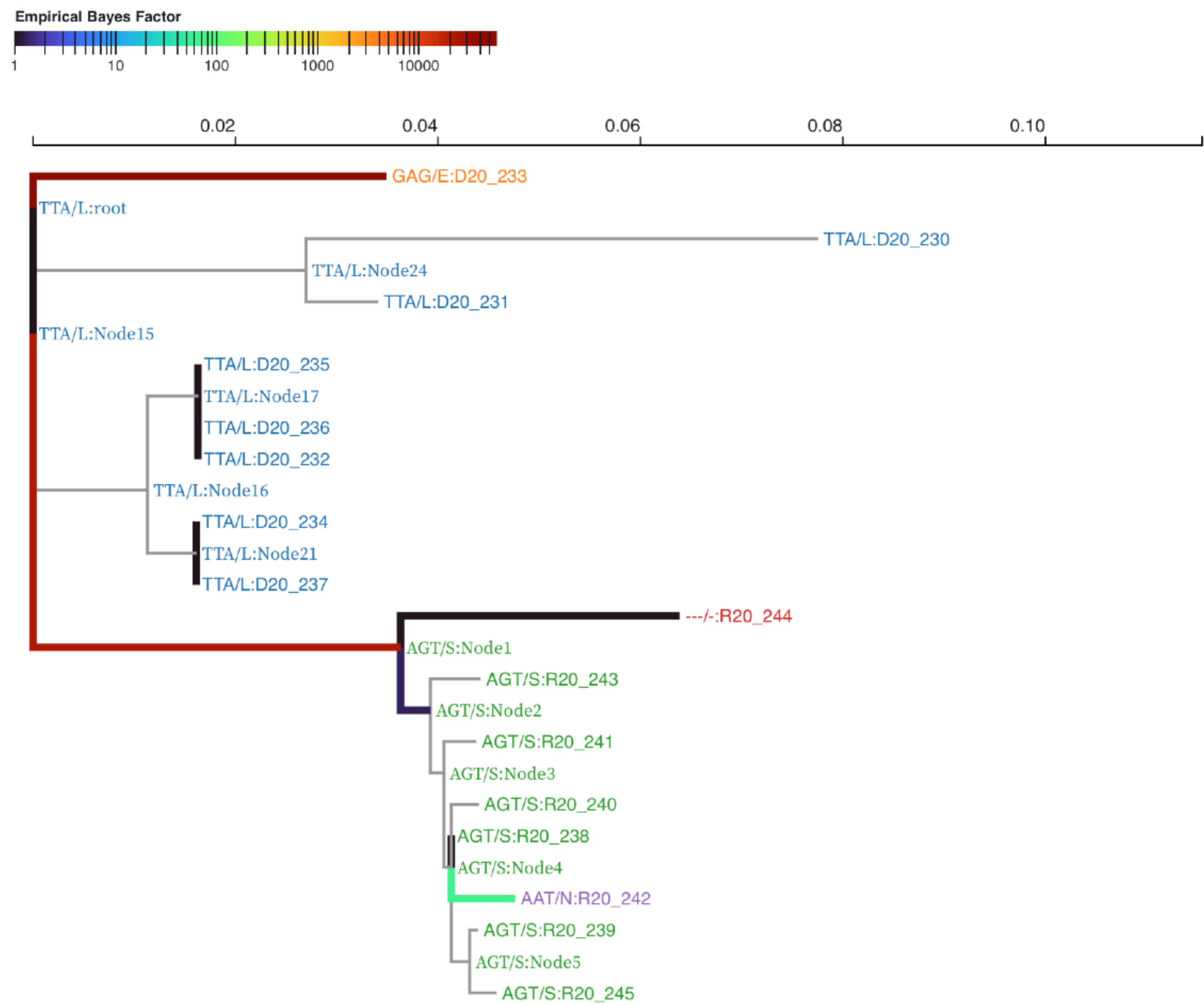


Codon 270



# Gene-wide selection analysis using a branch-site method (BUSTED), WNV NS3

hyphy busted --srv No --alignment data/WestNileVirus\_NS3.fna --starting-points 5

Produces WestNileVirus\_NS3.fna.BUSTED.json file

View in <http://vision.hyphy.org/BUSTED>

Based on the likelihood ratio test, there **is no** evidence of *episodic diversifying selection* in this dataset ( $p=0.2691$ ).

BUSTED analysis (v4.0) was performed on the alignment from /Users/sergei/Dropbox/Talks/VEME-current/data/WestNileVirus\_NS3.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

19  
sequences in the alignment

•••

619  
codon sites in the alignment

•••

1  
partitions

^

33  
median branches/partition used for testing

🔗

3 classes  
non-synonymous rate variation

□□  
□□

None  
synonymous rate variation

📁

0.27  
p-value for episodic diversifying selection

⊕

0  
Sites with ER≥10 for positive selection

⚡

N/A:N/A  
Multiple hit rates (2H:3H)

🎯

Alignment-wide results

Model	Log (L)	AIC-c	Params.	Rate distribution	Rate plot
Unconstrained model	−6396.17	12896.8	52	<b>Tested <math>\omega</math></b> 0.003895 (98.862%) 0.004316 (0.40762%) 1.859 (0.73075%) Mean = <b>0.01745</b> , CoV = <b>9.054</b>	
Constrained model	−6396.79	12896.0	51	<b>Tested <math>\omega</math></b> 0.003674 (0.10704%) 0.003690 (98.824%) 1.000 (1.0691%) Mean = <b>0.01434</b> , CoV = <b>7.145</b>	

77

Murrell et al | Mol. Biol. Evol | 32(5) | 1365–1371