

Update: Sites of
Interest in Spike, 07/07/2020
47,648 Sequences

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Mutations of Interest in Spike other than D614G are RARE.

Other mutations in Spike that may be of interest are shown on the left

Very rare mutations that still important as they may be in or near antibody epitopes are shown on the right.

* **Bold Higher Priority**

Mutations of interest

***D 936 Y**
Most interesting
so far

L 5 F
A 829 T
D 839 Y

Natural Variants that could be useful for mapping antibodies

Domain A, NTD (5)

*H 49 Y
S 50 L
*T 76 I (glycan loss at N74)
*D 138 H
*H 146 Y
V 213 L
R 214 L
*D 215 G

RBD variants (7)

*V 341 I
*V 367 F
*N 439 K
*S 477 N
T 478 I
*V 483 A
*S 494 P
A 520 S
*A 522 V

Fab C105 contacts (+4)

*R 403 K
R 408 I
Q 414 R
G 446 V
*L 455 F
A 475 V
*G 476 S
*S 477 N
T 478 I
P 479 S
Q 493 L
*S 494 P
*N 501 Y


All of these would be best considered in a G614 clade background. They are either found in both D and G, or only G. There is only one exception: V483A was not ever found with G614. V483A was an early form in found in Washington state that is no longer sampled.

Example of a Site-of-Interest: from the spread sheet, which includes sites > 0.3% in Spike, >0.1% in the RDB:

ori	pos	mut	codon	mut	covariations	location	# of Occ	(total # of se
D	936	Y	GAC	TAC	D614G	Bosnia-and-Herzegovina_Ilijas	1	31
D	936	Y	GAC	TAC	D614G	Colombia_Cali	1	87
D	936	Y	GAC	TAC	D614G	Denmark_Unknown	6	640
D	936	Y	GAC	TAC	D614G	Estonia	2	19
D	936	Y	GAC	TAC	D614G	Finland_Uusimaa	175	260
D	936	Y	GAC	TAC	D614G	Hong-Kong	1	162
D	936	Y	GAC	TAC	D614G	Iceland_Reykjavik	3	506
D	936	Y	GAC	TAC	D614G	Kenya	3	55
D	936	Y	GAC	TAC	D614G	Netherlands	4	1490
D	936	Y	GAC	TAC	D614G	Netherlands_Zuid-Holland	1	1490
D	936	Y	GAC	TAC	D614G	Norway	1	42
D	936	Y	GAC	TAC	D614G	Oman_Muscat	1	49
D	936	Y	GAC	TAC	D614G	Poland_Pomorskie	1	80
D	936	Y	GAC	TAC	D614G	Singapore	1	516
D	936	Y	GAC	TAC	D614G	Sweden_Dalarna	1	531
D	936	Y	GAC	TAC	D614G	Sweden_Gavleborg	1	531
D	936	Y	GAC	TAC	D614G	Sweden_Halland	10	531
D	936	Y	GAC	TAC	D614G	Sweden_Jonkoping	2	531
D	936	Y	GAC	TAC	D614G	Sweden_Kalmar	1	531
D	936	Y	GAC	TAC	D614G	Sweden_Norrboten	5	531
D	936	Y	GAC	TAC	D614G	Sweden_Orebro	1	531
D	936	Y	GAC	TAC	D614G	Sweden_Ostergotland	3	531
D	936	Y	GAC	TAC	D614G	Sweden_Skane	1	531
D	936	Y	GAC	TAC	D614G	Sweden_Sormland	7	531
D	936	Y	GAC	TAC	D614G	Sweden_Stockholm	27	531
D	936	Y	GAC	TAC	D614G	Sweden_Uppsala	17	531
D	936	Y	GAC	TAC	D614G	Sweden_Varmland	1	531
D	936	Y	GAC	TAC	D614G	Sweden_Vasterbotten	1	531
D	936	Y	GAC	TAC	D614G	Sweden_Vasternorrland	1	531
D	936	Y	GAC	TAC	D614G	Sweden_Vastmanland	14	531
D	936	Y	GAC	TAC	D614G	Sweden_Vastra-Gotaland	21	531
D	936	Y	GAC	TAC	D614G	Turkey_Istanbul	1	112
D	936	Y	GAC	TAC	D614G	USA_Minnesota	2	9681
D	936	Y	GAC	TAC	D614G	USA_Utah	1	9681
D	936	Y	GAC	TAC	D614G	USA_Washington	1	9681
D	936	Y	GAC	TAC	D614G	United-Kingdom_England	13	21348
D	936	Y	GAC	TAC	D614G	United-Kingdom_England_BRIS	16	21348
D	936	Y	GAC	TAC	D614G	United-Kingdom_England_CAMB	82	21348
D	936	Y	GAC	TAC	D614G	United-Kingdom_England_EXET	2	21348
D	936	Y	GAC	TAC	D614G	United-Kingdom_England_HECH	1	21348
D	936	Y	GAC	TAC	D614G	United-Kingdom_England_LIVE	1	21348
D	936	Y	GAC	TAC	D614G	United-Kingdom_England_LOND	37	21348
D	936	Y	GAC	TAC	D614G	United-Kingdom_England_NOTT	2	21348
D	936	Y	GAC	TAC	D614G	United-Kingdom_England_OXON	5	21348
D	936	Y	GAC	TAC	D614G	United-Kingdom_England_SHEF	10	21348
D	936	Y	GAC	TAC	D614G	United-Kingdom_Scotland	1	21348
D	936	Y	GAC	TAC	D614G	United-Kingdom_Wales	123	21348
D	936	Y	GAC	TAC	L5F,D614G	Finland_Uusimaa	4	260
D	936	Y	GAC	TAC	L5F,D614G	United-Kingdom_England_CAMB	1	21348
D	936	Y	GAC	TAC	L5F,D614G	United-Kingdom_England_SHEF	1	21348
D	936	Y	GAC	TAC	R211,D614G	United-Kingdom_Wales	2	21348

This enables one to see if the site is coming up in any particular region.

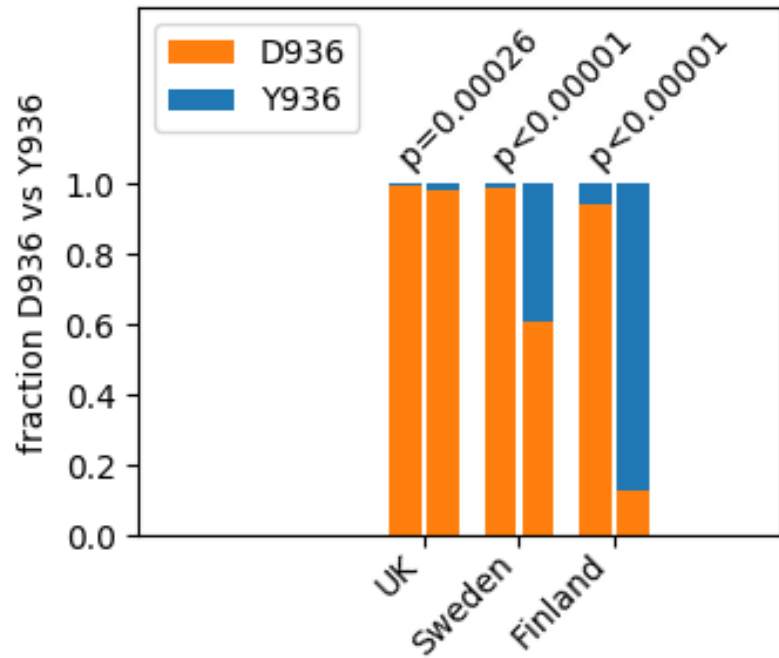
The last two columns indicate how many times it is found in a geographic region, and how many times that region is sampled.

For example, Y936 was found 13 times in UK samples with no additional geographic information, 16 times in Bristol (BRIS), 82 in Cambridge (CAMB)... 

