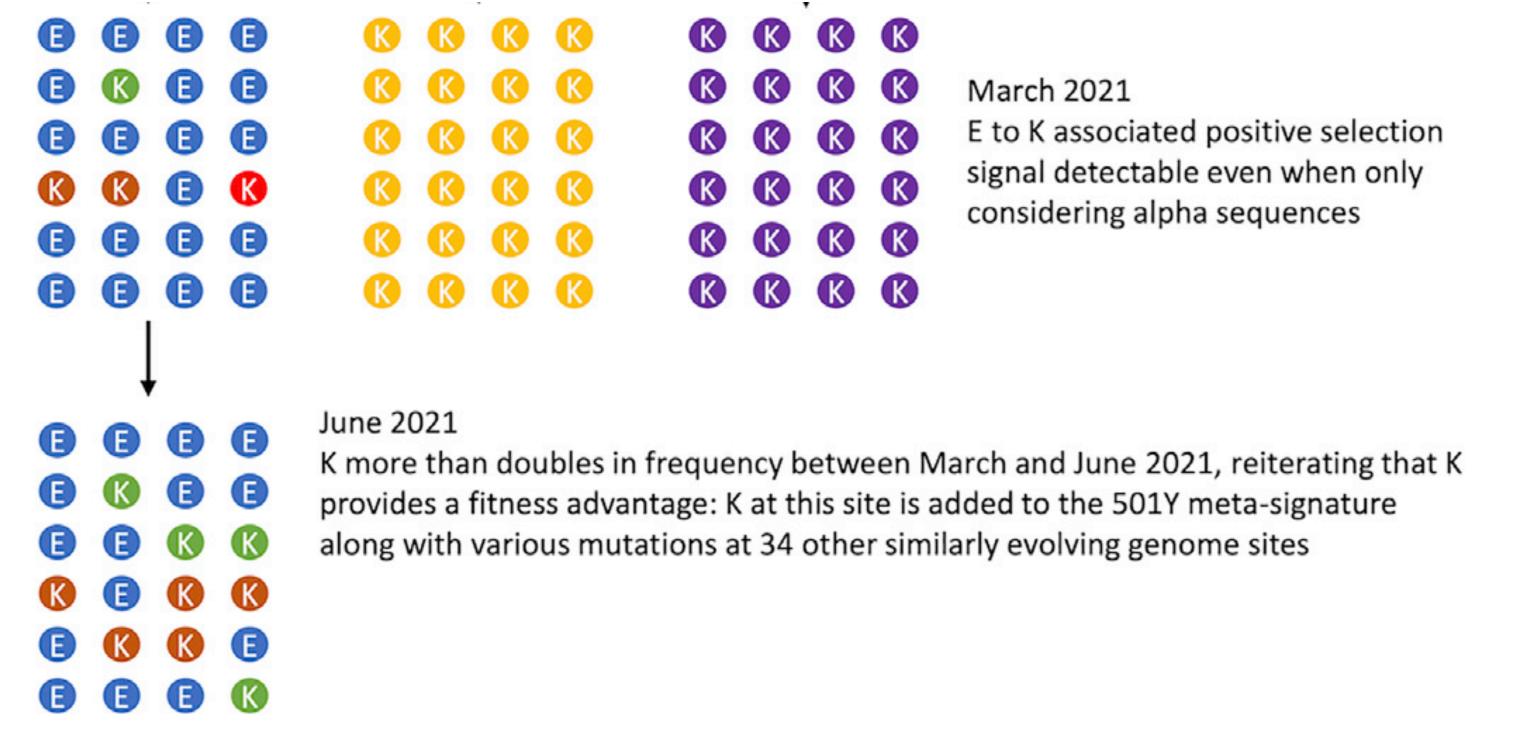


Decemb	er 2019	November 2020	May 2021	



Martin et al., 2021, Cell 184, 5189–5200 The emergence and ongoing convergent evolution of the SARS-CoV-2 N501Y lineages



