Codon 270

Empirical Bayes Factor

GAG/E:D20_233
TTA/L:root
TTA/L:D20_230
TTA/L:Node24
TTA/L:D20_231
TTA/L:Node15
TTA/L:D20_235
TTA/L:Node17
TTA/L:D20_236
TTA/L:D20_232
TTA/L:Node16
TTA/L:D20_234
TTA/L:Node21
TTA/L:D20_237
---/-:R20_244
AGT/S:Node1
AGT/S:R20_243
AGT/S:Node2
AGT/S:R20_241
AGT/S:Node3
AGT/S:R20_240
AGT/S:R20_238
AGT/S:Node4
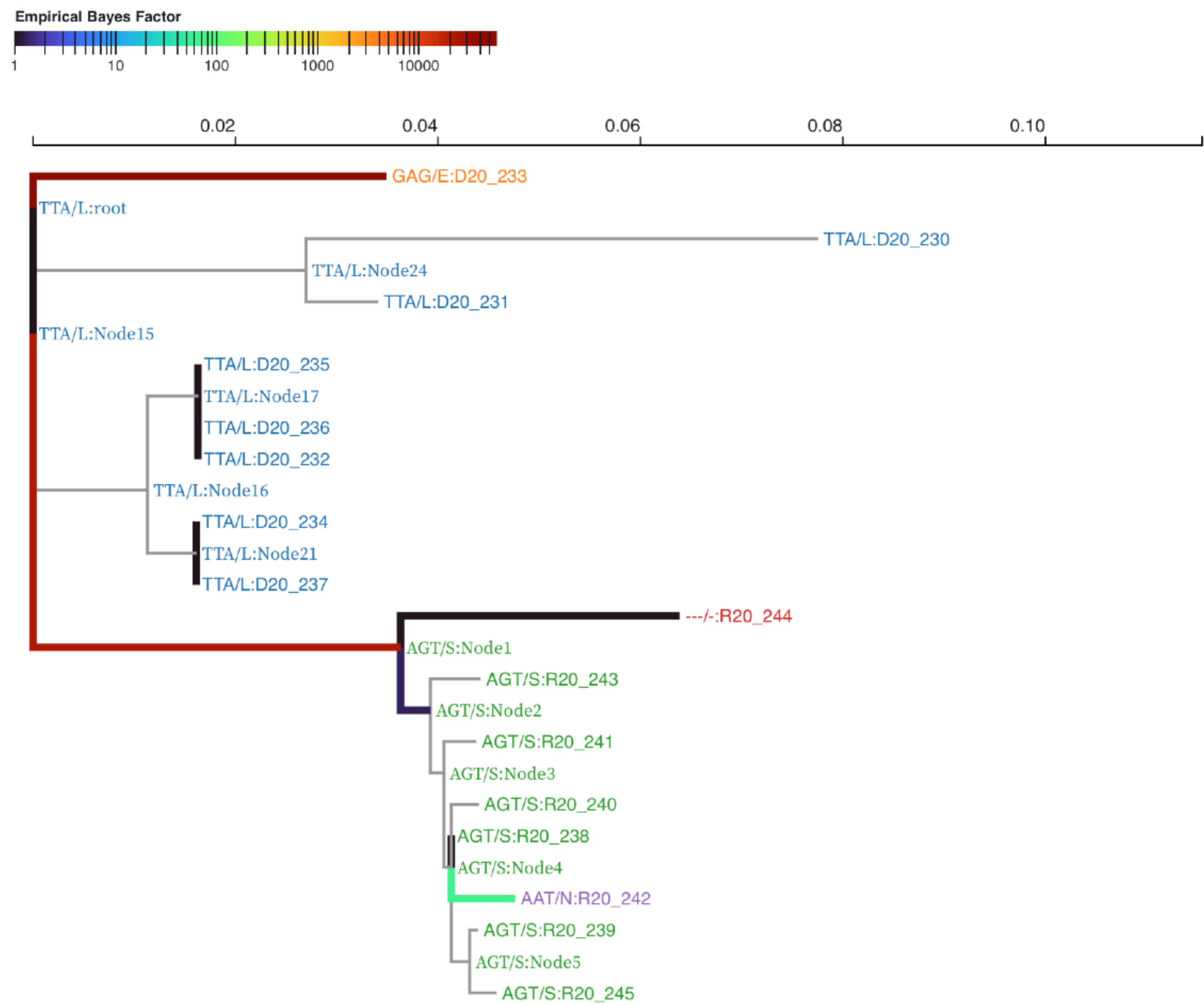AAT/N:R20_242
AGT/S:R20_239
AGT/S:Node5
AGT/S:R20_245

64

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

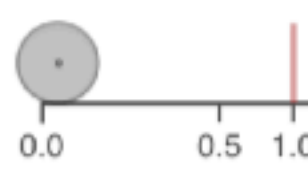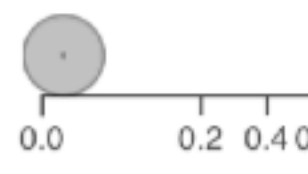**0.27** p-value for episodic diversityfing selection

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	Tested ω 0.003895 (98.862%) 0.004316 (0.40762%) 1.859 (0.73075%) Mean = **0.01745**, CoV = **9.054**	0.0 0.5 1.0
Constrained model	−6396.79	12896.0	51	Tested ω 0.003674 (0.10704%) 0.003690 (98.824%) 1.000 (1.0691%) Mean = **0.01434**, CoV = **7.145**	0.0 0.2 0.40