Fast Unconstrained Bayesian AppRoximation

results summary

INPUT DATA | 6096240f238adf71a515f5a1 | 90 sequences | 239 sites

Export

FUBAR **found evidence** of

episodic positive/diversifying selection at 1 sites

episodic negative/purifying selection at 215 sites

with posterior probability of 0.9.

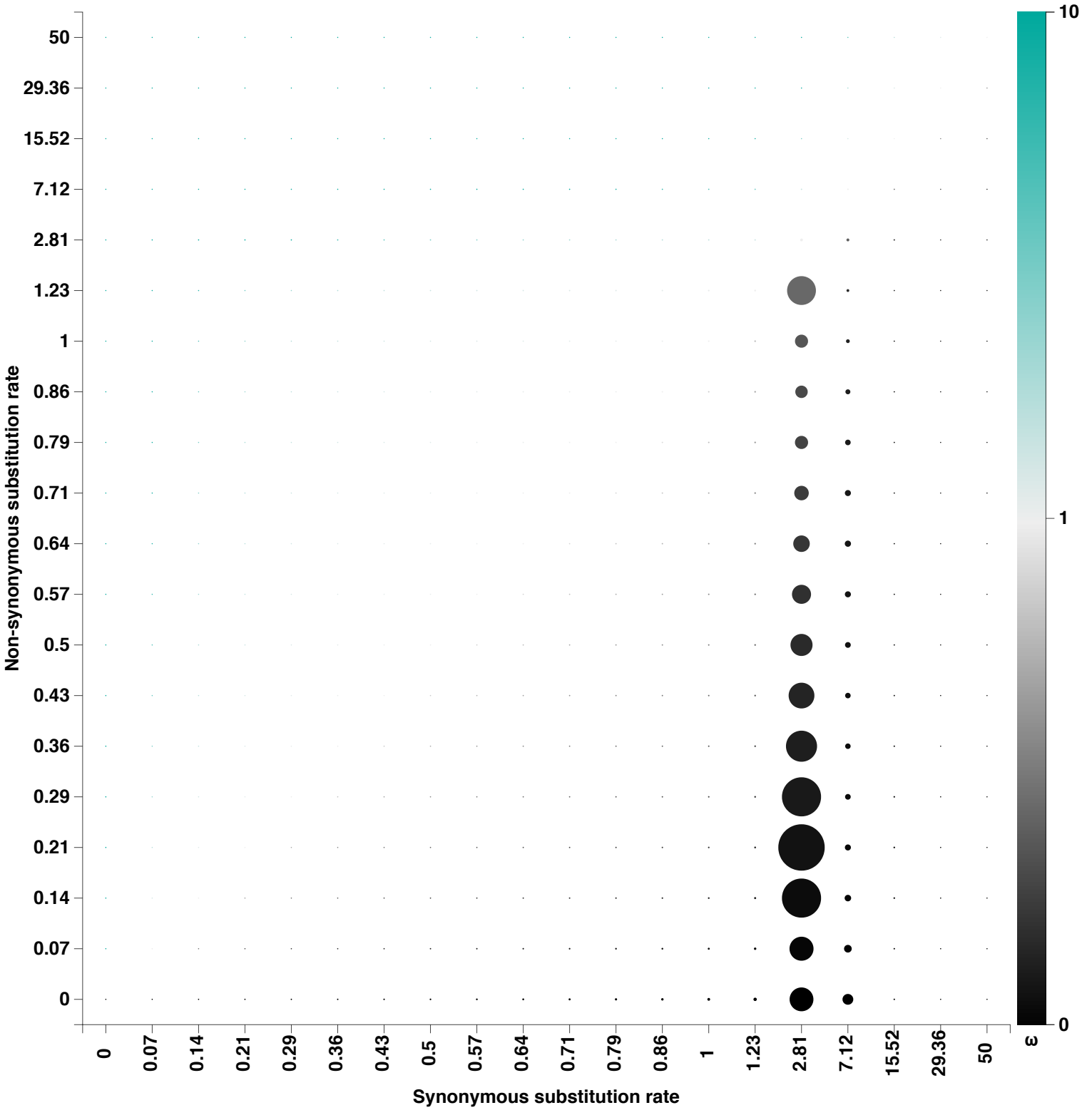
See **here** for more information about the FUBAR method.

