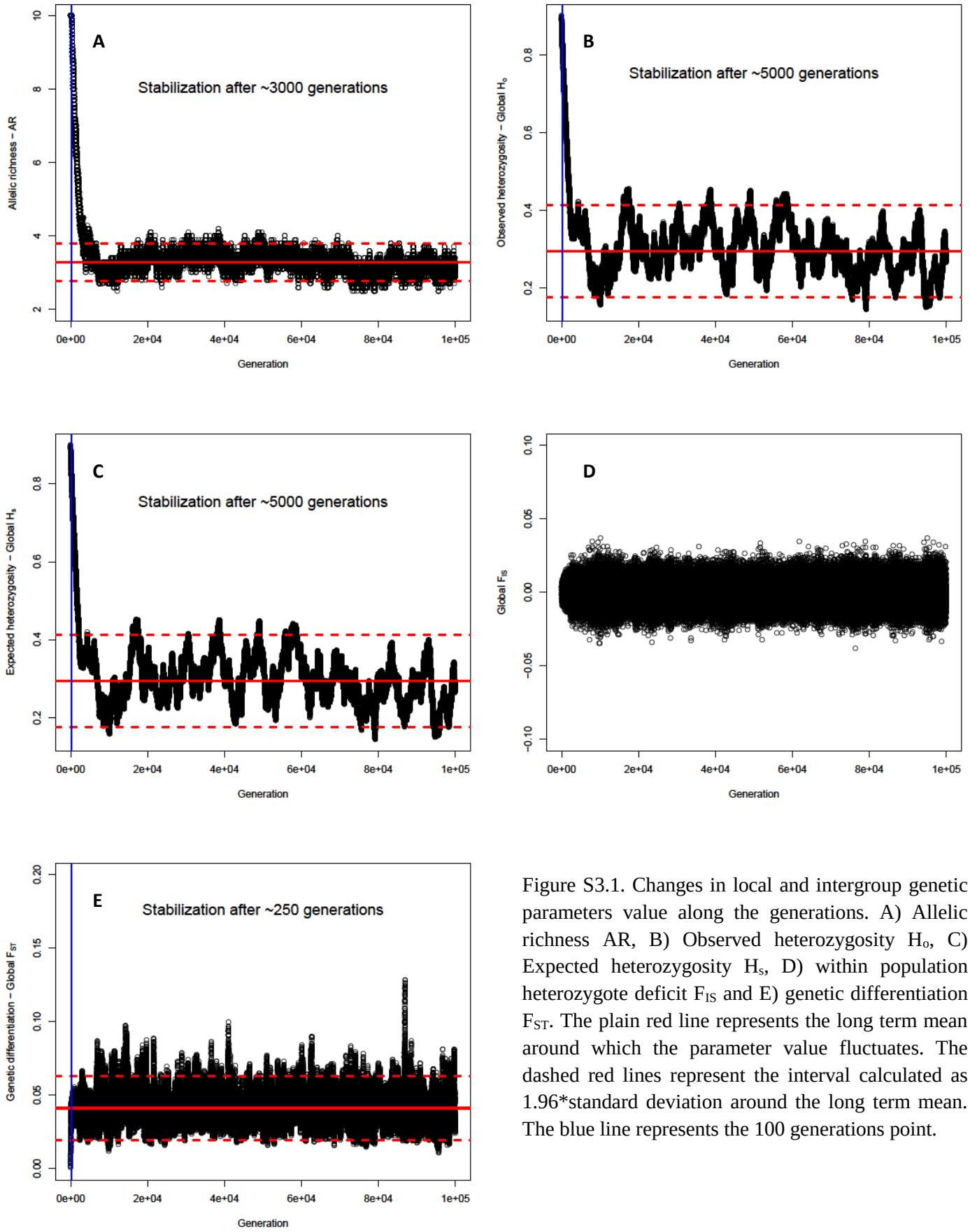

Figure S3.1. Changes in local and intergroup genetic parameters value along the generations. A) Allelic richness AR, B) Observed heterozygosity H_o, C) Expected heterozygosity H_s, D) within population heterozygote deficit F_{IS} and E) genetic differentiation F_{ST}. The plain red line represents the long term mean around which the parameter value fluctuates. The dashed red lines represent the interval calculated as 1.96*standard deviation around the long term mean. The blue line represents the 100 generations point.