

Table S1 Comparison of pairwise F_{ST} estimates

F_{ST}	n	Pool-seq		Ind-seq
		Cov.	\hat{F}_{ST}^{pool}	WC ₈₄
0.05	10	20×	0.051 (0.004)	
0.05	10	50×	0.051 (0.004)	0.051 (0.003)
0.05	10	100×	0.051 (0.003)	
0.05	100	20×	0.051 (0.003)	
0.05	100	50×	0.051 (0.003)	0.051 (0.002)
0.05	100	100×	0.051 (0.002)	
0.20	10	20×	0.203 (0.007)	
0.20	10	50×	0.202 (0.006)	0.202 (0.007)
0.20	10	100×	0.201 (0.006)	
0.20	100	20×	0.201 (0.006)	
0.20	100	50×	0.201 (0.006)	0.201 (0.005)
0.20	100	100×	0.202 (0.005)	

Pairwise multilocus \hat{F}_{ST}^{pool} estimates were computed for various conditions of expected F_{ST} , pool size (n) and coverage (Cov.) in an island model with $n_d = 8$ subpopulations (pools). 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).