



Figure S4 Precision and accuracy of alternative estimators of F_{ST} with varying pool size, for various levels of differentiation (A–D). The haploid pool size n drawn independently for each deme from a Gaussian distribution with mean 100 and standard deviation 30; n was rounded up to the nearest integer, with min. 20 and max. 300 haploids per deme. We considered three estimators based on allele count data inferred from individual genotypes (Ind-seq): WC_{84} , $\hat{F}_{ST} \equiv (\hat{Q}_1 - \hat{Q}_2) / (1 - \hat{Q}_2)$ (where \hat{Q}_1 and \hat{Q}_2 are the weighted frequencies of identical pairs of genes within and between subpopulations, respectively, with weights equal to the number of pairs of genes) and $\tilde{F}_{ST} \equiv (\tilde{Q}_1 - \tilde{Q}_2) / (1 - \tilde{Q}_2)$ (where \tilde{Q}_1 and \tilde{Q}_2 are the unweighted frequencies of identical pairs of genes within and between subpopulations, respectively). For Pool-seq data, we considered the estimators \hat{F}_{ST}^{pool} (Equation 12), $\hat{F}_{ST}^{pool-PID}$ (Equation A44) and $\tilde{F}_{ST}^{pool-PID}$ (Equation A45). Each boxplot represents the distribution of multilocus F_{ST} over 50 independent replicates of the *ms* simulations. 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} and the dotted line indicates the median of the distribution of WC_{84} estimates.