

## Fast Unconstrained Bayesian AppRoximation results summary

INPUT DATA | 6096f188238adf71a5160e3e | 77 sequences | 121 sites

 Export ▾

FUBAR **found evidence** of

⊕ episodic positive/diversifying selection at 3 sites

⊖ episodic negative/purifying selection at 68 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.

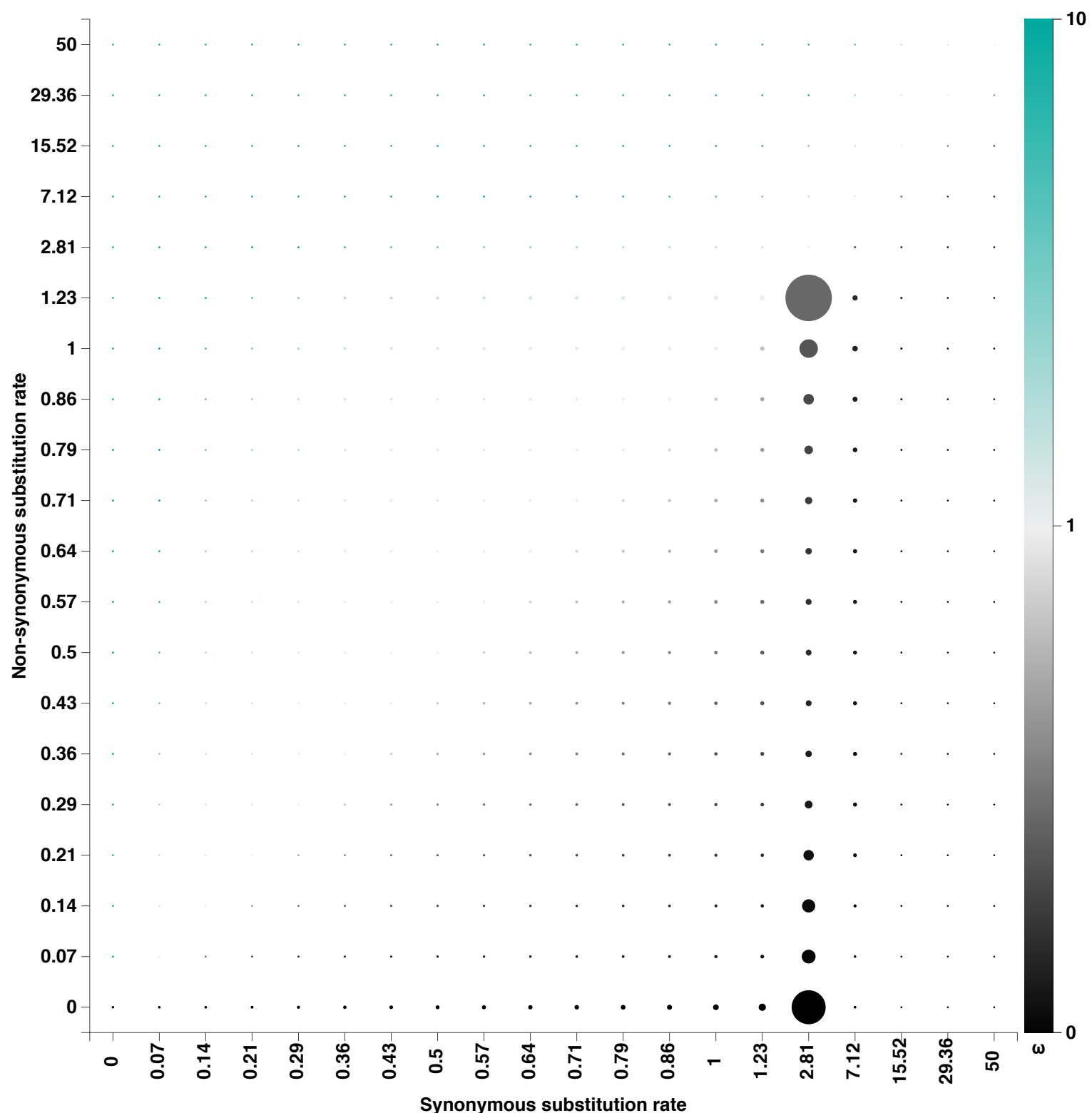
### Posterior rate distribution



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 1 through 20 out of 121.

