

Supplemental Information

Table S1: BUSTED false positive rates on null simulations from Murrell et al. (2012b). N is the number of sequences used in the simulation. All alignments were simulated with 250 codon sites. BUSTED was conservative on average.

N	BUSTED at $p \leq 0.05$
8	0.00
16	0.025
32	0.025
64	0.05
128	0.025