## Used data up to February to define 34 convergent sites between three N501Y lineages

## Used data up to June to validate convergent sites

	0.000001	0	.0001	0.	01	0.05	0.5
Nucleotide	Site	V1	V2	V3	V1 subs to	V2 subs to	V3 subs to
21574	S/5	Ж	Ж	X	F	F	F
21613	S/18	Xξ	ル¥	ni	F	F	F
21619	S/20			n		T I	N
21637	S/26	×		ni	S	R	s
21799	S/80	×	nx		A	A D S	
21853	S/98	ж	×		F	F	S
21973	S/138	Ж	ж	n)K	HY	Y	Y D
22129	S/190			n			S
22204	S/215	Ж	nx		G	G V D H	
22810	\$/417		nx	ni		NK	TK
23011	S/484	×	<b>ル</b> 無	nii	K Q	KE	K
23062	S/501	n	ni	ni	YNE	YN	YN

## Selection legend

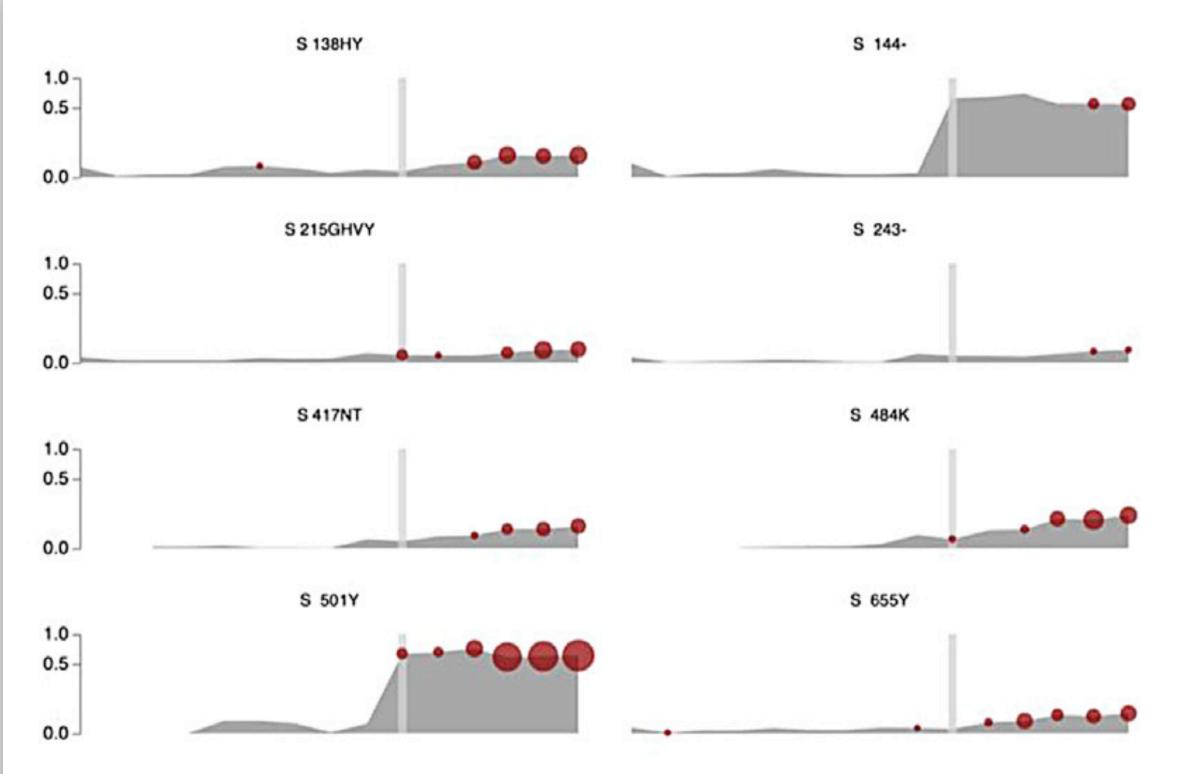
1. > : Signtature mutation

**Evolutionary Probability** 

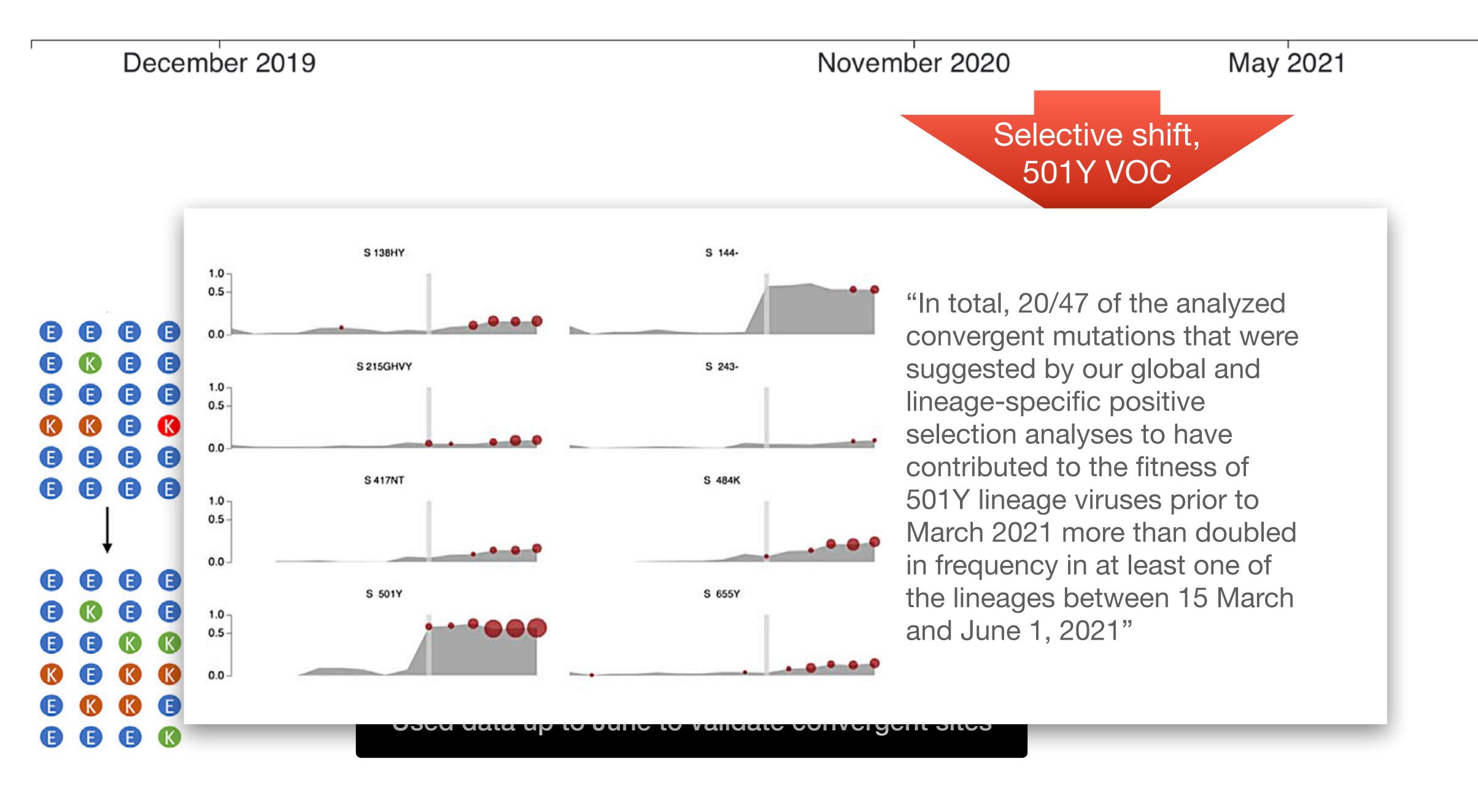
2. 
: MEME support

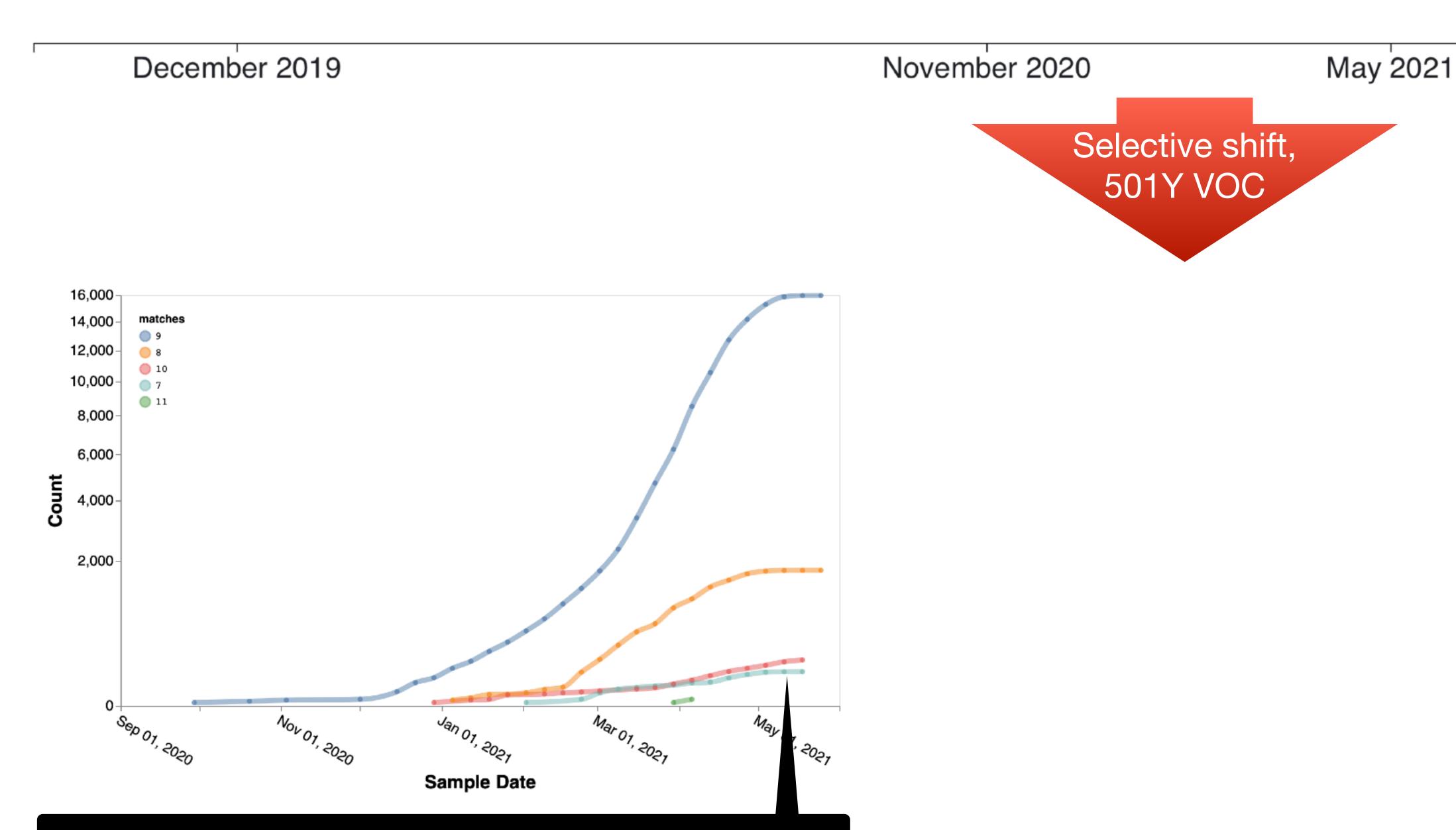
3. 💥 : convergent substitutions to another lineage (no MEME support)

4. 💥 : convergent substitutions to another lineage AND MEME support



"In total, 20/47 of the analyzed convergent mutations that were suggested by our global and lineage-specific positive selection analyses to have contributed to the fitness of 501Y lineage viruses prior to March 2021 more than doubled in frequency in at least one of the lineages between 15 March and June 1, 2021"





Sequences acquiring additional mutations in Spike (V3)