

Table S2 Effect of unequal sampling on pairwise F_{ST} estimates

F_{ST}	n	Pool-seq		Ind-seq
		Cov.	\hat{F}_{ST}^{pool}	WC ₈₄
0.05	$\mathcal{N}(100, 30)$	20×	0.051 (0.003)	
0.05	$\mathcal{N}(100, 30)$	50×	0.052 (0.003)	0.051 (0.002)
0.05	$\mathcal{N}(100, 30)$	100×	0.051 (0.002)	
0.20	$\mathcal{N}(100, 30)$	20×	0.202 (0.007)	
0.20	$\mathcal{N}(100, 30)$	50×	0.202 (0.006)	0.202 (0.006)
0.20	$\mathcal{N}(100, 30)$	100×	0.202 (0.006)	

Pairwise multilocus \hat{F}_{ST}^{pool} estimates were computed for various conditions of expected F_{ST} and coverage (Cov.) in an island model with $n_d = 8$ subpopulations (pools). The pool size (n) was variable across demes, with haploid sample 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. 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 (Weir and Cockerham 1984) estimates from allele count data inferred from individual genotypes (Ind-seq).