


# adaptive Branch Site REL results summary

INPUT DATA | HIV-sets.fas | 16 sequences | 288 sites

Export

aBSREL **found evidence** of episodic diversifying selection on **3** out of **26** branches in your phylogeny. 

A total of **26** 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.

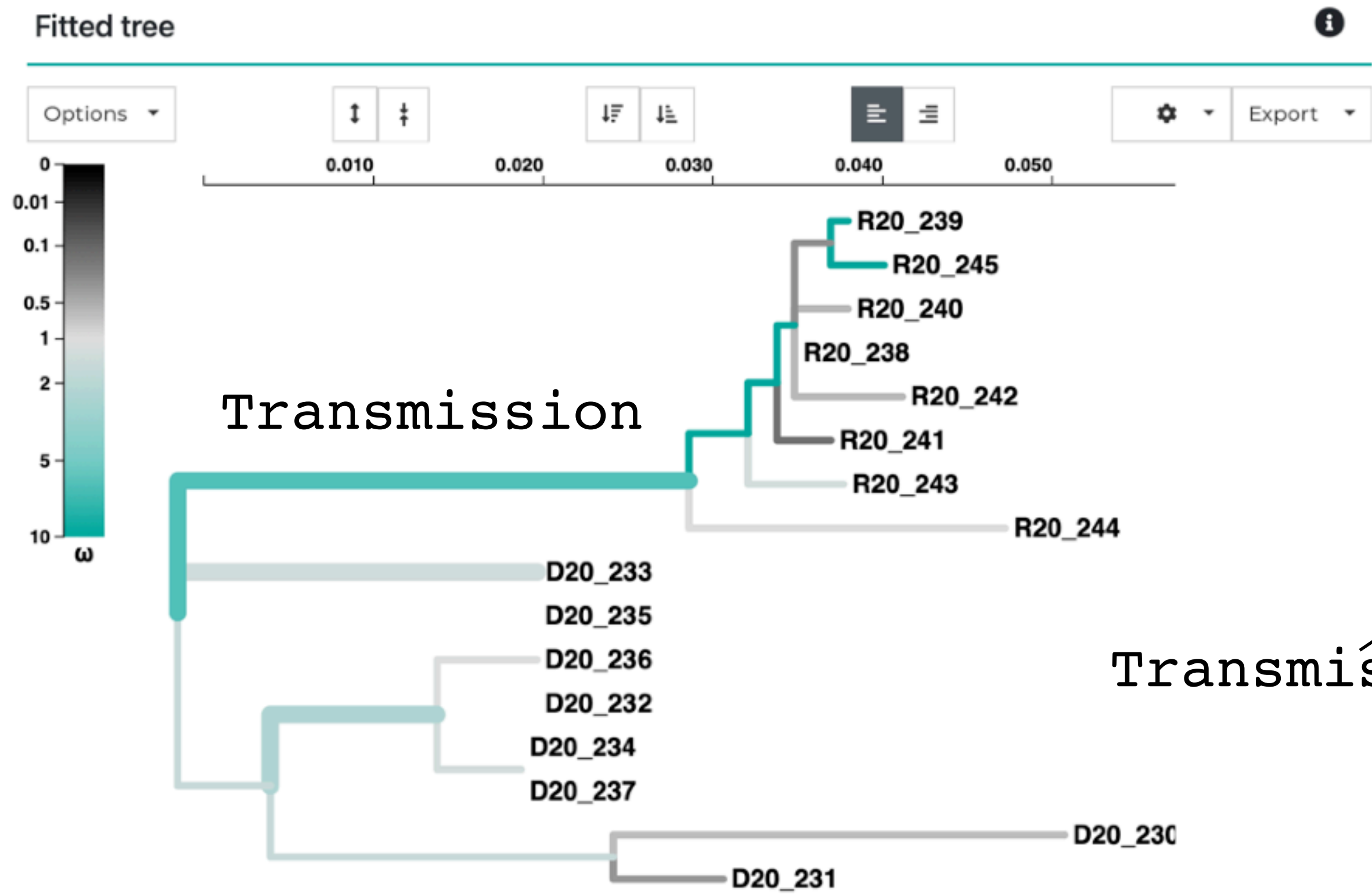
## Tree summary

$\omega$ rate classes	# of branches	% of branches	% of tree length	# under selection
1	21	81%	0.49%	0
2	5	19%	100%	3

