

Based on the likelihood ratio test, *episodic diversifying selection* has acted on **6 sites** in this dataset ($p \leq 0.1$).

MEME analysis (v3.0) was performed on the alignment from /Users/sergei/Dropbox/Talks/VEME-current/data/spike.fas using HyPhy v2.5.40.

p-value threshold

0.1

Update

Suggested citation: Detecting Individual Sites Subject to Episodic Diversifying Selection. *PLoS Genet* 8(7): e1002764.

118

sequences in the alignment

1273

codon sites in the alignment

1

partitions

162

median branches/partition used for testing

N/A

bootstrap replicates

6

sites subject to episodic diversifying selection

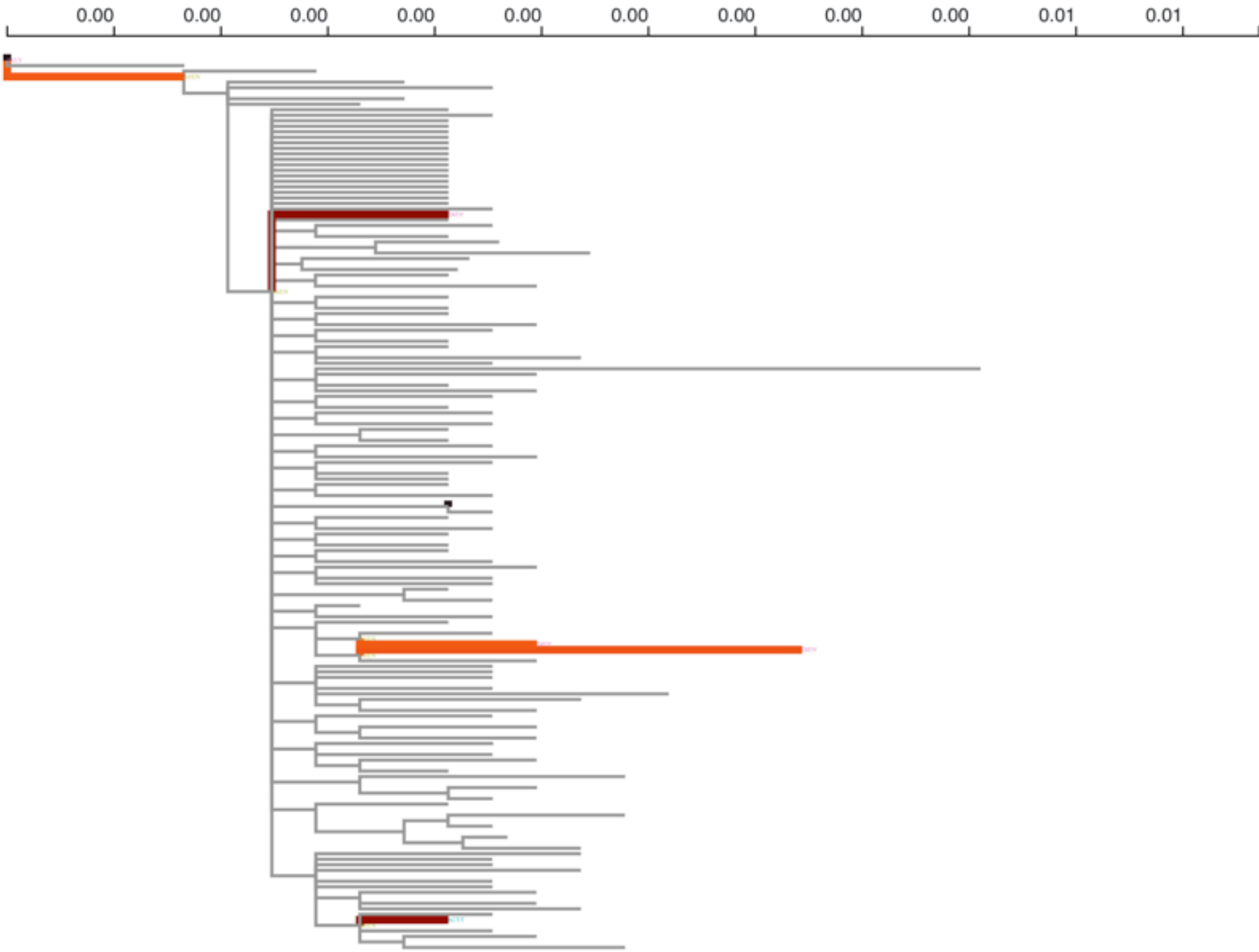
3.00

median branches with support for selection/selected site

3

sites with variable ω across branches

Codon	α	β^-	p^-	β^+	p^+	LRT	$-p\text{-value}$	# branches under selection	MEME LogL	FEL LogL	Δ
1	1.213	0.543	0.994	2,732.12	0.006	9.76	0.003	1	-19.143	-14.262	4.881
1,243	0	0	0.983	552.73	0.017	8.846	0.005	2	-23.278	-19.431	3.847
452	0	0	0.01	14.48	0.99	8.771	0.005	5	-36.485	-36.486	-0.001
470	3.168	0.727	0.994	10,000	0.006	8.012	0.008	1	-24.317	-19.832	4.485
501	0.004	0.002	0.925	343.752	0.075	5.017	0.037	5	-37.067	-36.202	0.865
157	0	0	0.01	7.313	0.99	3.708	0.074	4	-29.546	-29.547	-0.001



```
hyphy meme --alignment data/spike.fas --tree data/spike.tree
```

Interpreting dN/dS for intra-host and intra-species pathogen

- **dN/dS** can be estimated for all sorts of sequence data (e.g., it has been done for cancer SNP data)
- Traditional interpretation of dN/dS is based on the assumption that **substitution ~ fixation**
- Not the same for intra-species / intra-host pathogens
 - Much of variation is due to polymorphism, or even dead-end mutations
 - This is because selection has not had a chance to “filter” mutations (except for patently deleterious ones)
 - This often manifests as differences in selective “regimes” between tips and internal branches