WNV NS3

adaptive Branch Site REL
results summary

INPUT DATA | WestNileVirus_NS3.fas | 19 sequences | 619 sites

Export

aBSREL **found no evidence** of episodic diversifying selection in your phylogeny.

A total of **33** branches were formally tested for diversifying selection. Significance was assessed using the Likelihood Ratio Test at a threshold of $p \leq 0.05$, after correcting for multiple testing. Significance and number of rate categories inferred at each branch are provided in the detailed results table.

See here for more information about this method.

Please cite PMID 25697341 if you use this result in a publication, presentation, or other scientific work.

Tree summary

ω rate classes	# of branches	% of branches	% of tree length	# under selection
1	30	91%	37%	0
2	3	9.1%	63%	0

This table contains a summary of the inferred aBSREL model complexity. Each row provides information about the branches that were best described by the given number of ω rate categories.

```
hyphy absrel --alignment data/WestNileVirus_NS3.fas
```

SARS-CoV-2 spike

adaptive Branch Site REL
results summary

INPUT DATA | **spike.fas** | **118** sequences | **1273** sites

Export

aBSREL **found no evidence** of episodic diversifying selection in your phylogeny.

A total of **44** branches were formally tested for diversifying selection. Significance was assessed using the Likelihood Ratio Test at a threshold of $p \leq 0.05$, after correcting for multiple testing. Significance and number of rate categories inferred at each branch are provided in the detailed results table.

See here for more information about this method.

Please cite PMID 25697341 if you use this result in a publication, presentation, or other scientific work.

Tree summary

ω rate classes	# of branches	% of branches	% of tree length	# under selection
1	161	99%	61%	0
2	1	0.62%	39%	0

This table contains a summary of the inferred aBSREL model complexity. Each row provides information about the branches that were best described by the given number of ω rate categories.

```
hyphy absrel --alignment data/spike.fas --tree data/spike.tree --branches Internal
```