Please cite **PMID 23420840** if you use this result in a publication, presentation, or other scientific work.

Posterior rate distribution

Site: Alignment wide

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.

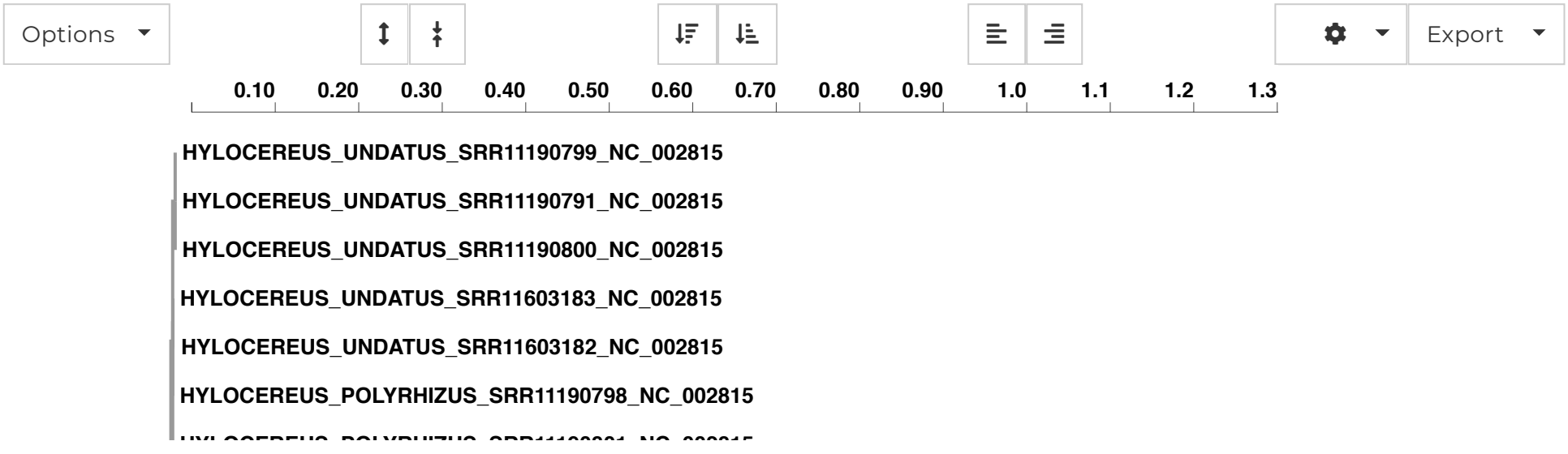
Showing entries 1 through 20 out of 239.

