Table S2

Linear regression model summary statistics for comparison of two approaches (pooled and individual) based on nucleotide diversity (π) and pairwise population differentiation (F_{ST}) estimates from only "non-zero" values of *Leiopelma hochstetteri 16S* and 830-bp *Cyt b* data.

Statistics	N	Intercept (SE)	Slope β (95% CI)	R^2
16S				
π	7	0.002 (0.007)	0.964 (0.756 - 1.172)	0.94
F_{ST}	186	0.330 (0.043)	0.638 (0.546 - 0.731)	0.50
Cyt b				
π	11	0.007 (0.010)	0.475 (-0.301 - 1.252)	0.14
F_{ST}	190	0.378 (0.060)	0.597 (0.470 - 0.725)	0.31

N: number of populations (π) or population-pairs (F_{ST})