

Table S3 Effect of variable coverage on pairwise F_{ST} estimates

F_{ST}	n	Pool-seq		Ind-seq
		Δ	\hat{F}_{ST}^{pool}	WC ₈₄
0.05	10	20	0.050 (0.006)	
0.05	10	50	0.050 (0.004)	0.050 (0.004)
0.05	10	100	0.050 (0.004)	
0.05	100	20	0.051 (0.003)	
0.05	100	50	0.051 (0.002)	0.051 (0.002)
0.05	100	100	0.051 (0.002)	
0.20	10	20	0.200 (0.007)	
0.20	10	50	0.200 (0.007)	0.200 (0.007)
0.20	10	100	0.200 (0.007)	
0.20	100	20	0.202 (0.006)	
0.20	100	50	0.203 (0.006)	0.203 (0.005)
0.20	100	100	0.203 (0.005)	

Pairwise multilocus \hat{F}_{ST}^{pool} estimates were computed for various conditions of expected F_{ST} and pool size (n) in an island model with $n_d = 8$ subpopulations (pools). The coverage (δ_i) was varying across demes and loci, with $\delta_i \sim \text{Pois}(\Delta)$. The mean (RMSE) is computed for a single pair of subpopulations, over 50 independent simulated datasets, each made of 5,000 loci. For comparison, we computed multilocus WC₈₄ estimates from allele count data inferred from individual genotypes (Ind-seq).