

Fast Unconstrained Bayesian AppRoximation

results summary

INPUT DATA | [6096f1c9238adf71a5160e9e](#) | 78 sequences | 134 sites

 Export ▾

FUBAR **found evidence** of

⊕ episodic positive/diversifying selection at 3 sites

⊖ episodic negative/purifying selection at 33 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.

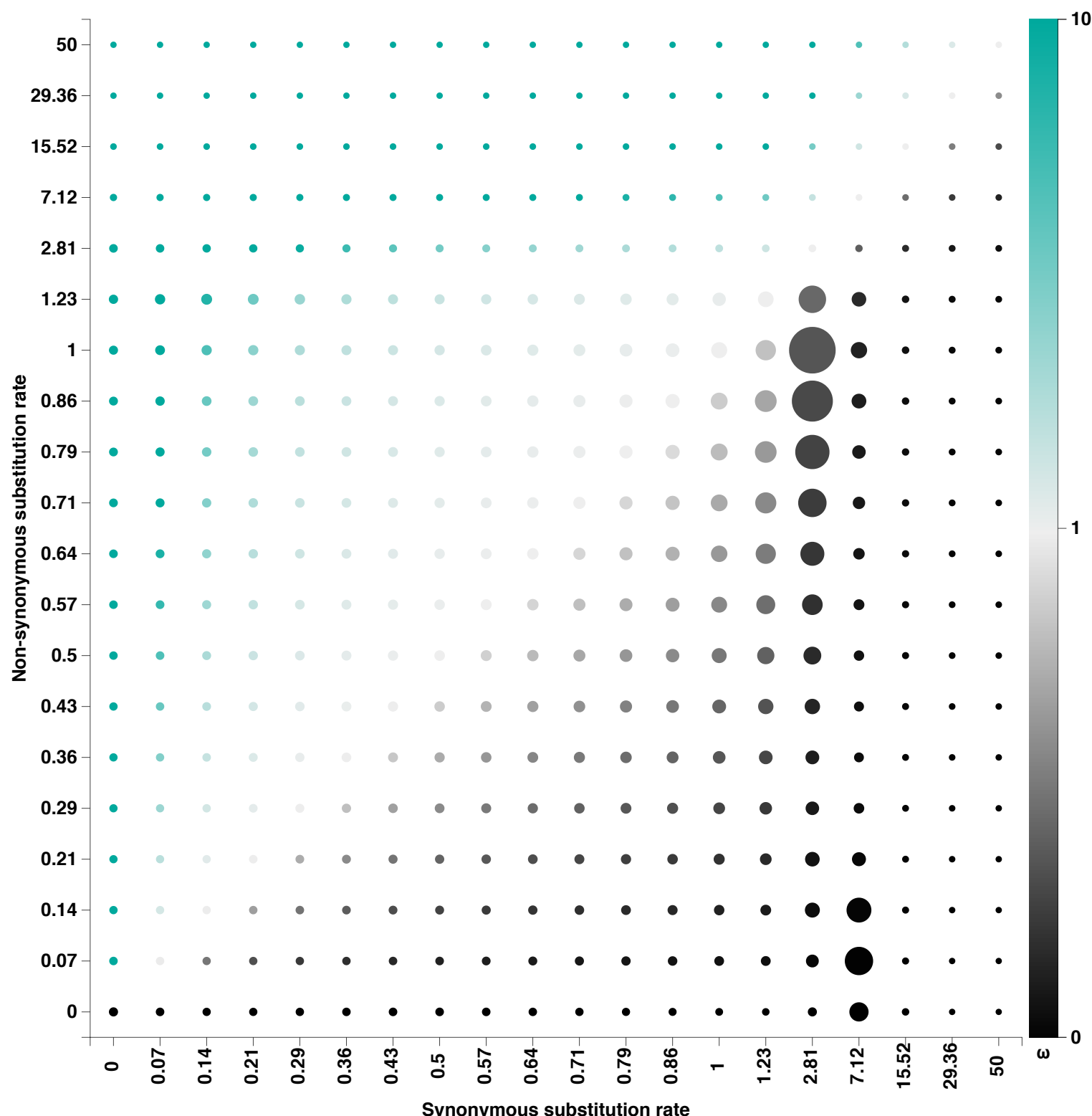
Posterior rate distribution



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.

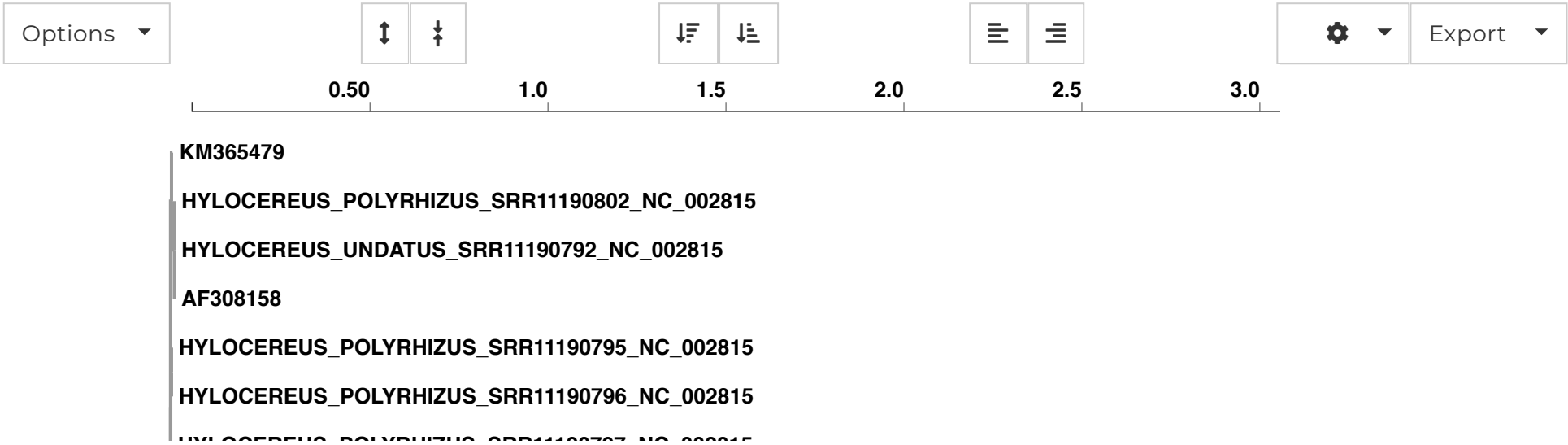
Showing entries 15 through 34 out of 134.

