

Table S5 Indels affected levels of nucleotide diversity and divergence. Illustrated are results from Student t -tests (t) with Welch corrections for unequal variances. P -values were determined parametrically (P) and non-parametrically (P_{perm}) using permutations. The permutation-based tests randomized the data with respect to presence or absence of indels and then used the distribution for the t -statistic based on 10,000 randomizations as the null distribution with which to compare to the observed t -statistic. Note that parametric t -tests were used here because we were interested in comparing means (which the Wilcoxon-rank sum test does not). Use of nonparametric tests gave the same results (data not shown).

Statistic	mean (- indels)	mean (+ indels)	t	df	P	P_{perm}
S	3.03	7.79	-19.34	1200.157	<2.2e-16	<1.0e-04
h_1	1.64	4.09	-13.33	1179.734	<2.2e-16	<1.0e-04
θ_{π}	0.0028	0.0074	-13.33	1178.909	<2.2e-16	<1.0e-04
D_{xy} (Pira)	0.0073	0.0106	-7.24	875.017	9.537e-13	<1.0e-04
D_{xy} (Pila)	0.0415	0.0515	-4.26	157.005	3.441e-05	0.0008
k	2.82	4.17	-19.85	1447.415	<2.2e-16	<1.0e-04
H_d	0.39	0.62	-24.17	1854.041	<2.2e-16	<1.0e-04
Tajima's D	-0.47	-0.36	-3.15	1538.623	0.001660	0.009
n	11.99	12.10	-1.56	1851.381	0.116912	0.225
Noncoding (bp)	203.46	226.93	-2.86	578.456	0.004265	0.047

Abbreviations: bp, base pairs; df , degrees of freedom; D_{xy} , nucleotide divergence; H_d , haplotypic diversity; indels, insertion-deletion events; k , the number of haplotypes; n , sample size; h_1 , singletons or the first class of the folded site-frequency spectrum; Pila, *Pinus lambertiana*; Pira, *Pinus radiata*; S , segregating sites; θ_{π} , nucleotide diversity based on the average number of pairwise differences (per site).