

Table 2. PAML results

Rooting strategy	<i>Hsmar1</i> consensus	<i>Mmmar1</i> consensus	No consensus
1) K_A/K_S analyses			
<u>Entire transposase sequence (1,029 bp)</u>			
Free K_A/K_S ratio vs. single K_A/K_S ratio	$P = 0.162$	$P = 0.118$	$P = 0.053$
Single K_A/K_S ratio estimate	0.311	0.387	0.289
Single K_A/K_S ratio vs. $K_A/K_S = 1$ (neutrality)	$P < 0.000001$	$P < 0.000001$	$P < 0.000001$
<u>5' half (positions 1-513)</u>			
Free K_A/K_S ratio vs. single K_A/K_S ratio	$P = 0.504$	$P = 0.144$	$P = 0.489$
Single K_A/K_S ratio estimate	0.106	0.202	0.084
Single K_A/K_S ratio vs. $K_A/K_S = 1$ (neutrality)	$P < 0.000001$	$P < 0.000001$	$P < 0.000001$
<u>3' half (positions 514-1,029)</u>			
Free K_A/K_S ratio vs. single K_A/K_S ratio	$P = 0.087$	$P = 0.086$	$P = 0.064$
Single K_A/K_S ratio estimate	0.695	0.673	0.721
Single K_A/K_S ratio vs. $K_A/K_S = 1$ (neutrality)	$P = 0.163$	$P = 0.111$	$P = 0.282$
2) Site selection analyses			
Model M1a (no positive selection) vs. model M2a (positive selection)	$P = 0.833$	$P = 0.457$	$P = 0.354$