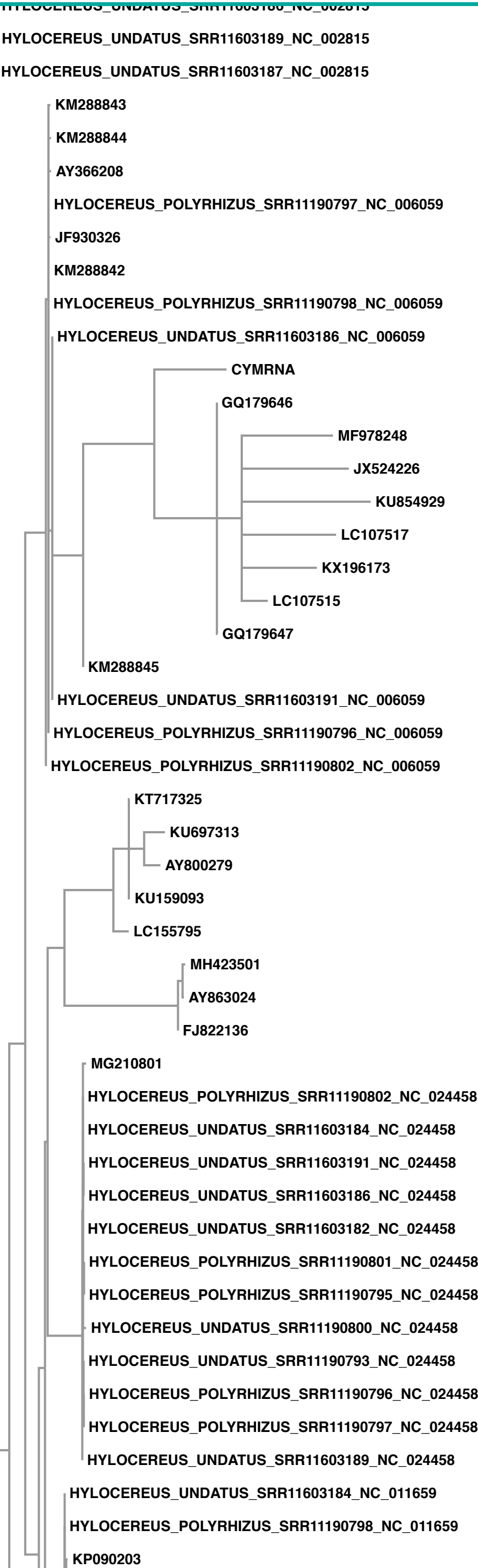
Export Table to CSV

Navigation buttons: double left arrow, left arrow, right arrow, double right arrow

Site ↕	Partition ↕	α ↕	β ↕	$\beta - \alpha$ ↕	Prob[$\alpha > \beta$] ↕	Prob[$\alpha < \beta$] ↕	BayesFactor[$\alpha < \beta$] ↕		
15	1	0.480	0.647	0.167	0.319	0.621	2.353	0.000	0.000
16	1	1.360	0.418	-0.943	0.764	0.187	0.332	0.000	0.000
17	1	0.694	0.596	-0.097	0.414	0.522	1.574	0.000	0.000
18	1	2.127	0.338	-1.788	0.843	0.120	0.196	0.000	0.000
19	1	0.505	0.409	-0.095	0.508	0.416	1.026	0.000	0.000
20	1	0.665	0.334	-0.331	0.578	0.343	0.753	0.000	0.000
21	1	1.827	0.669	-1.158	0.556	0.387	0.907	0.000	0.000
24	1	0.523	0.576	0.053	0.373	0.563	1.851	0.000	0.000
25	1	11.305	1.811	-9.494	0.716	0.244	0.464	0.000	0.000
26	1	1.494	1.159	-0.335	0.502	0.426	1.066	0.000	0.000
27	1	0.603	1.349	0.746	0.187	0.762	4.603	0.000	0.000
28	1	0.665	0.322	-0.343	0.588	0.333	0.719	0.000	0.000
29	1	2.757	0.606	-2.151	0.719	0.226	0.420	0.000	0.000
30	1	0.773	0.763	-0.010	0.314	0.627	2.417	0.000	0.000
31	1	7.069	4.094	-2.975	0.700	0.235	0.442	0.000	0.000
32	1	0.641	0.649	0.008	0.446	0.490	1.383	0.000	0.000
33	1	0.764	2.010	1.247	0.234	0.708	3.492	0.000	0.000
34	1	0.647	0.403	-0.244	0.540	0.393	0.932	0.000	0.000

Fitted tree









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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