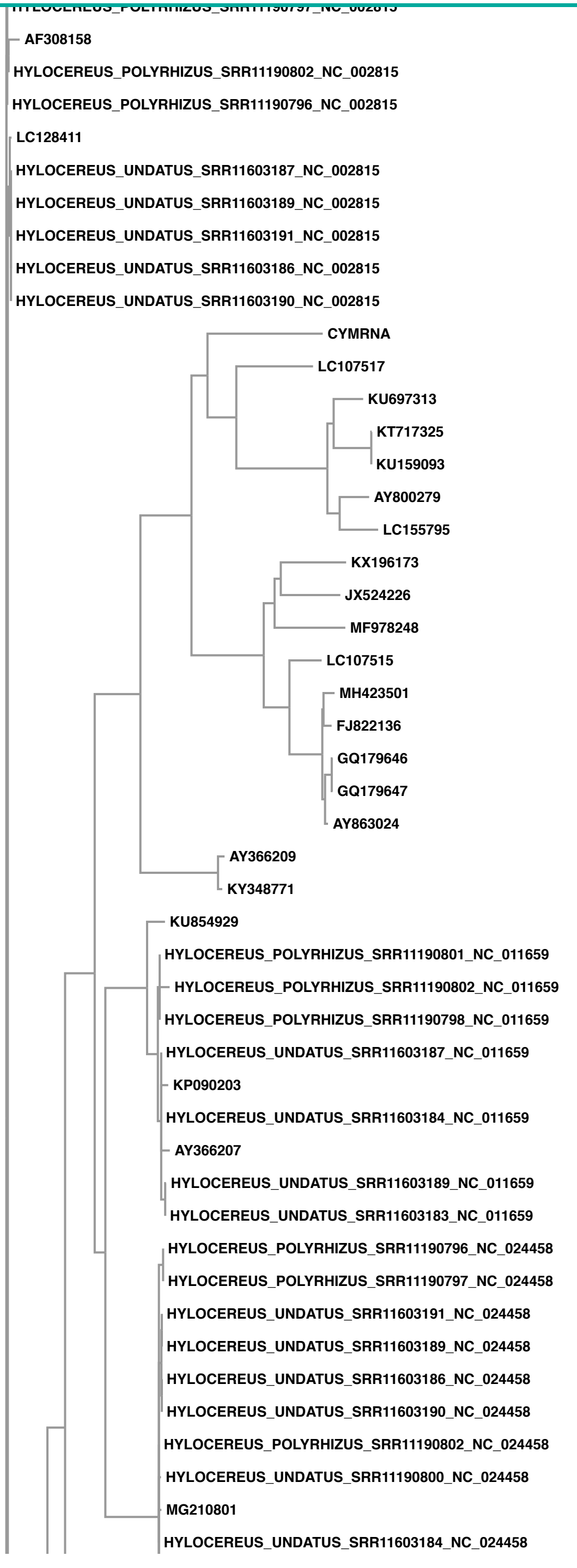
« ‹ › »

Export Table to CSV

Site	Partition	α	β	β-α	Prob[α>β]	Prob[α<β]	BayesFactor[α<β]		
3	1	2.346	0.378	-1.967	0.810	0.161	0.627	0.000	0.000
4	1	2.133	0.788	-1.345	0.835	0.120	0.446	0.000	0.000
15	1	8.951	3.714	-5.238	0.815	0.012	0.039	0.000	0.000
17	1	2.955	1.260	-1.695	0.723	0.236	1.008	0.000	0.000

