

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
```

aBSREL analysis

- **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.