



Gene-wide selection  
random effects over sites and branches [BUSTED]



Sites



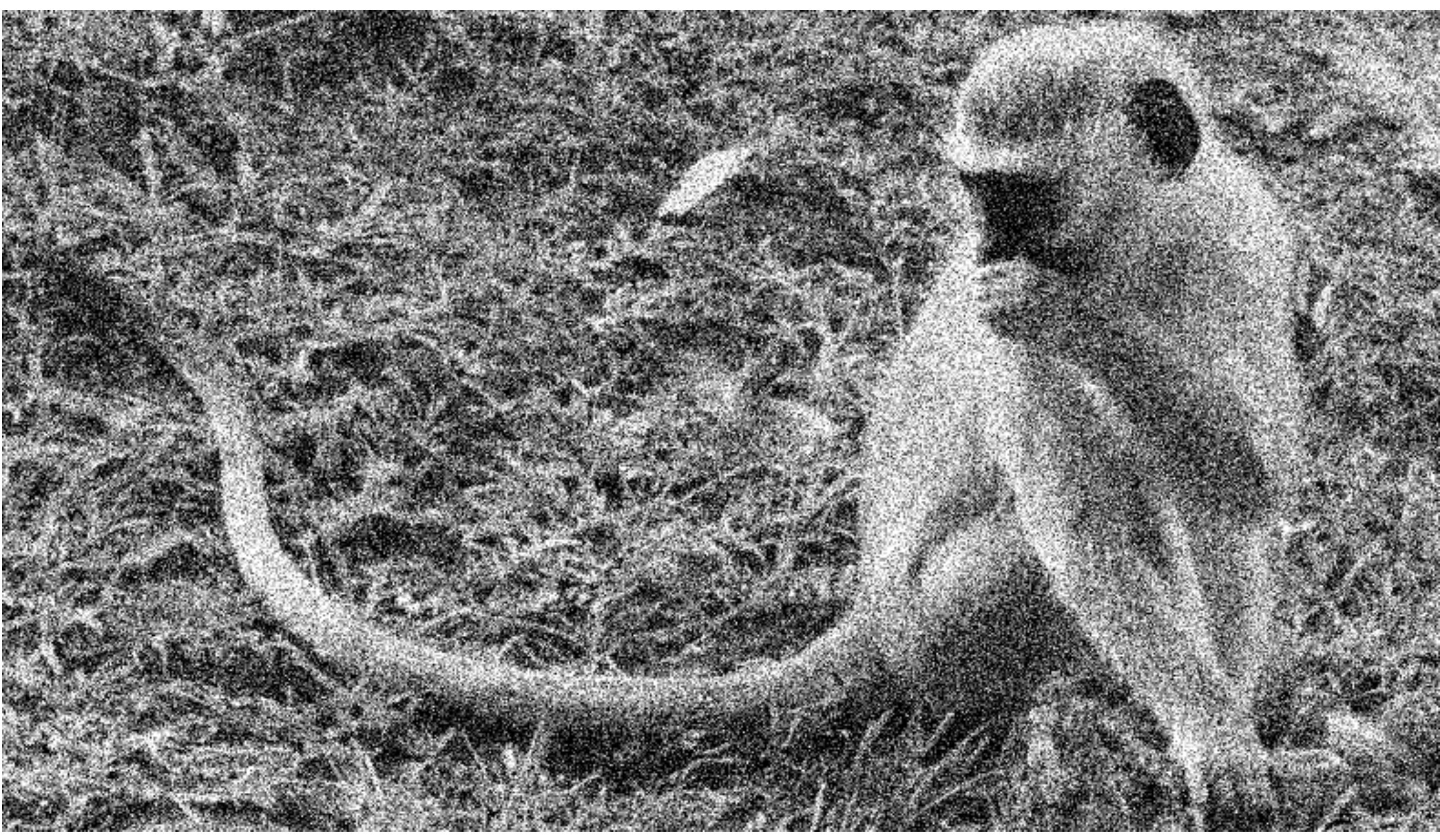




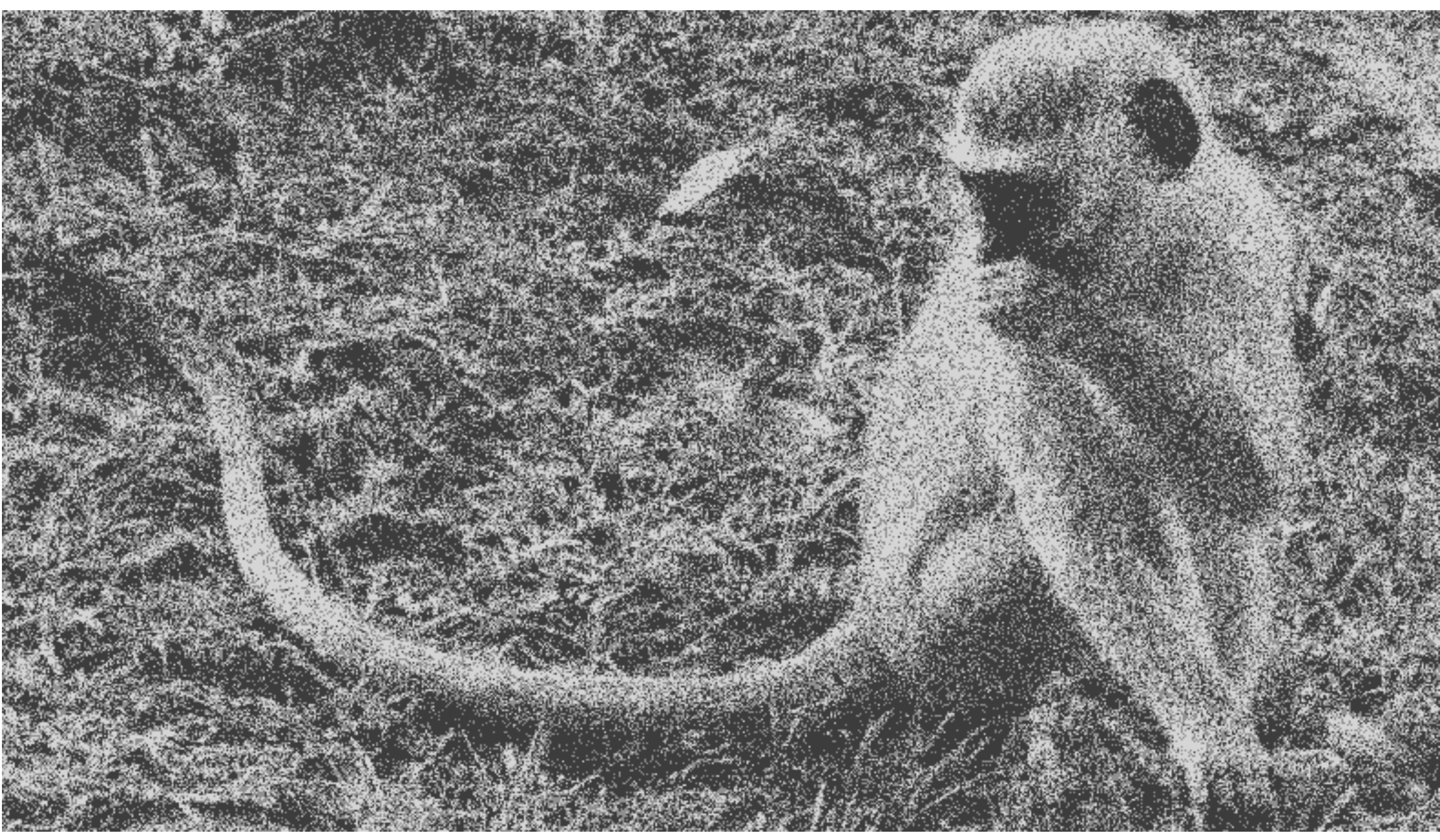
Is there enough **image area** that is sufficiently bright; allow each pixel to be one of  $K$  ( $=3$ ) colors, chosen adaptively, e.g. to minimize perceptual differences



[BUSTED]: each branch-site combination is drawn from a  $K$ -bin ( $dS, dN$ ) distribution. The distribution is estimated from the entire alignment. Tests if  $dN/dS > 1$  for some branch/site pairs in the alignment