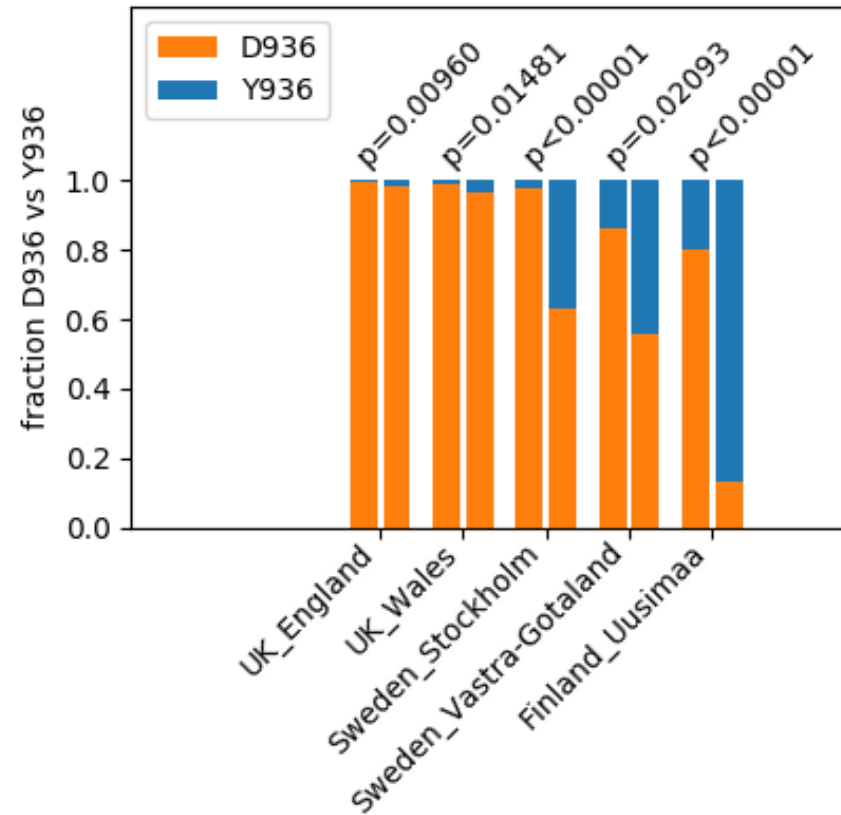
The UK is really heavily sampled, the 21348 is for the whole UK.

These graphs show all data from geographic regions in GISAID where there was enough samples to look, and a significant change in frequencies of a position's amino acid before and after a two week interval in sampling was observed (like figure 1b in Korber et al)

There was a change in 3 countries.



There was a change in 5 more local regions



5/5 –
not significant
($p=0.065$), but
suggestive.

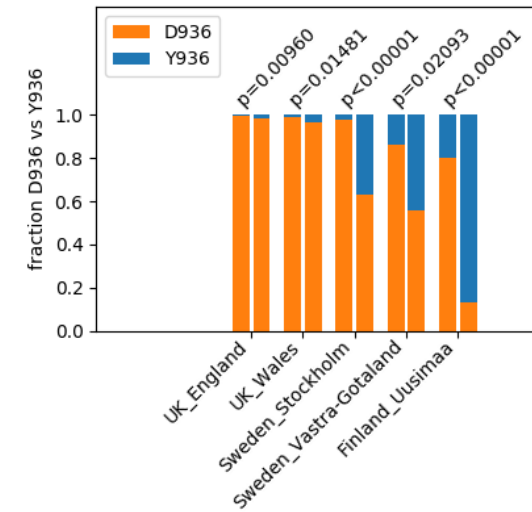
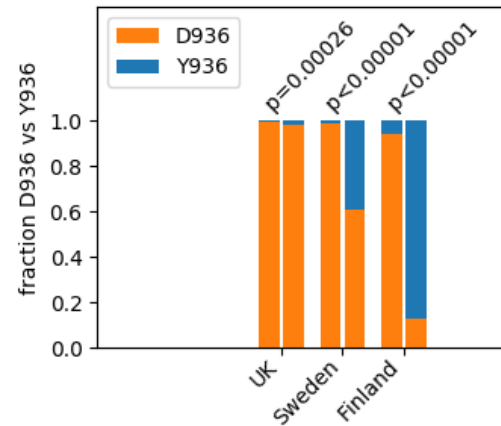
There are no other significant changes regional changes in GISAID...

Using this and the previous slide as a guide, we can look at in detail at the 5 geographic regions of interest.

D936Y: From the spread sheet:

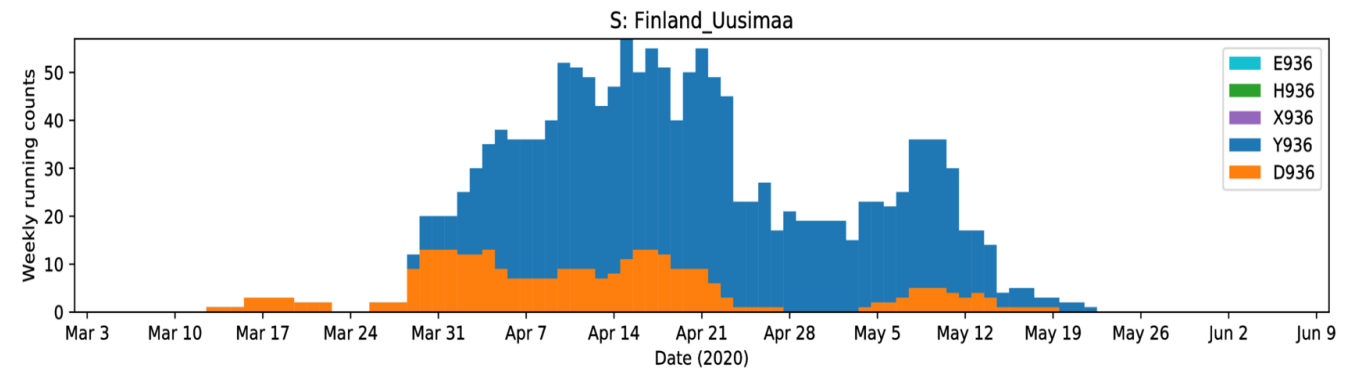
D	936	Y	GAC	TAC	D614G	Bosnia-and-Herzegovina_Ilijas	1	31
D	936	Y	GAC	TAC	D614G	Colombia_Cali	1	87
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D	936	Y	GAC	TAC	D614G	Kenya	3	55
D	936	Y	GAC	TAC	D614G	Netherlands	4	1490
D	936	Y	GAC	TAC	D614G	Netherlands_Zuid-Holland	1	1490
D	936	Y	GAC	TAC	D614G	Norway	1	42
D	936	Y	GAC	TAC	D614G	Oman_Muscat	1	49
D	936	Y	GAC	TAC	D614G	Poland_Pomorskie	1	80
D	936	Y	GAC	TAC	D614G	Singapore	1	516
D	936	Y	GAC	TAC	D614G	Sweden_Dalarna	1	531
D	936	Y	GAC	TAC	D614G	Sweden_Gavleborg	1	531
D	936	Y	GAC	TAC	D614G	Sweden_Halland	10	531
D	936	Y	GAC	TAC	D614G	Sweden_Jonkoping	2	531
D	936	Y	GAC	TAC	D614G	Sweden_Kalmar	1	531
D	936	Y	GAC	TAC	D614G	Sweden_Norrbottn	5	531
D	936	Y	GAC	TAC	D614G	Sweden_Orebro	1	531
D	936	Y	GAC	TAC	D614G	Sweden_Ostergotland	3	531
D	936	Y	GAC	TAC	D614G	Sweden_Skane	1	531
D	936	Y	GAC	TAC	D614G	Sweden_Sormland	7	531
D	936	Y	GAC	TAC	D614G	Sweden_Stockholm	27	531
D	936	Y	GAC	TAC	D614G	Sweden_Uppsala	17	531
D	936	Y	GAC	TAC	D614G	Sweden_Varmland	1	531
D	936	Y	GAC	TAC	D614G	Sweden_Vasterbotten	1	531
D	936	Y	GAC	TAC	D614G	Sweden_Vasternorrland	1	531
D	936	Y	GAC	TAC	D614G	Sweden_Vastmanland	14	531
D	936	Y	GAC	TAC	D614G	Sweden_Vastra-Gotaland	21	531
D	936	Y	GAC	TAC	D614G	Turkey_Istanbul	1	112
D	936	Y	GAC	TAC	D614G	USA_Minnesota	2	9681
D	936	Y	GAC	TAC	D614G	USA_Utah	1	9681
D	936	Y	GAC	TAC	D614G	USA_Washington	1	9681
D	936	Y	GAC	TAC	D614G	United-Kingdom_England	13	21348
D	936	Y	GAC	TAC	D614G	United-Kingdom_England_BRIS	16	21348
D	936	Y	GAC	TAC	D614G	United-Kingdom_England_CAMB	82	21348
D	936	Y	GAC	TAC	D614G	United-Kingdom_England_EXET	2	21348
D	936	Y	GAC	TAC	D614G	United-Kingdom_England_HECH	1	21348
D	936	Y	GAC	TAC	D614G	United-Kingdom_England_LIVE	1	21348
D	936	Y	GAC	TAC	D614G	United-Kingdom_England_LOND	37	21348
D	936	Y	GAC	TAC	D614G	United-Kingdom_England_NOTT	2	21348
D	936	Y	GAC	TAC	D614G	United-Kingdom_England_OXON	5	21348
D	936	Y	GAC	TAC	D614G	United-Kingdom_England_SHEF	10	21348
D	936	Y	GAC	TAC	D614G	United-Kingdom_Scotland	1	21348
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D	936	Y	GAC	TAC	L5F,D614G	United-Kingdom_England_SHEF	1	21348
D	936	Y	GAC	TAC	R211,D614G	United-Kingdom_Wales	2	21348

There is a trend in this data, it is quite weak and could be consistent with a founder effect. In 5 cases with mixed infections, the D936 frequencies have diminished, Y936 have increased. Usimaa is the strongest case. Y936 is very rare in the UK, and rare in Sweden, and but may have increased very slightly over time particularly in Stockholm and Vastra-Gotland



5/5 – not significant (p=0.065), but suggestive.