Export Table to CSV

«

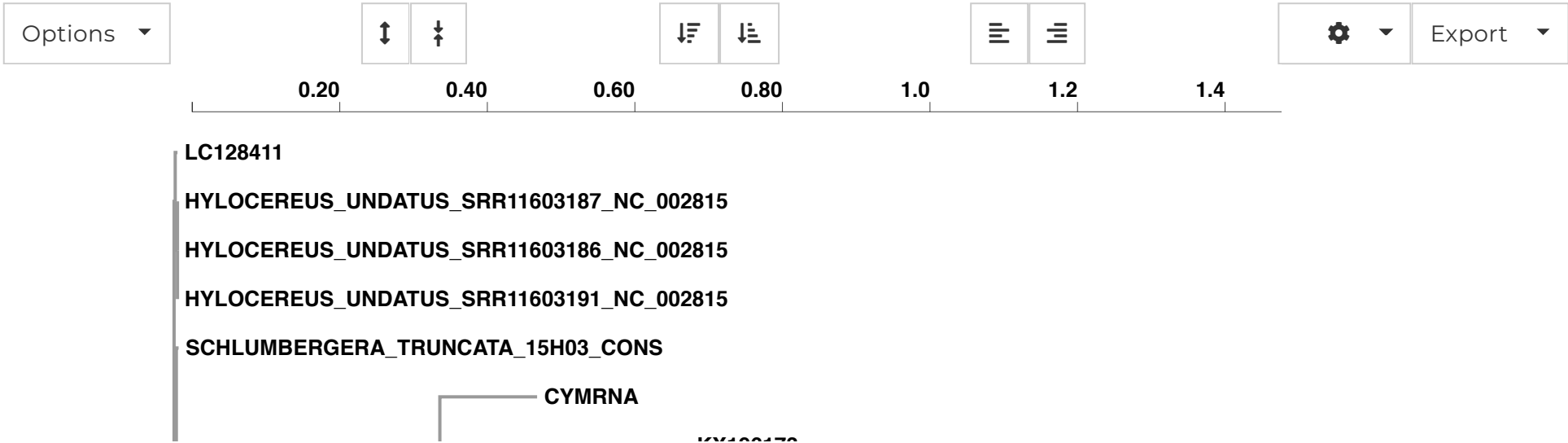
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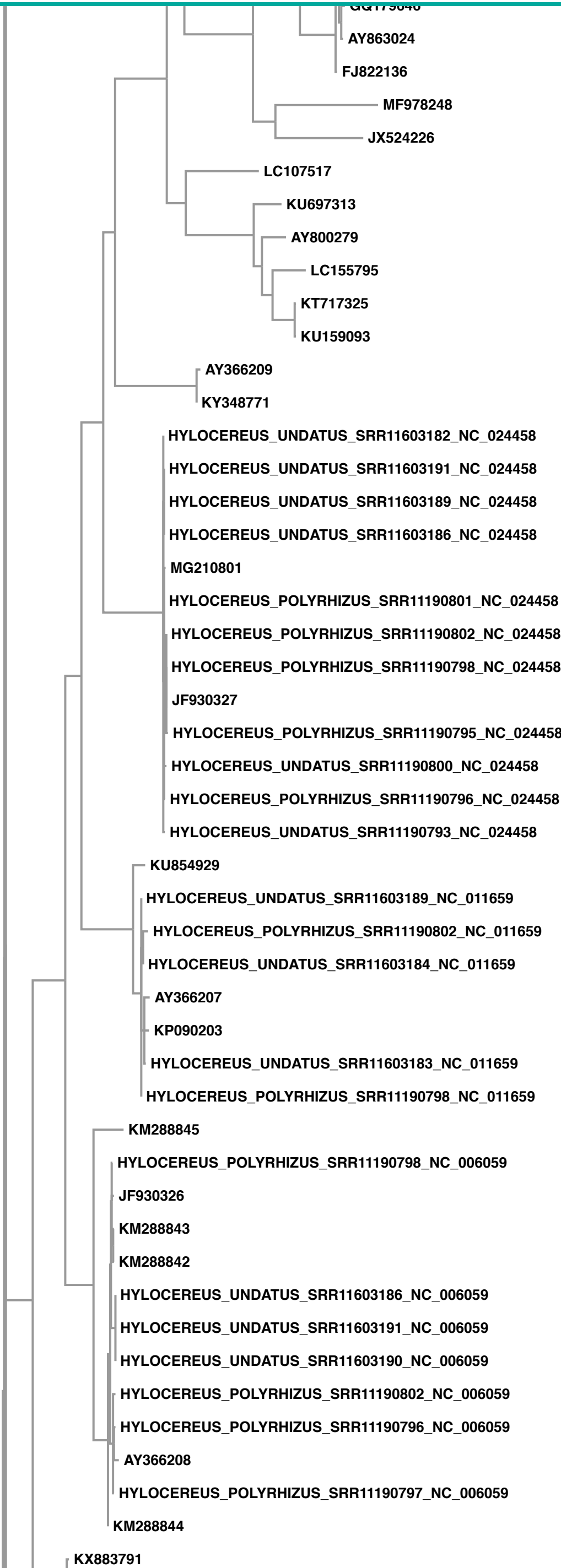
>

