Table S3 A summary of statistical tests used to assess the effects of coverage variation on basic alignment summaries.

Measure	Statistical Test	Statistical Test Results	Interpretation
Nucleotide diversity (θ_π)	Kruskal-Wallis	$\chi^2 = 97.63$, df=16, $P = 9.62\text{e-}14$	Average ranks of diversity vary significantly across coverage classes
Nucleotide divergence (Pira)	Kruskal-Wallis	$\chi^2 = 95.61$, df=16, $P = 2.29\text{e-}14$	Average ranks of divergence vary significantly across coverage classes
Nucleotide divergence (Pila)	Kruskal-Wallis	$\chi^2 = 29.41$, df=16, $P = 0.02134$	Average ranks of divergence vary significantly across coverage classes
The number of SNPs	Kruskal-Wallis	$\chi^2 = 174.31$, df=16, $P < 2.2\text{e-}16$	Average ranks of SNPs vary significantly across coverage classes
Alignment length (bp)	Kruskal-Wallis	$\chi^2 = 236.24$, df=16, $P < 2.2\text{e-}16$	Average ranks of alignment lengths vary significantly across coverage classes
Noncoding sites (bp)	Kruskal-Wallis	$\chi^2 = 24.24$, df=16, $P = 0.08437$	Average ranks of noncoding sites do not vary significantly across coverage classes
Coding sites (bp)	Kruskal-Wallis	$\chi^2 = 42.08$, df=16, $P = 0.00038$	Average ranks of coding sites vary significantly across coverage classes
The proportion of masked bases	Goodness-of-fit	$\chi^2 = 3559.68$, df=17, $P < 2.2\text{e-}16$	Too few masked bases with high coverage, too many masked bases with low coverage
Proportion of annotated genes	Goodness-of-fit	$\chi^2 = 16.64$, df=17, $P = 0.47900$	Annotated genes within each coverage class occurred in proportion to overall fraction of genes that were annotated
Indels	Goodness-of-fit	$\chi^2 = 36.32$, df=16, $P = 0.00415$	Too many indels at intermediate coverage classes
OG (Pira)	Goodness-of-fit	$\chi^2 = 418.84$, df=17, $P < 2.2\text{e-}16$	Too many genes with Pira outgroup when coverage was high and too few when coverage was low.
OG (Pila)	Goodness-of-fit	$\chi^2 = 171.03$, df=17, $P < 2.2\text{e-}16$	Too many genes with Pila outgroup when coverage was high and too few when coverage was low.

Abbreviations: bp, base pairs; Indels, insertion-deletion events; OG, outgroup present (i.e. either a single sequence of *Pinus lambertiana* or *P. radiata* or both is available for the amplicon); Pila, *Pinus lambertiana*; Pira, *Pinus radiata*; SNPs, single nucleotide polymorphisms.