



Figure S6 Root mean square deviation of the inbreeding coefficient estimates, as a function of the mean depth of coverage, estimated from a fixed number of total sequence reads. The product of the mean depth of coverage μ and number of sampled individuals N is fixed at 1,000 such that a two-fold increase in μ resulted in a two-fold decrease in N . The root mean square deviation (RMSD) when the inbreeding coefficient is A) minimized, B) equal to zero (Hardy-Weinberg equilibrium), or C) maximized is shown. Results are conditioned on significant polymorphism at the 5% level. The error rate $\epsilon = 0.01$. A total of 10,000 simulation replications were run for each set of parameter values.