

Figure 1 Panel	BI	ML	ratio(BI/ML)
a	0.020	0.016	1.25
b	0.027	0.021	1.27
c	0.024	0.018	1.38
d	0.038	0.019	2.02

**Table S1** Bayesian integration (BI) requires more phylogenetic signal to recover the correct tree than maximum likelihood (ML). For each panel in Figure 1, we calculate the  $BL_{95}$ —the internal branch length at which the correct phylogeny is recovered from 95% of replicates—for BI and ML using logistic regression:  $1/(1 + e^{(x-c)s})$ , where  $x$  is the internal branch length;  $c$  is the internal length at which 50% accuracy is achieved, and  $s$  is the slope of the curve.