»

Site ↕	Partition ↕	$\alpha$ ↕	$\beta$ ↕	$\beta - \alpha$ ↕	Prob[ $\alpha > \beta$ ] ↕	Prob[ $\alpha < \beta$ ] ↕	BayesFactor[ $\alpha < \beta$ ] ↕		
3	1	0.735	0.448	-0.287	0.777	0.162	0.345	0.000	0.000
7	1	1.205	0.561	-0.643	0.835	0.119	0.243	0.000	0.000
14	1	0.892	0.670	-0.222	0.526	0.391	1.151	0.000	0.000
17	1	1.666	0.992	-0.674	0.643	0.241	0.570	0.000	0.000
19	1	0.912	0.638	-0.273	0.636	0.288	0.727	0.000	0.000
20	1	0.688	0.292	-0.396	0.899	0.062	0.118	0.000	0.000

Fitted tree





SCHLUMBERGERA\_TRUNCATA\_19JSF\_STY\_NC\_002815  
SCHLUMBERGERA\_TRUNCATA\_15H04\_CONS  
SCHLUMBERGERA\_TRUNCATA\_15H06\_CONS  
HYLOCEREUS\_UNDATUS\_SRR11190793\_NC\_002815  
HYLOCEREUS\_UNDATUS\_SRR11190792\_NC\_002815  
KM365479  
HYLOCEREUS\_POLYRHIZUS\_SRR11190797\_NC\_002815  
HYLOCEREUS\_POLYRHIZUS\_SRR11190798\_NC\_002815  
HYLOCEREUS\_POLYRHIZUS\_SRR11190801\_NC\_002815  
HYLOCEREUS\_UNDATUS\_SRR11190799\_NC\_002815  
HYLOCEREUS\_UNDATUS\_SRR11603184\_NC\_002815  
HYLOCEREUS\_UNDATUS\_SRR11603182\_NC\_002815  
HYLOCEREUS\_UNDATUS\_SRR11603183\_NC\_002815  
HYLOCEREUS\_POLYRHIZUS\_SRR11190796\_NC\_002815  
HYLOCEREUS\_POLYRHIZUS\_SRR11190795\_NC\_002815  
AF308158  
HYLOCEREUS\_POLYRHIZUS\_SRR11190802\_NC\_002815

Model fits



Model	AIC <sub>c</sub>	log L	Parameters	Rate distributions
Nucleotide GTR	13357.97	-6519.07	159	

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  $\omega$  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.

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