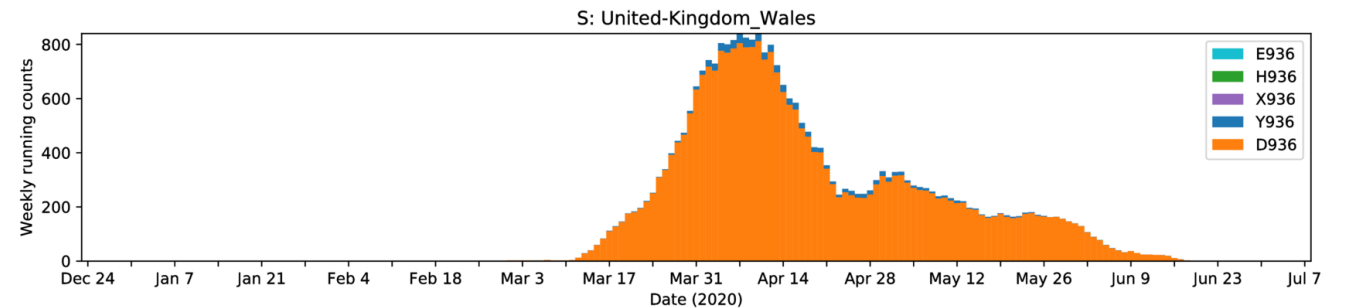
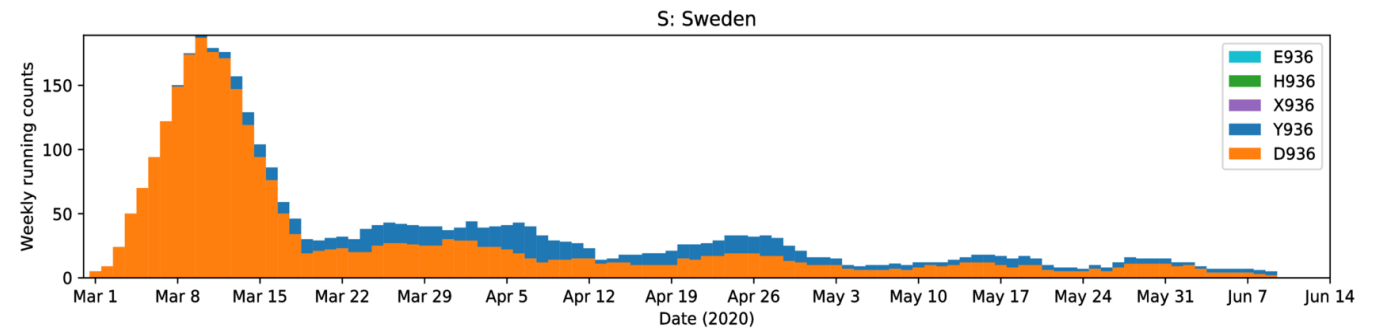
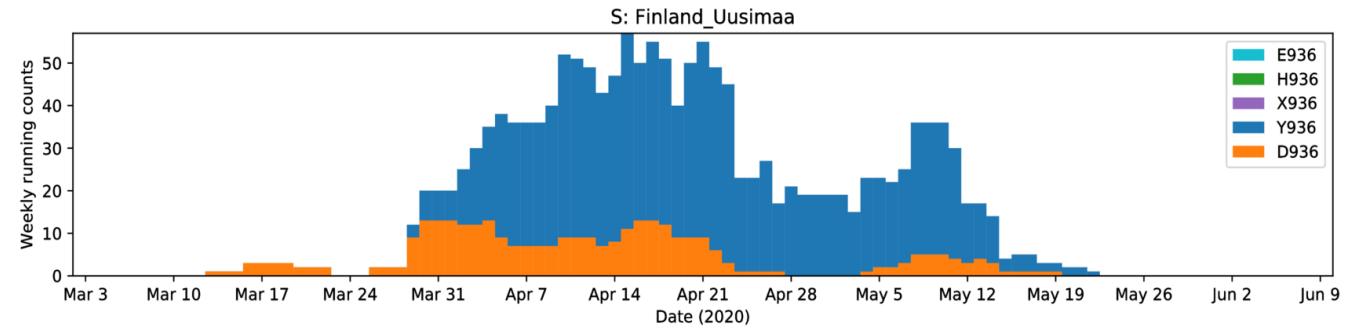
Y936 is almost always with G614 forms



Weekly running counts of D936Y

932 is not compelling like 614, (I think 614 was a selective sweep), but still is potentially interesting.

932 could be a founder effect, or it could be subtle sign of positive selection

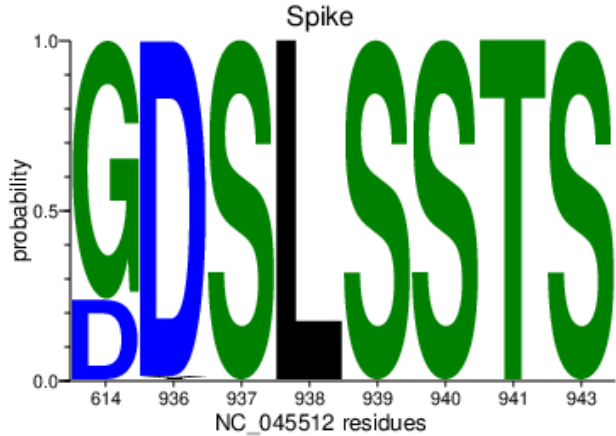


From the Spike Variation in the spread sheet:

Wuhan Reference NC_045512	Spike Regions from Duke	Barnes... Bjorkman	1st seq position	1st seq in input set	07/06/2020 common form	07/06/2020 Variants	07/06/2020 Entropy	07/06/2020 Ave Entropy 10mer	10 mer
D	HR1		936	D	D(46416)	E(1) H(2) X(10) Y(625)	0.071	0.0087	DSLS-STASA
S	HR1		937	S	S(47051)	L(2) X(1)	0	0.0016	SLS-STASAL
L	HR1		938	L	L(47043)	F(8) I(1) X(2)	0.002	0.0016	LS-STASALG
S	HR1		939	S	S(47014)	F(34) X(5) Y(1)	0.006	0.0014	S-STASALGK
S	HR1		939	-	-47053	X(1)	0	0.0008	-STASALGKL
T	HR1		940	S	S(47033)	F(14) T(1) X(6)	0.003	0.0008	STASALGKLQ
A	HR1		941	T	T(47048)	A(2) I(2) X(2)	0.001	0.0007	TASALGKLQD
S	HR1		942	A	A(47042)	S(9) X(3)	0.002	0.0006	ASALGKLQDV
A	HR1		943	S	S(46929)	I(4) P(5) X(116)	0.002	0.0004	SALGKLQDVV

