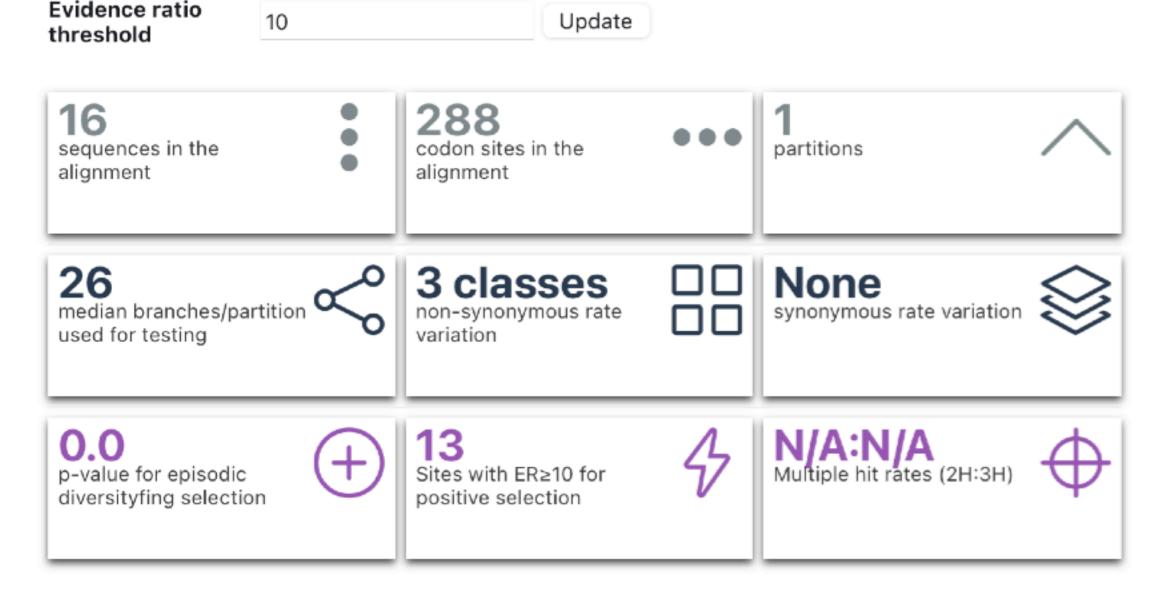
Based on the likelihood ratio test, there **is** evidence of *episodic diversifying* selection in this dataset (p=0.000).

BUSTED analysis (v4.0) was performed on the alignment from /Users/sergei/Dropbox/Talks/VEME-current/data/HIV-sets.fas using HyPhy v2.5.40. This analysis **did not include** site-to-site synonymous rate variation.

Suggested citation: Gene-wide identification of episodic selection, Mol Biol Evol.

32(5):1365-71, Synonymous Site-to-Site Substitution Rate Variation Dramatically Inflates
False Positive Rates of Selection Analyses: Ignore at Your Own Peril, Mol Biol Evol.

37(8):2430-2439



Gene-wide selection analysis using a branch-site method (BUSTED), HIV-1 env

hyphy busted --srv No --alignment data/HIV-sets.nex --starting-points 5

Produces *HIV-sets.nex.BUSTED.json* file View in http://vision.hyphy.org/BUSTED

Alignment-wide results

Model	Log (L)	AIC-c	Params.	Rate distribution	Rate plot
Unconstrained model	-2039.96	4170.83	45	Tested ω 0.5596 (86.941%) 0.9885 (10.960%) 96.09 (2.0981%) Mean = 2.611, CoV = 5.242	0 20 40 60 80100
Constrained model	-2078.31	4245.48	44	Tested ω 1.000 (14.819%) 1.000 (20.229%) 1.000 (64.952%) Mean = 1.000, CoV = NaN 47	1

Figure 1. Empirical Bayes Factors for $\omega > 1$ at a particular branch and site (only tested branches are included).

