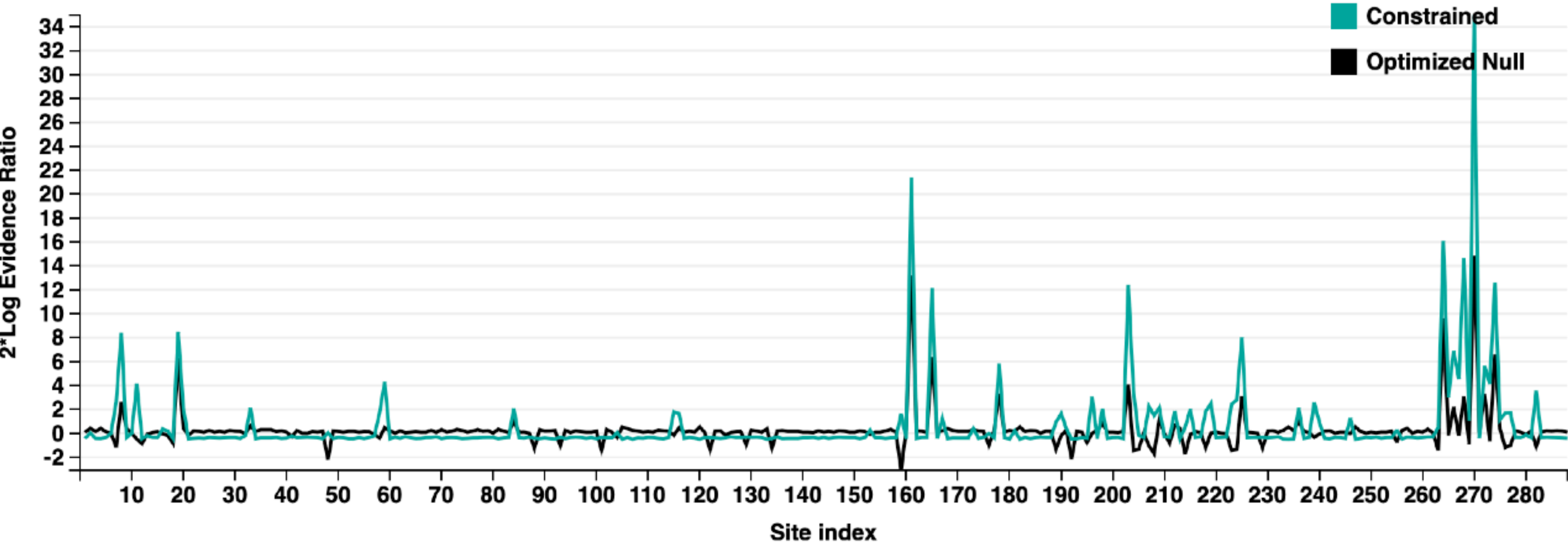




Export Chart to PNG

Export Chart to SVG



Constrained Test Statistic

5

Optimized Null Test Statistic

-Infinity

Showing entries 1 through 13 out of 13.

Export Table to CSV

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Site index ⬆	Unconstrained likelihood ⬆	Constrained likelihood ⬆	Optimized Null Likelihood	Constrained Statistic	Optimized Null Statistic
8	-25.12	-29.31	-26.42	8.38	2.6
19	-13.12	-17.34	-16.24	8.45	6.23

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

BUSTED without synonymous rate variation **found no evidence** (LRT, p-value = 0.262 \geq .05) of gene-wide episodic diversifying selection in the selected test branches of your phylogeny. Therefore, there is no evidence that any sites have experienced diversifying selection along the test branch(es). 

See [here](#) for more information about this method.
Please cite [PMID 25701167](#) if you use this result in a publication, presentation, or other scientific work.

Model fits

Model	<i>log L</i>	#. params	<i>AIC_c</i>	Branch set	ω_1	ω_2	ω_3	
Unconstrained model	-6396.1	52	12896.7	Test	0.00 (75.70%)	0.00 (23.57%)	1.89 (0.73%)	
Constrained model	-6396.7	51	12895.9	Test	0.00 (25.78%)	0.00 (73.15%)	1.00 (1.07%)	

This table reports a statistical summary of the models fit to the data. Here, **Unconstrained model** refers to the BUSTED alternative model for selection, and **Constrained model** refers to the BUSTED null model for selection.

```
hyphy busted --srv No --alignment WestNileVirus_NS3.fas --starting-points 5
```