Non-synonymous substitution rates within BESs

Locus	Subspecies	Parameters (M1a)	Parameters (M2a)	2Δ ln L	p-value
ESAG6	**T.b.g.**	$\omega 0=0.000,\ p0=0.560$	$\omega 0=0.157,\ p0=0.752$	3.460	0.177
		$\omega 1=1.000,\ p1=0.440$	$\omega 1=1.000,\ p1=0.216$		
			$\omega 2=7.215,\ p2=0.032$		
	T.b.b.	$\omega 0=0.031,\ p0=0.708$	$\omega 0=0.043,\ p0=0.724$	61.58	4.25×10^{-14}
		$\omega 1=1.000,\ p1=0.292$	$\omega 1=1.000,\ p1=0.220$		
			$\omega 2=4.132,\ p2=0.056$		
	T. eq.	$\omega 0=0.000,\ p0=0.536$	$\omega 0=0.000,\ p0=0.711$	6.276	0.043
		$\omega 1=1.000,\ p1=0.464$	$\omega 1=1.000,\ p1=0.022$		
			$\omega 2=2.207,\ p2=0.266$		
ESAG5	**T.b.g.**	$\omega 0=0.691,\ p0=1.000$	$\omega 0=0.557,\ p0=0.686$	-0.010	1.000
		$\omega 1=1.000,\ p1=0.000$	$\omega 1=1.000,\ p1=0.314$		
			$\omega 2=1.010,\ p2=0.000$		
	T.b.b.	$\omega 0=0.000,\ p0=0.484$	$\omega 0=0.262,\ p0=0.852$	71.95	2.22×10^{-16}
		$\omega 1=1.000,\ p1=0.516$	$\omega 1=1.000,\ p1=0.000$		
			$\omega 2=4.056,\ p2=0.148$		
	T. eq.	$\omega 0=0.000,\ p0=0.441$	$\omega 0=0.000,\ p0=0.544$	14.70	6.42×10^{-4}
		$\omega 1=1.000,\ p1=0.559$	$\omega 1=1.000,\ p1=0.317$		
			$\omega 2=3.186,\ p2=0.140$		
ESAG2	**T.b.g.**	$\omega 0=0.021,\ p0=0.714$	$\omega 0=0.032,\ p0=0.735$	10.63	0.005
		$\omega 1=1.000,\ p1=0.286$	$\omega 1=1.000,\ p1=0.236$		
			$\omega 2=5.335,\ p2=0.029$		
	T.b.b.	$\omega 0=0.058,\ p0=0.691$	$\omega 0=0.060,\ p0=0.689$	40.72	0.000
		$\omega 1=1.000,\ p1=0.309$	$\omega 1=1.000,\ p1=0.289$		
			$\omega 2=5.220,\ p2=0.021$		
	T. eq.	$\omega 0=0.163,\ p0=0.848$	$\omega 0=0.217,\ p0=0.970$	7.521	0.023
		$\omega 1=1.000,\ p1=0.152$	$\omega 1=1.000,\ p1=0.000$		
			$\omega 2=6.592,\ p2=0.030$		

Sup. Table 2. Non-synonymous substitution rates for different genes located within trypanosome BESs. Sequences from different BES loci from *Trypanosoma brucei gambiense* DAL 972 (T.b.g.), *T. b. brucei* EATRO 2340 (T.b.b.), or *T. equiperdum* STIB 818 (T. eq) were analysed. The dN/ dS ratio (ω) and weights (p) of discrete priors for the relative rate of non-synonymous (dN) to synonymous (dS) substitutions under models M1a (2 atoms) and M2a (3 atoms); p-value of the difference in log-likelihoods between M2a and M1a under a χ^2-distribution with two degrees of freedom. Rows with a p value of < 0.05 indicate significant support for adaptive evolution.