HR1 D936Y

614 + Variable region 936-943



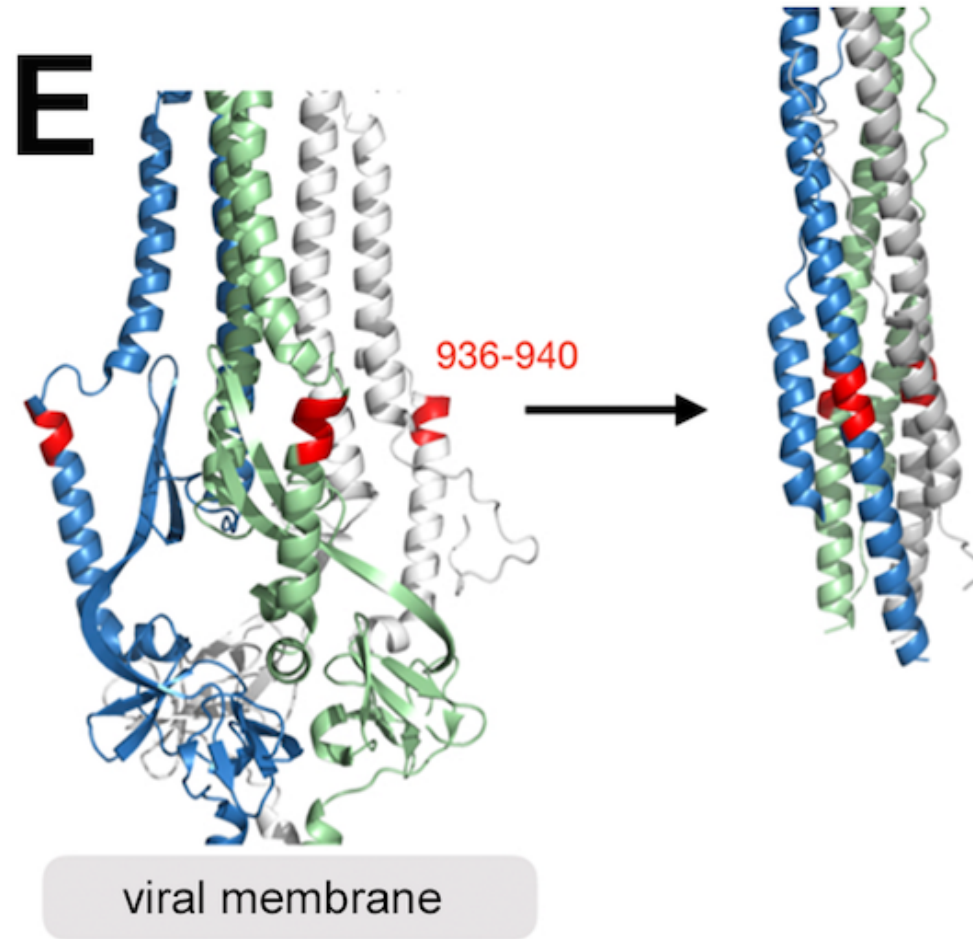
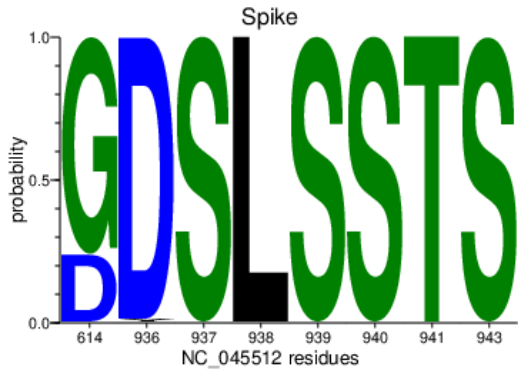
Position number under the LOGO

1. Country lists are not complete, just the most common
2. I'm not including ambiguous base calls -> uncertain amino acids unless they are very common
3. I'm not including variants that were just found once

Variant	Count	%	#mut	Locations
G DSLSSTS	36938	74.6	0	
- - - - -				
- Y - - - - -	638	1.29	1	United-Kingdom 308, Finland 179, Sweden 114...
D Y - - - - -	4	0.01	2	Sweden 2, France 1, United-Kingdom 1
D H - - - - -	2	0	2	Singapore 1, United-Kingdom 1
D E - - - - -	1	0	2	Singapore 1
- - - - F - - - -	31	0.06	1	USA 16, United-Kingdom 6, Austria 4...
D - - - F - - - -	4	0.01	2	Kazakhstan 1, Switzerland 1...
- - - - Y - - - -	1	0	1	Bangladesh 1
- - - - - F - - - -	10	0.02	1	USA 4, France 2, Netherlands 2, Canada 1...
D - - - - F - - - -	6	0.01	2	USA 3, Australia 2, South-Korea 1
- - - - - T - - - -	1	0	1	Taiwan 1
- - - F - - - - -	7	0.01	1	United-Kingdom 3, Germany 2, Denmark 1...
D - - F - - - - -	1	0	2	United-Kingdom 1
- - - I - - - - -	1	0	1	United-Kingdom 1
- - - - - I - - - - -	6	0.01	1	United-Kingdom 6
D - - - - - P - - - - -	1	0	2	India 1
- - - - - P - - - - -	3	0.01	1	China 3
- - L - - - - - -	3	0.01	1	United-Kingdom 2, Netherlands 1
D - - - - - A - - - - -	2	0	2	United-Kingdom 2
- - - - - I - - - - -	2	0	1	USA 2

HR1 D936Y

614 + Variable region:



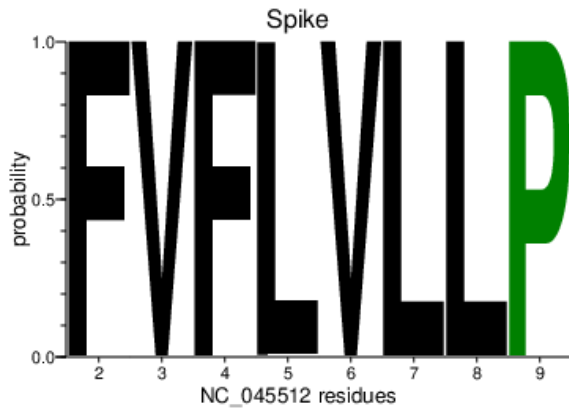
From Gnana, in our paper Korber et al:

“Variable cluster 936-940 (red), in the HR1 region of S_2 . These residues occur in a region that undergoes conformational transition during fusion: pre-fusion (PDB:6VSB) and post-fusion (PDB: 6LXT) conformations of HR1 are shown, left and right.”

“Variable cluster 936-940 (red), in the HR1 region of S_2 . These residues occur in a region that undergoes conformational transition during fusion: pre-fusion (PDB:6VSB) and post-fusion (PDB: 6LXT) conformations of HR1 are shown, left and right.”

Signal Peptide 2-9: L5F

LF5 may be interesting, stable frequency and recurrent.

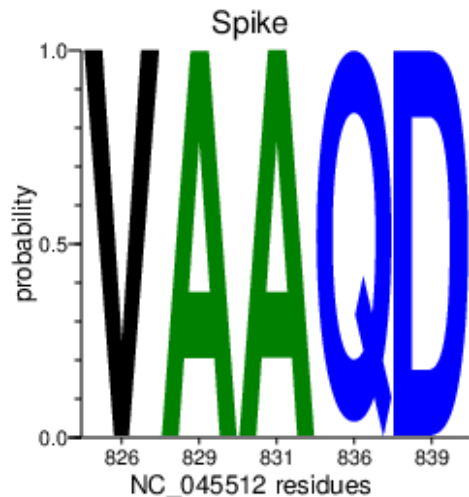


Variant	Count	%	#mut	Locations	FVFLVLLP
-----	47103	98.9	0		
--F----	359	0.75	1	Stable	
--X----	41	0.09	1		
X-F----	4	0.01	2		
-----V-	40	0.08	1	Transient	
---F---	34	0.07	1	Transient	
X-----	10	0.02	1		
L-----	9	0.02	1		
-----S	8	0.02	1		
-----L	6	0.01	1		
-----X	6	0.01	1		

United-Kingdom 189, USA 105...
 United-Kingdom 24, USA ...
 Egypt 2, United-Kingdom 2
 Hong-Kong 39, Canada 1
 USA 29, (CA Imperial County) Morocco 4,
 India 4, United-Kingdom 4,
 United-Kingdom 7, India 1, USA 1
 United-Kingdom 5, Netherlands 2, China 1
 United-Kingdom 3, Netherlands 1, Turkey 1, USA 1
 United-Kingdom 4, Australia 1, India 1

Fusion Peptide region: A829T

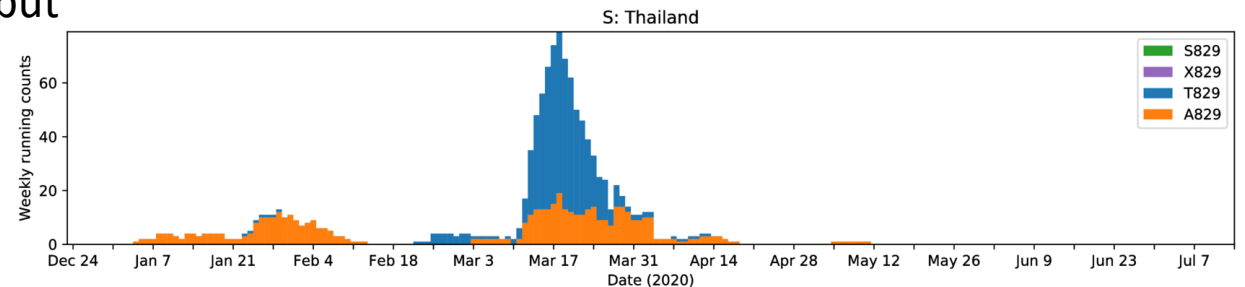
Near FP region: D839Y



Variant	Count	%	#mut	Locations
-----	47280	99.23	0	
----Y	170	0.36	1	Stable
-T---	94	0.2	1	?
--V--	32	0.07	1	
L----	28	0.06	1	
---H-	16	0.03	1	
---L-	3	0.01	1	

