

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.

Free summary

ω rate classes	# of branches	% of branches	% of tree length	# under selection
1	161	99%	66%	0
2	1	0.62%	34%	0

```
hyphy absrel --alignment spike.fas --tree 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 branches can be explained with simple single dN/dS models
- 1 long terminal branches (~34% of tree length) has evidence of multiple dN/dS rate classes over sites
- No evidence of branch level selection on internal branches.