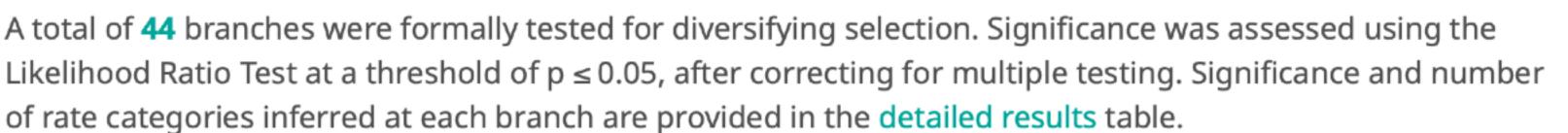
SARS-CoV-2 spike

adaptive Branch Site REL results summary

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



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



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.