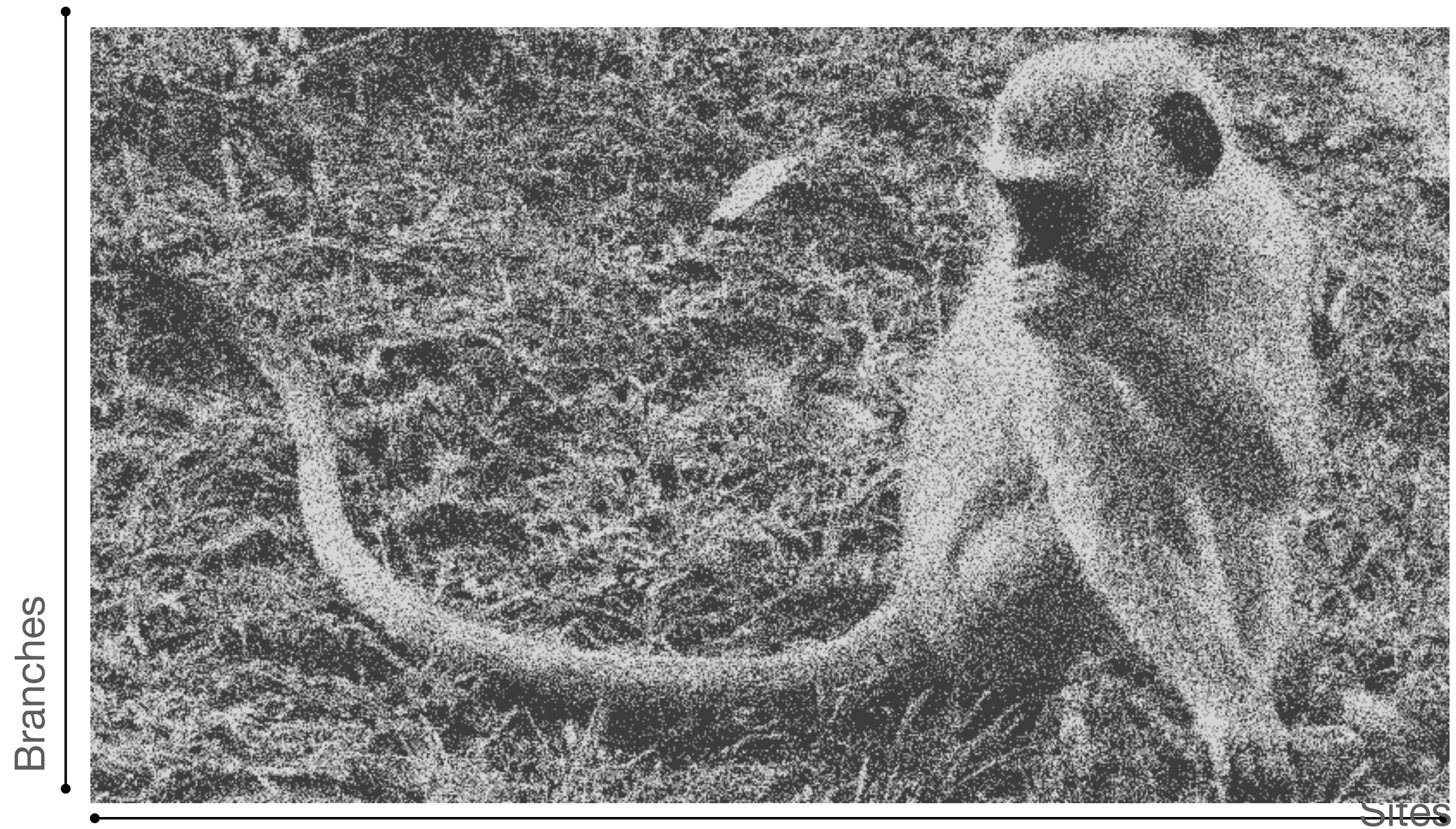






## Gene-wide selection

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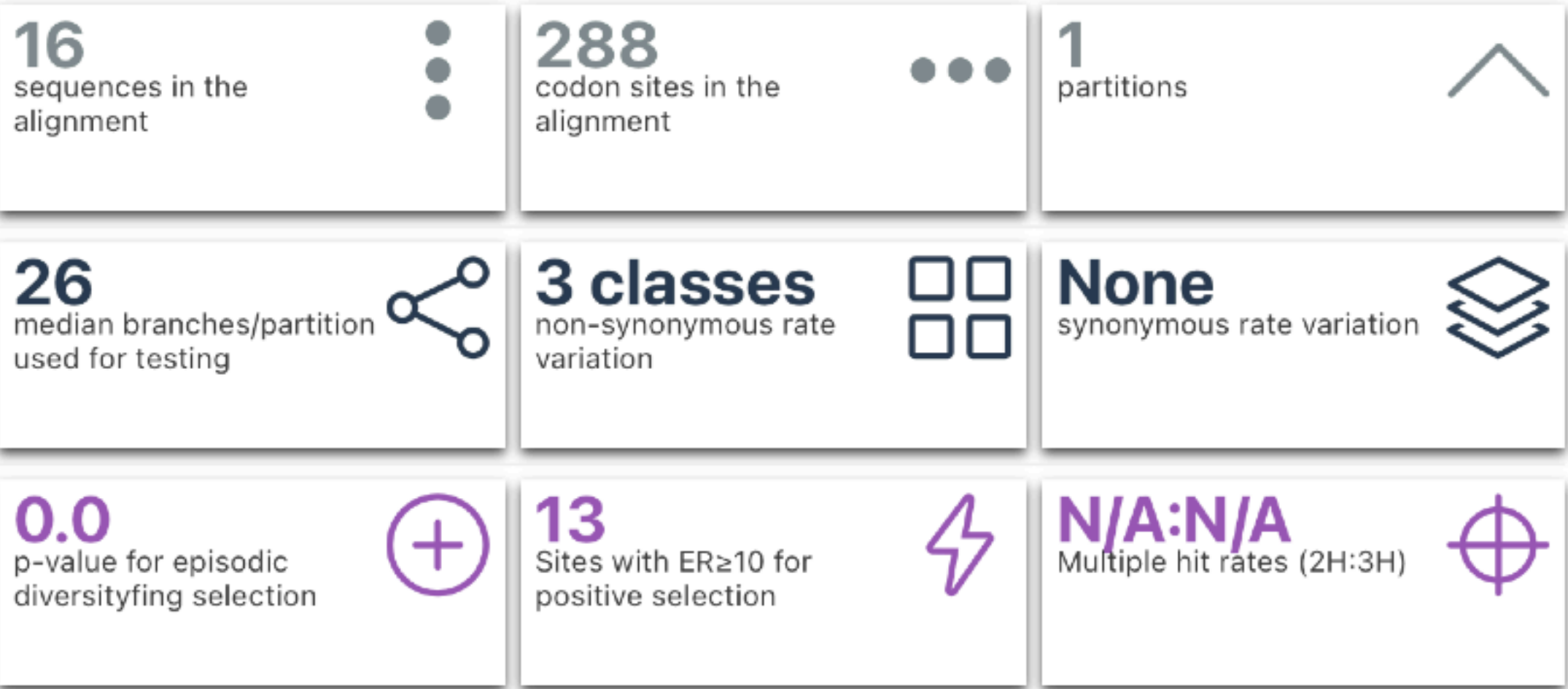


Based on the likelihood ratio test, there **is** evidence of *episodic diversifying selection* in this dataset (p=0.000).

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

Evidence ratio threshold 10 Update



Alignment-wide results

Model	Log (L)	AIC-c	Params.	Rate distribution	Rate plot
Unconstrained model	−2039.96	4170.83	45	<b>Tested ω</b> 0.5596 (86.941%) 0.9885 (10.960%) 96.09 (2.0981%) Mean = <b>2.611</b> , CoV = <b>5.242</b>	
Constrained model	−2078.31	4245.48	44	<b>Tested ω</b> 1.000 (14.819%) 1.000 (20.229%) 1.000 (64.952%) Mean = <b>1.000</b> , CoV = <b>NaN</b>	

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> or <https://observablehq.com/@spond/busted>