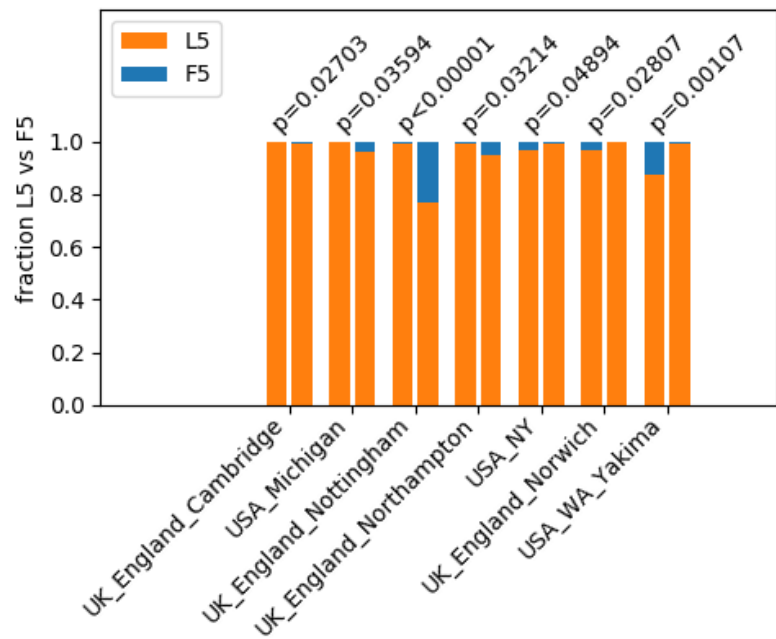
Portugal 101, United-Kingdom 37
 Thailand 90,
 Iceland 27, United-Kingdom 4,
 United-Kingdom 28
 United-Kingdom 16
 USA 3

Likely just a founder effect, but
 a shift in Thailand, in the FP

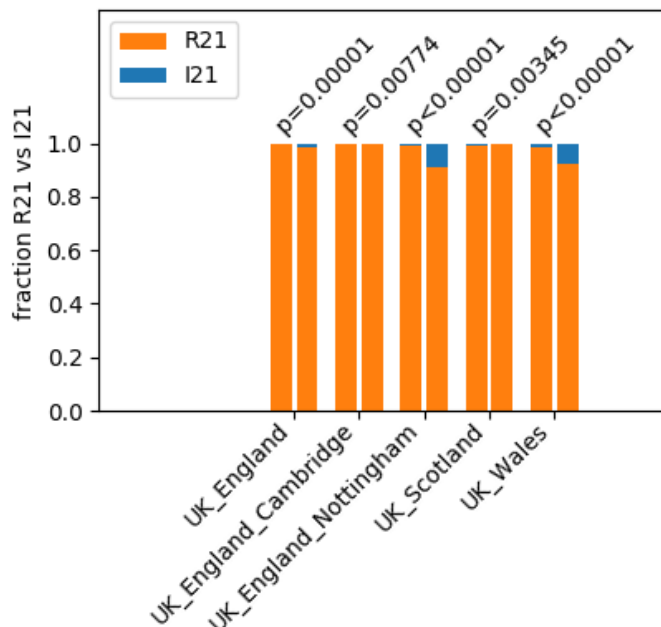


No other mutation that is present at 0.3% has even a hint of gaining ground:

