



Figure S1 Pairwise estimators of F_{ST} . A. Multilocus estimates \hat{F}_{ST}^{pool} computed from read counts, as a function of WC_{84} estimates computed from individual genotypes. B. Multilocus estimates $PP2_d$ computed from read counts, as a function of NC_{83} estimates computed from individual genotypes. C. Multilocus estimates \hat{F}_{ST}^{pool} as a function of multilocus $PP2_d$ estimates. In each graph, the dots represent multilocus estimates of F_{ST} across all pairs of subpopulations from an 8-island model, and over 50 replicate `ms` simulations. We specified the migration rate corresponding to $F_{ST} = 0.20$. The size of each pool was fixed to 100. The results are shown for different coverages (20X, 50X and 100X). The cross indicates the simulated value of the parameter F_{ST} .