Fitted tree




AF308158
HYLOCEREUS_POLYRHIZUS_SRR11190802_NC_002815
HYLOCEREUS_POLYRHIZUS_SRR11190796_NC_002815
LC128411
HYLOCEREUS_UNDATUS_SRR11603187_NC_002815
HYLOCEREUS_UNDATUS_SRR11603189_NC_002815
HYLOCEREUS_UNDATUS_SRR11603191_NC_002815
HYLOCEREUS_UNDATUS_SRR11603186_NC_002815
HYLOCEREUS_UNDATUS_SRR11603190_NC_002815
CYMRNA
LC107517
KU697313
KT717325
KU159093
AY800279
LC155795
KX196173
JX524226
MF978248
LC107515
MH423501
FJ822136
GQ179646
GQ179647
AY863024
AY366209
KY348771
KU854929
HYLOCEREUS_POLYRHIZUS_SRR11190801_NC_011659
HYLOCEREUS_POLYRHIZUS_SRR11190802_NC_011659
HYLOCEREUS_POLYRHIZUS_SRR11190798_NC_011659
HYLOCEREUS_UNDATUS_SRR11603187_NC_011659
KP090203
HYLOCEREUS_UNDATUS_SRR11603184_NC_011659
AY366207
HYLOCEREUS_UNDATUS_SRR11603189_NC_011659
HYLOCEREUS_UNDATUS_SRR11603183_NC_011659
HYLOCEREUS_POLYRHIZUS_SRR11190796_NC_024458
HYLOCEREUS_POLYRHIZUS_SRR11190797_NC_024458
HYLOCEREUS_UNDATUS_SRR11603191_NC_024458
HYLOCEREUS_UNDATUS_SRR11603189_NC_024458
HYLOCEREUS_UNDATUS_SRR11603186_NC_024458
HYLOCEREUS_UNDATUS_SRR11603190_NC_024458
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MG210801
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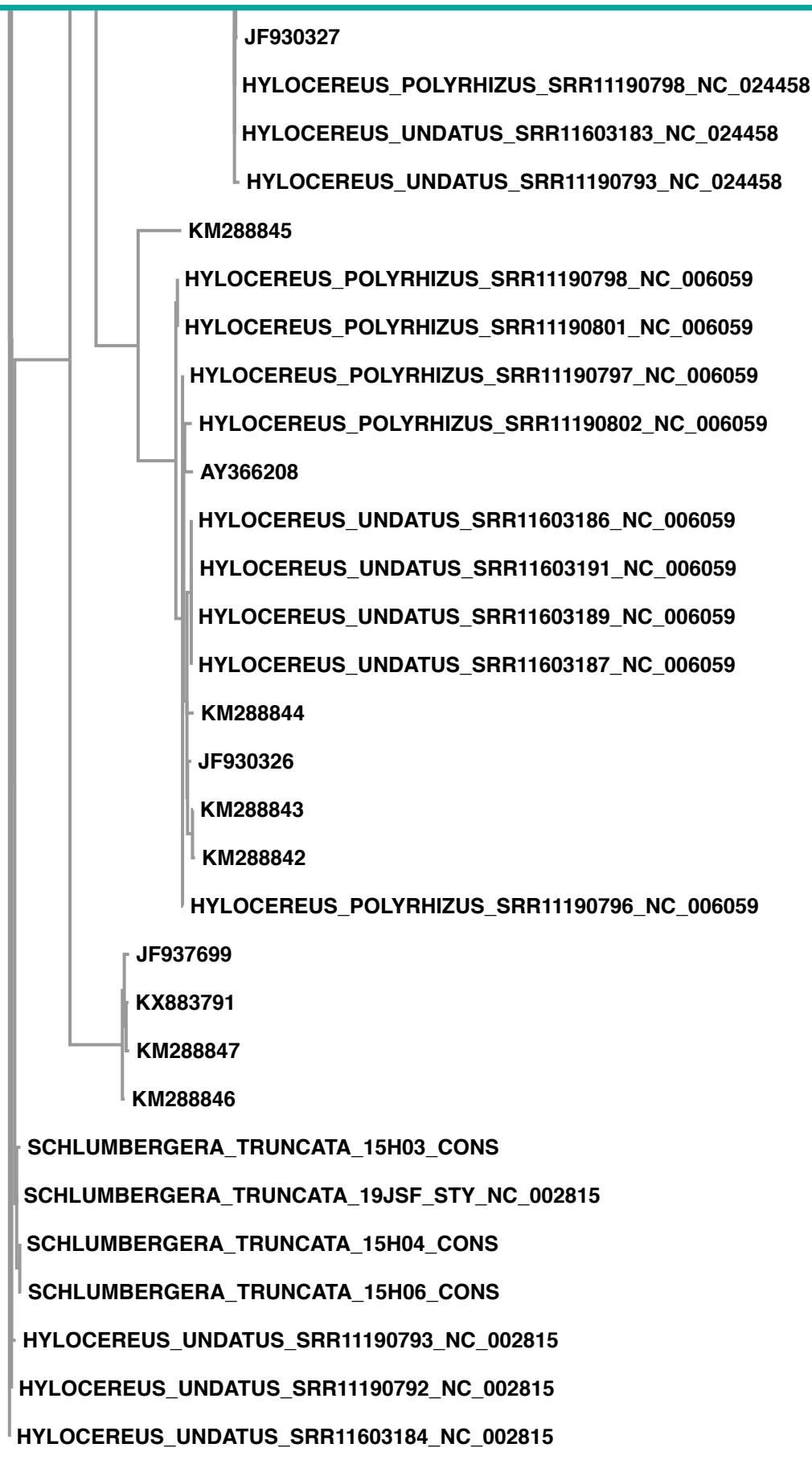

Model fits

Model	AIC_C	log L	Parameters	Rate distributions
Nucleotide GTR	**26567.04**	**-13097.99**	**185**	

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.

Datamonkey is funded jointly by MIDAS and NIH award R01 GM093939

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