

Fast Unconstrained Bayesian AppRoximation

results summary

INPUT DATA | **6096ed5d238adf71a5160d3b** | 87 sequences | 238 sites

[Export](#)

FUBAR **found evidence** of

⊕ episodic positive/diversifying selection at 4 sites

⊖ episodic negative/purifying selection at 210 sites

with posterior probability of .

See [here](#) for more information about the FUBAR method.

Please cite [PMID 23420840](#) if you use this result in a publication, presentation, or other scientific work.

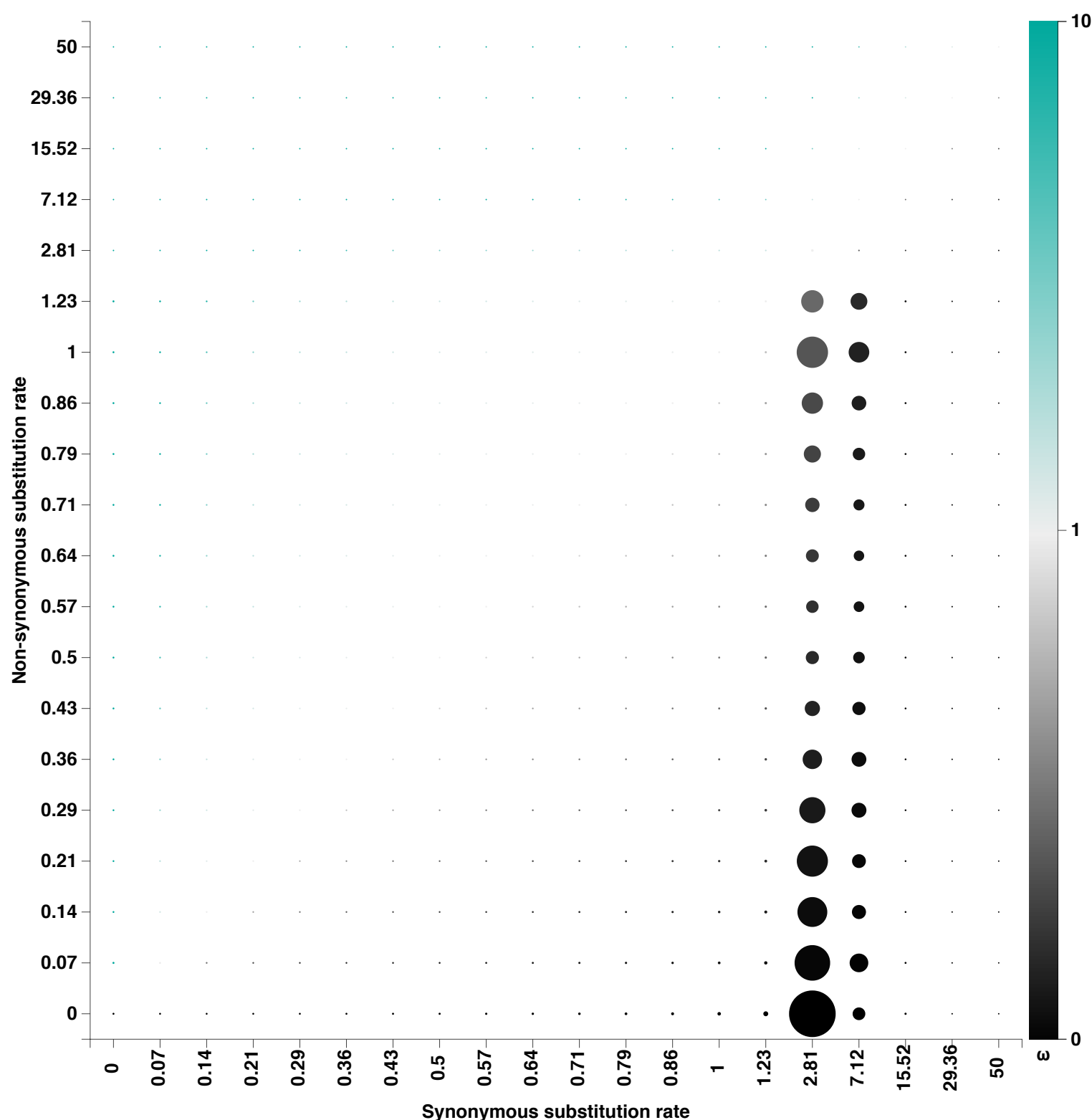
Posterior rate distribution



Site

[Export Chart to PNG](#)

