Table 4. False-positive rates of the branch-site likelihood method in detecting positive selection at the 5% significance level

	Relaxation of negative selection	
Sequence length (codons)	Partial (F1)*	Complete (F2)*
150	0.0050	0.0175
400	0.0400	0.0625
1,000	0.0450	0.0775

* The models used for foreground branches are in parentheses. Model B1 was used for the background branches.