

adaptive Branch Site REL

results summary

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

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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
```

aBSREL analysis - summary

- **West Nile Virus NS3 protein**

- 91% branches can be explained with simple (single dN/dS) models
- 3 branches (9%, 60% of tree length) have evidence of multiple dN/dS rate classes over sites, but **none** with significant proportions of sites with $dN/dS > 1$

- **HIV-1 transmission pair**

- 76% branches can be explained with simple (single dN/dS) models
- 5 branches (24%, ~100% of tree length) have evidence of multiple dN/dS rate classes over sites
- 3 branches have small (1–7%), but statistically significant ($p < 0.05$, multiple testing corrected) proportions of sites with $dN/dS > 1$, including the **transmission** branch

- **SARS-CoV-2 spike**

- All but **one** branch can be explained with simple (single dN/dS) models
- 1 long terminal branch (~34% of tree length) has evidence of multiple dN/dS rate classes over sites
- No evidence of branch level selection on internal branches.