4/7



3/5

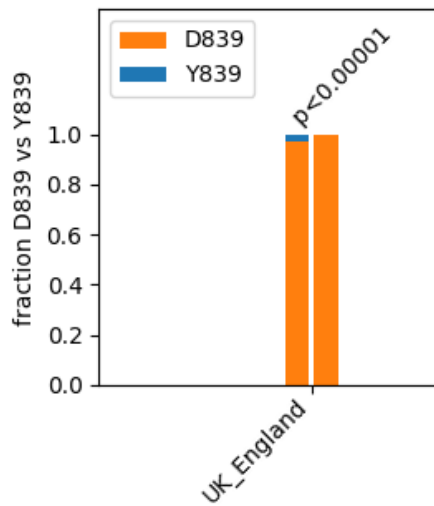


L 5 F
R 21 I

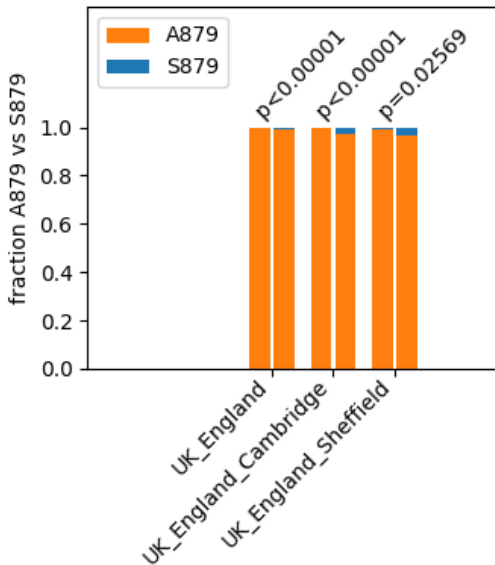
CTT
AGA

TTT
ATA

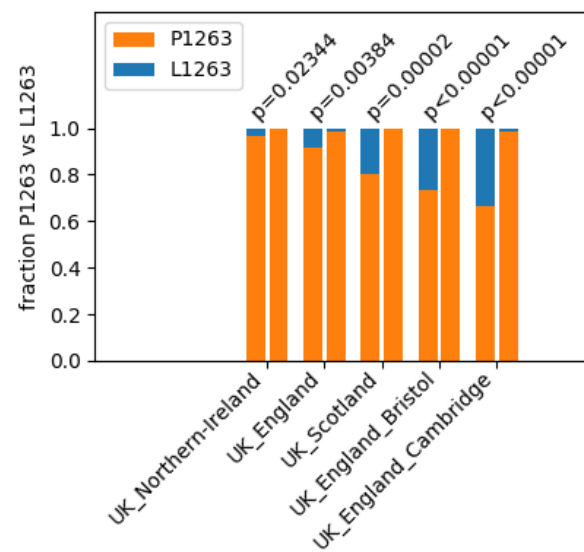
0/1



3/3

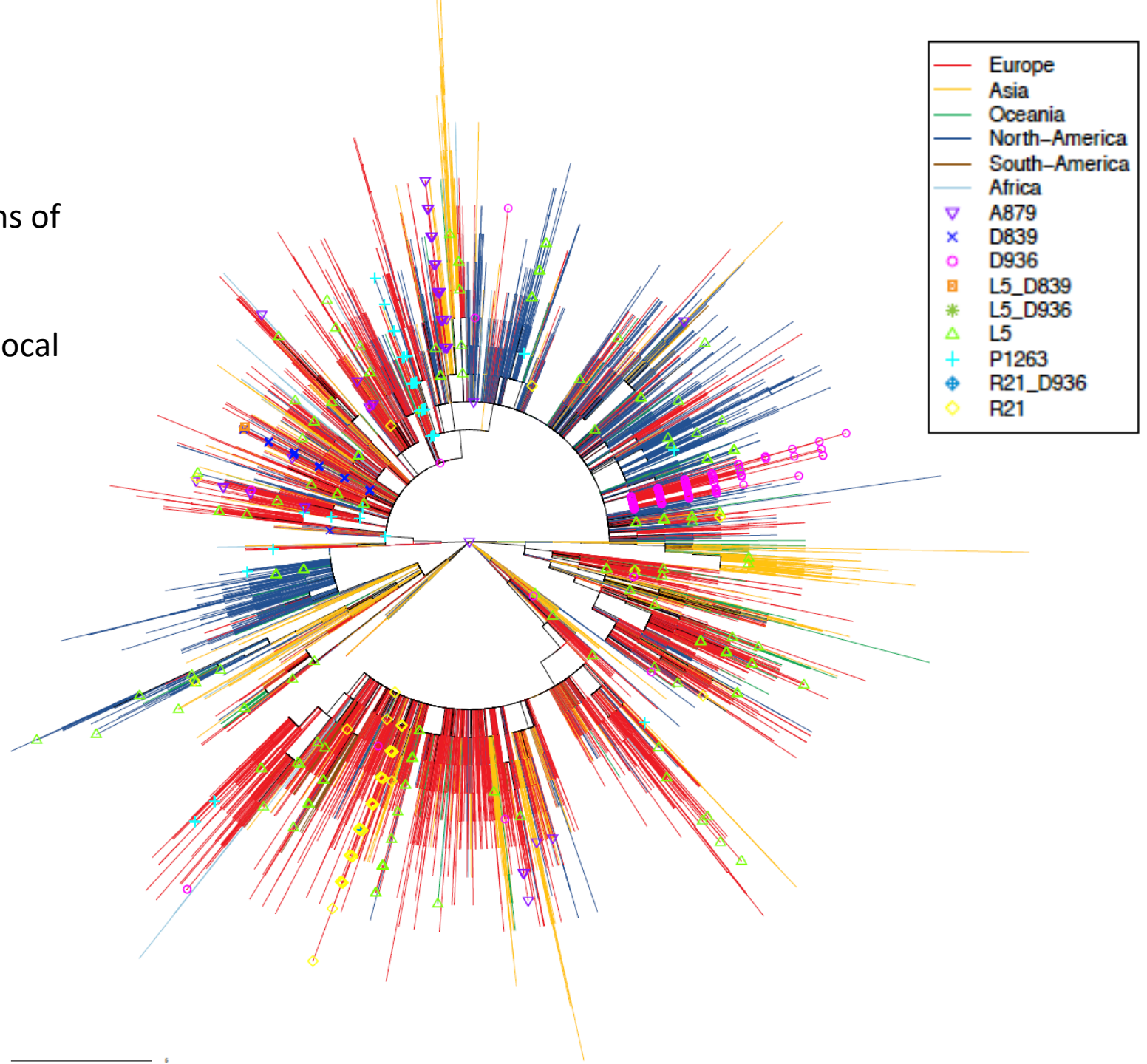


0/5

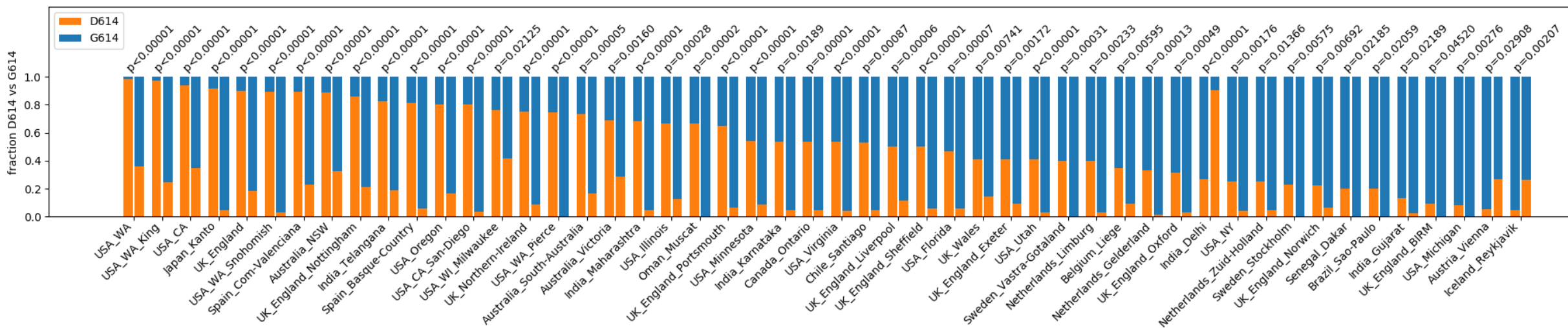
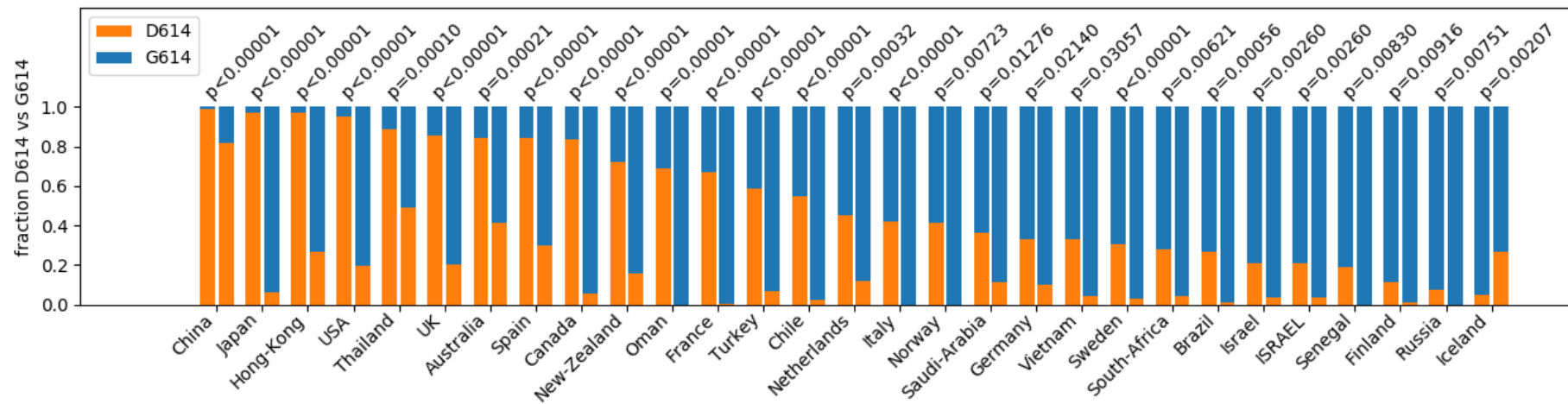
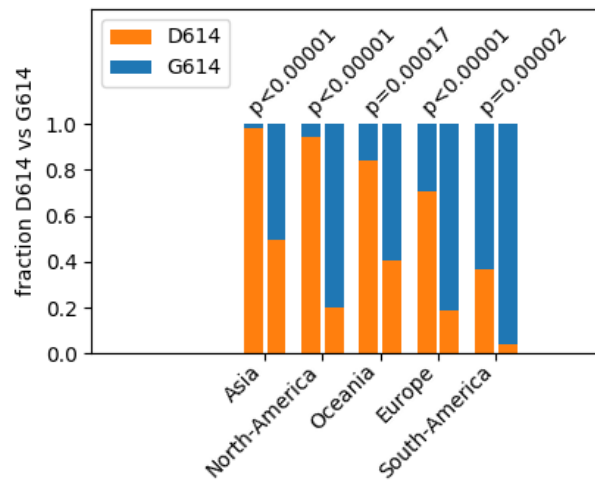


Full coding region tree with Spike mutations of Interests marked.

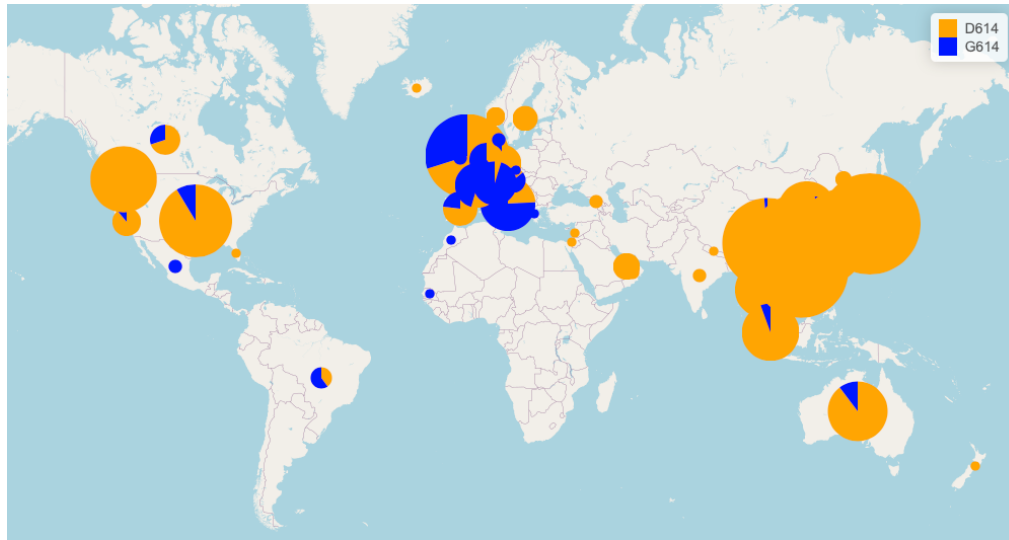
I think they are all viable: they form small local Clusters/lineages and recur in the tree.