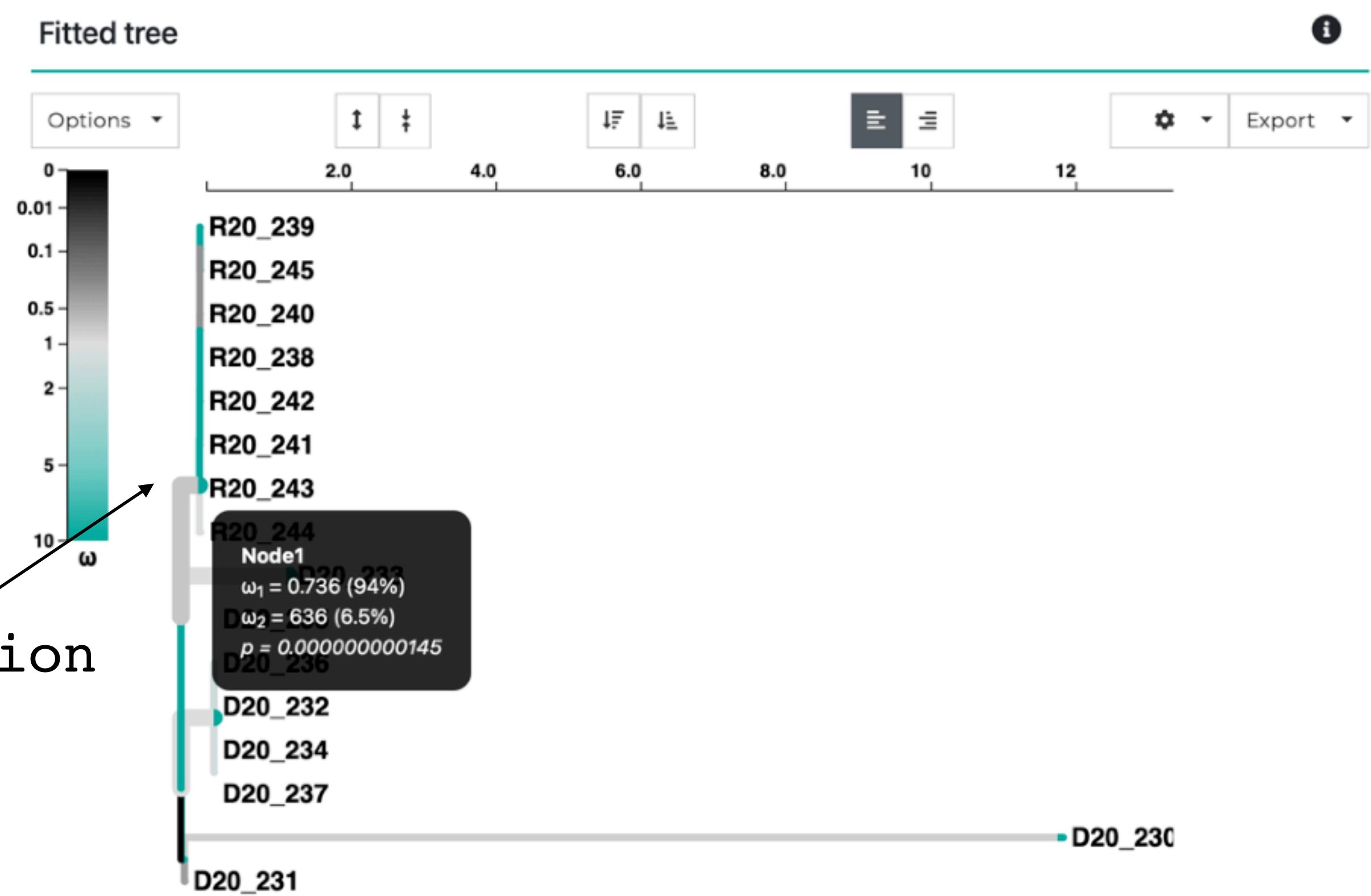
This table contains a summary of the inferred aBSREL model complexity. Each row provides information about the branches that were best described by the given number of  $\omega$  rate categories.

```
hyphy absrel --alignment data/HIV-sets.nex
```

HIV-1 env



One dN/dS per branch



Adaptive dN/dS per branch