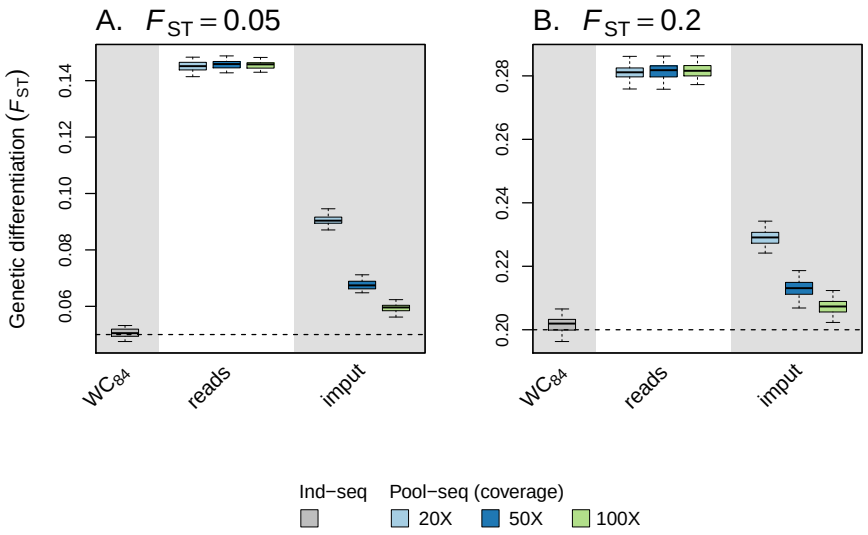

Figure S3 Precision and accuracy of naive estimators of F_{ST} for Pool-seq data. We compare WC_{84} estimates computed from allele count data inferred from individual genotypes (Ind-seq) to WC_{84} estimates computed: (*i*) directly from read counts, as if they were allele counts ("reads"); (*ii*) from allele counts imputed by maximum-likelihood ("imput"). Each boxplot represents the distribution of multilocus F_{ST} estimates across all demes in an 8-island model, and over 50 independent replicates of the `ms` simulations. We used two migration rates, corresponding to $F_{\mathrm{ST}} = 0.05$ (A) and $F_{\mathrm{ST}} = 0.20$ (B). The size of each pool was fixed to 10. For Pool-seq data, we show the results for different coverages (20X, 50X and 100X). In each graph, the dashed line indicates the simulated value of F_{ST}.