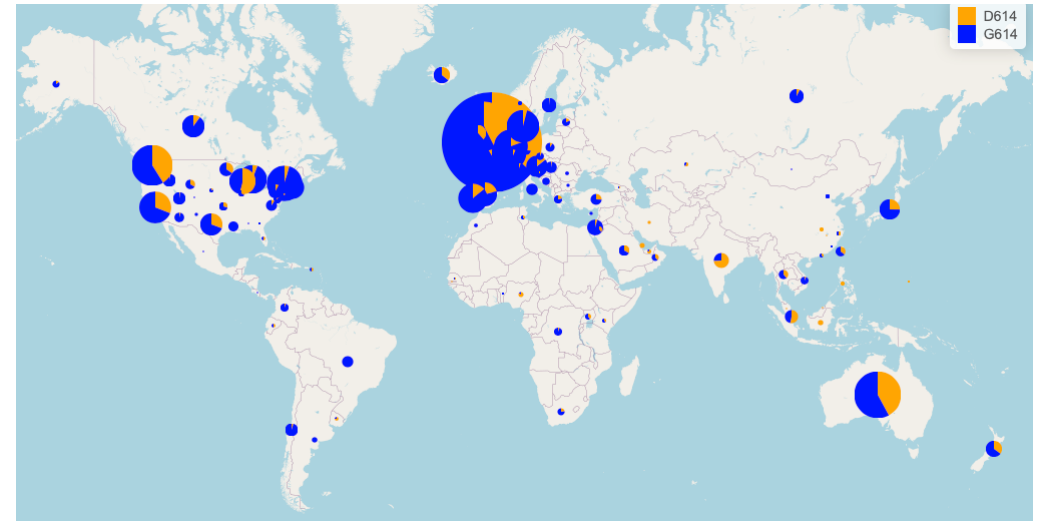
Update on D614G



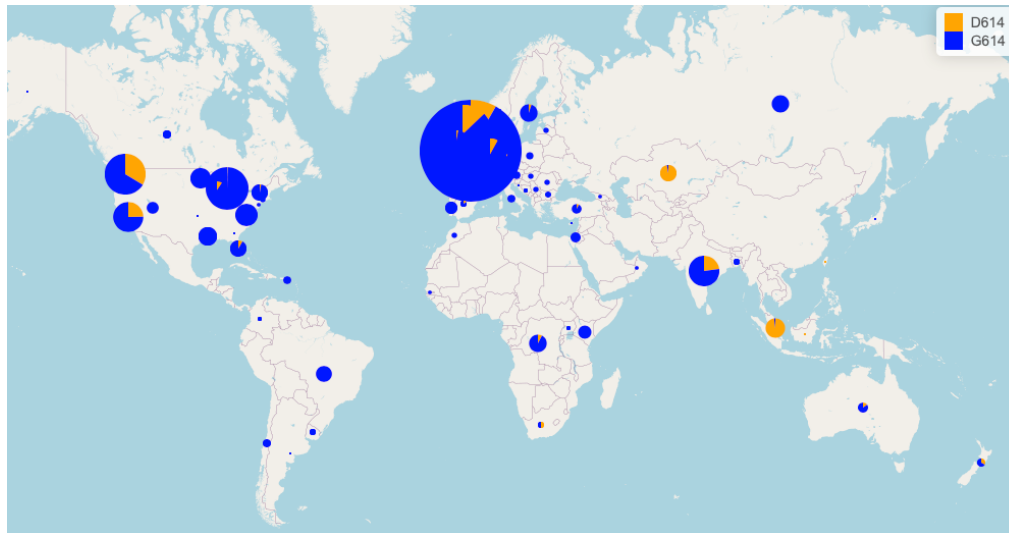
Up through March 1



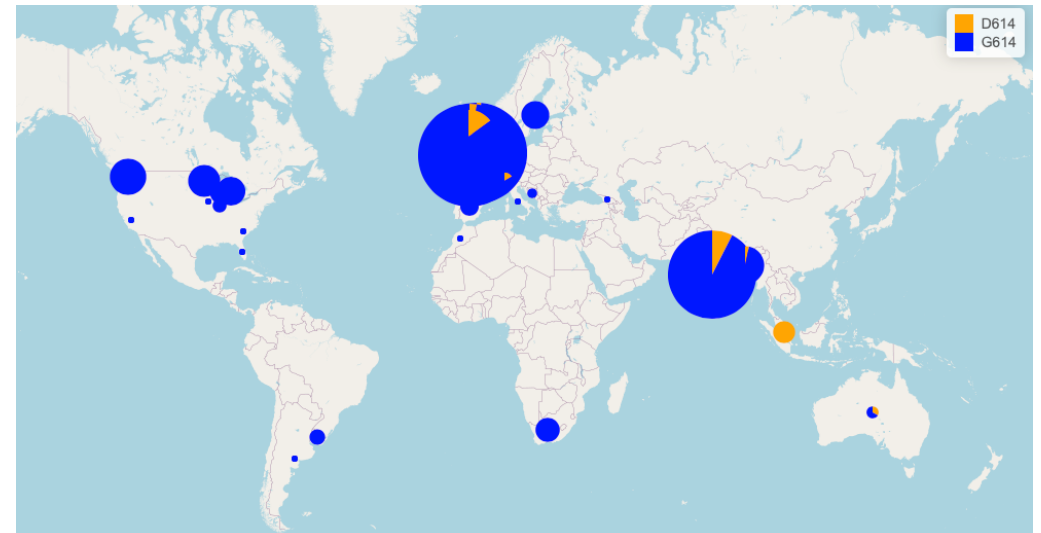
March 21-30



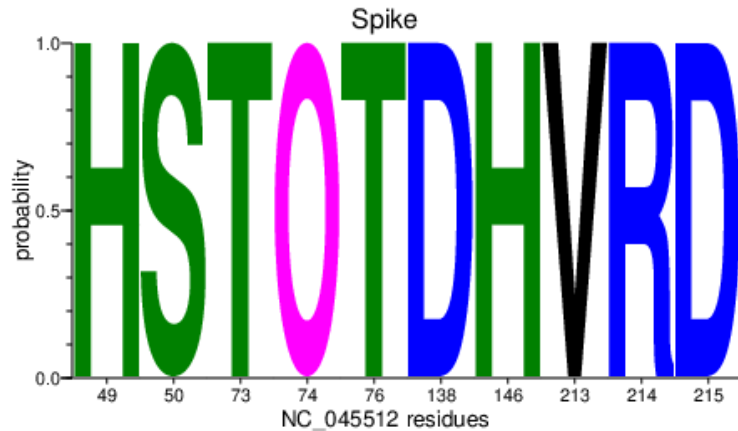
April 21-30



May 21-30



Domain A: N Terminal domain

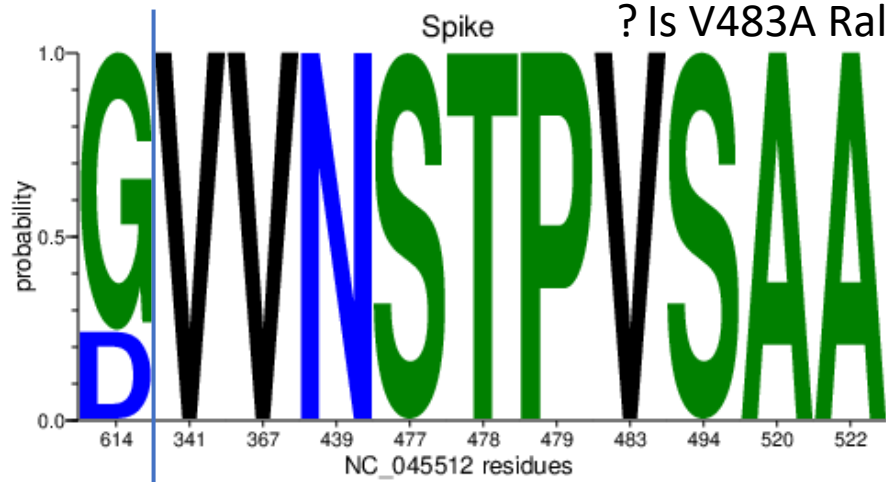


Variant	Count	%	#mut	Locations
HSTOTDHWVRD	47217	99.1	0	
Y-----	71	0.15	1	China 24, Denmark 13, USA 10, United-Kingdom 9, Mexico 5...
-----L-	51	0.11	1	United-Kingdom 46, USA 3,
-----Y-	41	0.09	1	USA 27, United-Kingdom 11, Switzerland 3
-----R-	6	0.01	1	United-Kingdom 6
-----Q-	3	0.01	1	United-Kingdom 2, Canada 1
-----N-	1	0	1	Colombia 1
---I-----	37	0.08	1	United-Kingdom 37
-----L-	20	0.04	1	United-Kingdom 13, Japan 5
-----A-	9	0.02	1	India 9
-----G-	36	0.08	1	Netherlands 34, China 1, France 1
-----N-	1	0	1	Israel 1
-----H-	11	0.02	1	USA 5, Sweden 2...
-----Y-	14	0.03	1	USA 13,
-----E-	1	0	1	United-Kingdom 1
-L-----	29	0.06	1	Australia 8, China 7, Canada 6, United-Kingdom 4...
---NI-----	22	0.05	1	United-Kingdom 13, USA 4, Singapore 3...
---NX-----	04	0.01	1	United-Kingdom 4
---K-----	2	0	1	Brazil 1, Turkey 1
Y--NI-----	1	0	2	Bangladesh 1
-----H-	25	0.05	1	USA 17, Australia 3...
-----Y-	13	0.03	1	Hong-Kong 7, India 3...