[Export Chart to SVG](#)



This graph shows the posterior distribution over the discretized rate grid. The size of a dot is proportional to the posterior weight allocated to that gridpoint, and the color shows the intensity of selection. Site-specific distributions can be viewed by entering a site number in the input box above the figure. When this is empty, the alignment-wide distribution will be shown.

Positively selected sites with evidence are highlighted in green.

Negatively selected sites with evidence are highlighted in black.

Showing entries 219 through 238 out of 238.

 **Export Table to CSV**

<<

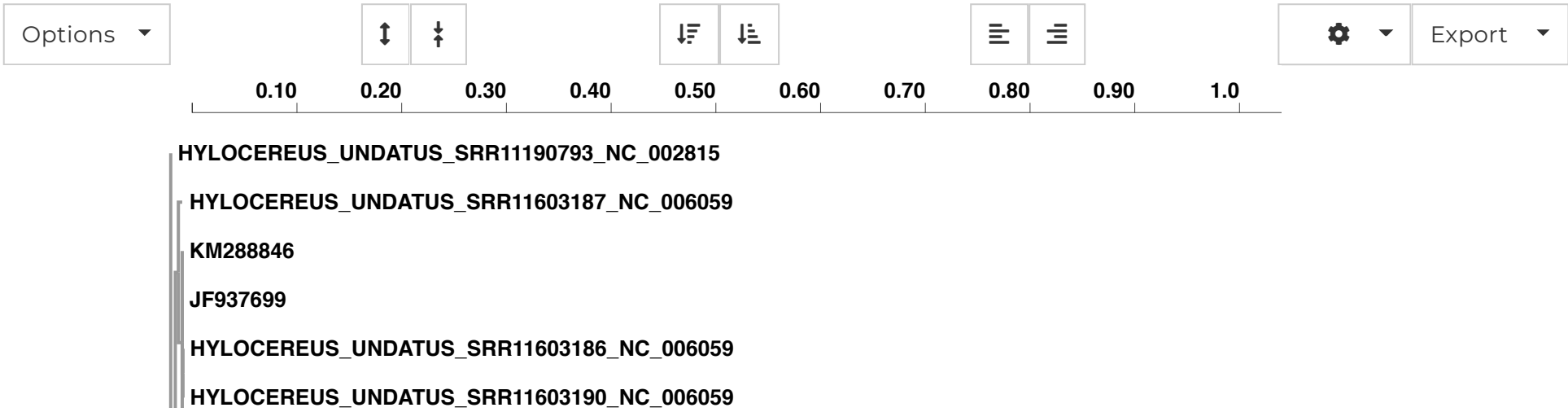
<

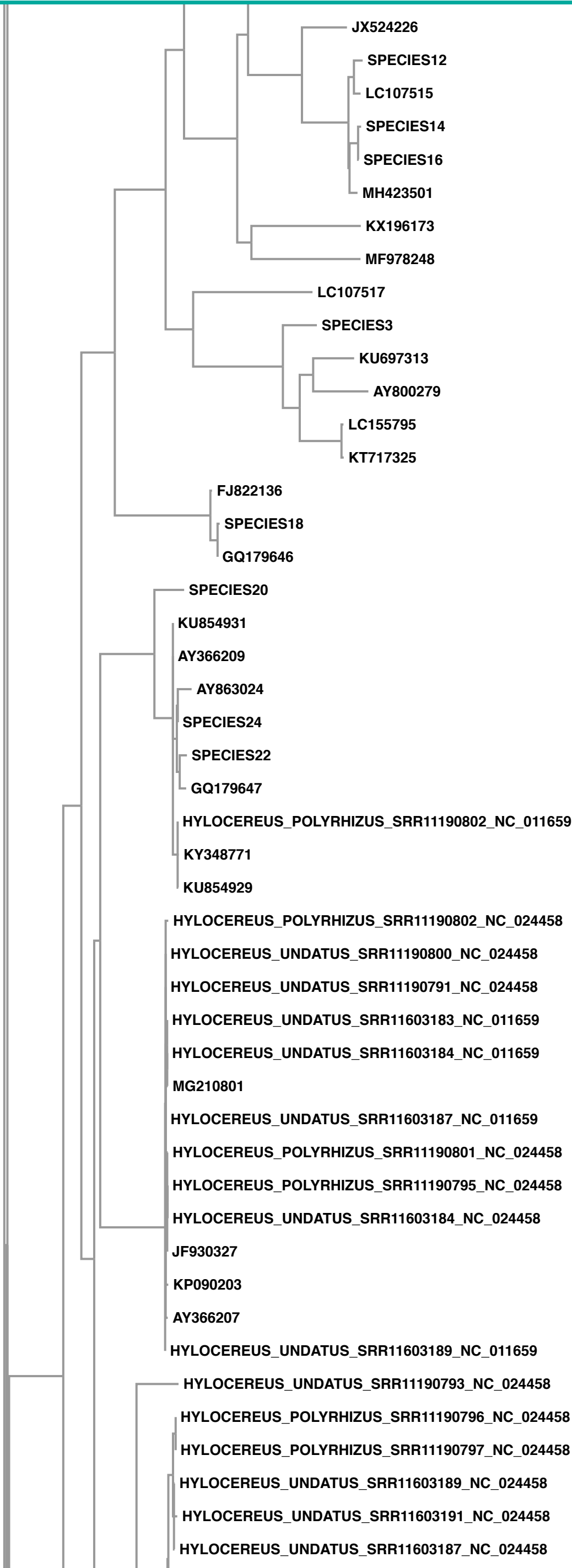
>

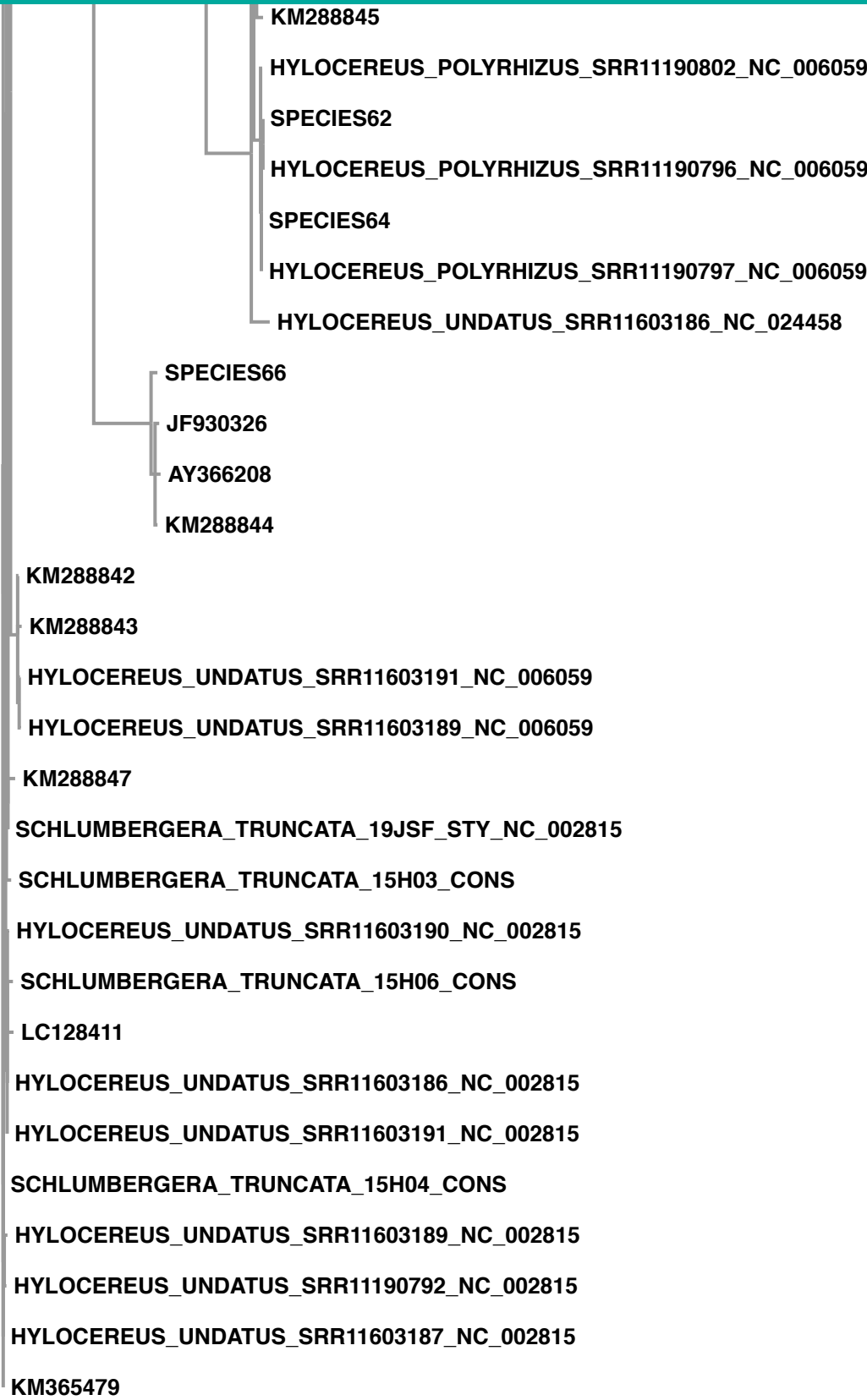
>>

Site ▾	Partition ▾	α ▾	β ▾	$\beta - \alpha$ ▾	Prob[$\alpha > \beta$] ▾	Prob[$\alpha < \beta$] ▾	BayesFactor[$\alpha < \beta$] ▾		
223	1	0.155	0.159	0.005	0.325	0.529	3.422	0.000	0.000
224	1	0.148	0.048	-0.100	0.541	0.188	0.706	0.000	0.000
228	1	0.502	0.769	0.266	0.178	0.757	9.503	0.000	0.000
229	1	1.262	0.936	-0.326	0.483	0.407	2.092	0.000	0.000
231	1	0.284	0.441	0.157	0.238	0.704	7.226	0.000	0.000
235	1	0.273	0.469	0.195	0.238	0.701	7.134	0.000	0.000
236	1	0.853	2.317	1.465	0.245	0.709	7.403	0.000	0.000
237	1	1.310	0.576	-0.733	0.506	0.447	2.466	0.000	0.000
238	1	4.754	2.856	-1.898	0.724	0.247	1.000	0.000	0.000

Fitted tree







Model fits i

Model	AIC _c	log L	Parameters	Rate distributions
Nucleotide GTR	27885.62	-13763.29	179	

This table reports a statistical summary of the models fit to the data. Here, **MG94** refers to the MG94xREV baseline model that infers a single ω rate category per branch.





Spyros Lytras

@SpyrosLytras

Replying to @SpyrosLytras

We used an array of methods implemented in [@hyphy_software](#) to search for site-, branch- and ORF-specific selection in the phylogenetic clade SARS-CoV-2 emerged from (we refer to as the 'nCoV' clade) 9/18



Mar 13, 2021



HyPhy Retweeted



Sergei Pond

@sergeilkp

Rapid app development is a must. Excited to start moving [Datamonkey.org](#) visualization development to embedded [@observablehq](#) notebooks. The new GARD analysis result page is one such example.

[Embed](#)

[View on Twitter](#)