74 O is an N-linked glycan,
so the N74 is actually stable, but T 76 I causes the loss of the glycan

*H 49 Y
S 50 L
*T 76 I (glycan loss at N74)
*D 138 H
*H 146 Y
V 213 L
R 214 L
*D 215 G

? Is V483A Ralph Baric's Washington sample?



All of these substitutions are very rare and show no sign of increasing, but all are in the RBD and seem to be tolerated as they are part of local transmission groups.

Thus this set might be a good set for evaluating antibody resistance patterns in the context of a functional Spike.

S494P in CoV-2: this is the same site that conferred SARS-CoV-1 antibody R80 resistance, but the D480A/G in SARS-CoV-1

- *V 341 I
- *V 367 F
- *N 439 K
- *S 477 N
- T 478 I
- *V 483 A
- *S 494 P
- A 520 S
- *A 522 V

RBD

G VVNSTPVSAA

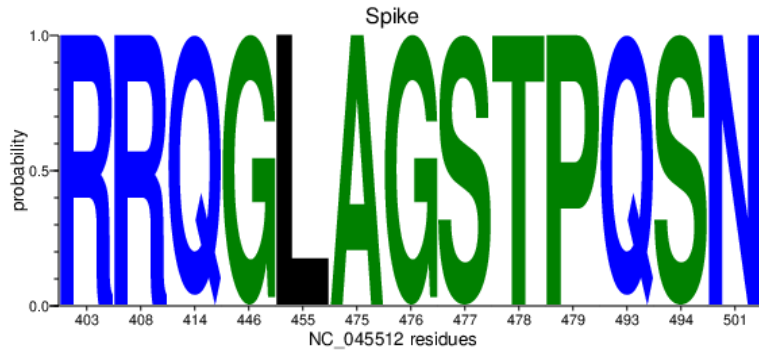
Residue	Count	Probability	Info	Origin
G	35684	74.89	0	
D	11331	23.78	1	
I	90	0.19	1	Rare, steady United-Kingdom 90, (CAMB NORW)
N	80	0.17	1	Rare, steady United-Kingdom 55, Australia 25 (NORW, Victoria)
K	57	0.12	1	Rare, transient United-Kingdom 56, Scotland
S	50	0.1	1	Rare, recent United-Kingdom 49, Wales
A	35	0.07	2	Rare, transient USA 35 WA, Transient, and always with D614
I	26	0.05	1	Rare, transient Sweden 22, Stockholm
F	19	0.04	2	France 5, United-Kingdom 4
F	17	0.04	1	Netherlands 9, United-Kingdom 5
S	14	0.03	1	India 6, USA 4
S	7	0.01	2	USA 5, Australia 1, United-Kingdom 1
V	14	0.03	1	United-Kingdom 11,
V	5	0.01	2	United-Kingdom 3,
S	7	0.01	1	United-Kingdom 4, Netherlands 2, USA 1
S	2	0	2	Australia 1, United-Kingdom 1
P	7	0.01	1	USA 3(Michigan), Sweden 2, Spain 1, United-Kingdom 1
P	3	0.01	2	India 1, Singapore 1, United-Kingdom 1

S494P == position to D480A/G in SARS-CoV1, nAb 80R escape

"In vitro immune pressure on this epitope using 2002/03 strain-specific nAb 80R recapitulated a dominant escape mutation that was present in all 2003/04 animal and human viruses" Sui et al. Broadening of neutralization activity to directly block a dominant antibody-driven SARS-coronavirus evolution pathway. PLoS Pathog 4, e1000197

COV107: Fab C105, PDB 6XCM

Barnes... Bjorkman. 2020 Jun 24;S0092-8674(20)30757-1



*R 403 K
 R 408 I
 Q 414 R
 G 446 V
 *L 455 F
 A 475 V
 *G 476 S
 *S 477 N
 T 478 I
 P 479 S
 Q 493 L
 *S 494 P
 *N 501 Y

Variant	Count	%	#muts	Locations
RRQGLAGSTPQSN	47261	99.19	0	
-----I-----	90	0.19	1	United-Kingdom 90
-----N-----	79	0.17	1	United-Kingdom 54, Australia 25
-----I-----	4	0.01	1	United-Kingdom 4
-----G-----	2	0	1	Austria 1, Japan 1
-----R-----	2	0	1	Egypt 1, United-Kingdom 1
-----S-----	50	0.1	1	United-Kingdom 49, USA 1
-----L-----	2	0	1	USA 1, United-Kingdom 1
-----S-----	13	0.03	1	USA 9, United-Kingdom 2, Belgium 1, India 1
-----A-----	1	0	1	United-Kingdom
-----Y-----	12	0.03	1	Australia 11, USA 1
-----T-----	1	0	1	Netherlands 1
-----P-----	10	0.02	1	USA 3, Sweden 2, United-Kingdom 2, India 1, Singapore 1, Spain 1
--R-----	9	0.02	1	United-Kingdom 8, Spain 1
--K-----	3	0.01	1	Israel 2, Sweden 1
--P-----	1	0	1	Romania 1
K-----	8	0.02	1	USA 8
S-----	1	0	1	United-Kingdom 1
-I-----	6	0.01	1	United-Kingdom 3, Egypt 2, India 1
---V-----	6	0.01	1	USA 5, Australia 1
---V-----	4	0.01	1	United-Kingdom 2, Australia 1, Finland 1
---S-----	2	0	1	United-Kingdom 2
-----L--	3	0.01	1	USA 3
-----R--	1	0	1	United-Kingdom 1
----F-----	3	0.01	1	United-Kingdom 3

Many of these have very low variability, but are very near C105.

So if you wanted natural repeated variants to assess C105-like antibody sensitivity, this might be a good panel.

1 UP RBD antibodies COV21:

Notes below are extracted directly from Barnes... Bjorkman. 2020 Jun 24;S0092-8674(20)30757-1

“From A 3D reconstruction of COV21 Fabs complexed with S showed recognizable density for the S trimer with a single extending density at the apex of the trimer corresponding to a Fab or mixture of Fabs bound to a similar epitope. The density could be fit to an S trimer with a Fab bound to a single RBD in an “up” position using coordinates from SARS-CoV-2 S trimer structures ([Walls et al., 2020](#); [Wrapp et al., 2020](#)), consistent with ELISA results mapping the COV21 response to the SARS-CoV-2 RBD ([Figure 3A](#)).”

“The complex structure and the position of the COV21 Fab(s) closely resembled a structure of SARS-CoV S bound to a Fab from the S230 mAb isolated from a SARS-CoV-infected individual, whose epitope overlaps with the binding site for the ACE2 receptor ([Walls et al., 2019](#))”

“It belongs to a set of 10 non-clonally related *VH3-30*-derived mAbs isolated from an individual infected with SARS-CoV, which represented 40% of the clones isolated from this individual ([Pinto et al., 2020](#)).”

“RBD residues 473 and 475 contacted by the antibody heavy chain in the S230 Fab-SARS-CoV structure ([Walls et al., 2019](#)) are conserved between SARS-CoV and SARS-CoV-2, and these residues are in the vicinity of antibody heavy chain residues N57 and K58. ”

S1A closed structure Pamela's paper

Notes below are extracted directly from Barnes... Bjorkman.
2020 Jun 24;S0092-8674(20)30757-1

- The COV57 Fab(s) density was in the vicinity of loops on the S1^A domain that were disordered in SARS-CoV-2 S trimer structures ([Walls et al., 2020](#); [Wrapp et al., 2020](#)). Such flexibility could explain the diffuse nature of the COV57 Fab(s) density in this reconstruction.
- COV107: Fab C105 potently neutralizing: epitopes overlaps ACE2 binding sites
- Interestingly, the C105-RBD interaction closely resembles the RBD interaction of another COVID-19 donor-derived neutralizing mAb, B38 ([Figure 5E](#)), as reported in a recent Fab-RBD crystal structure ([Wu et al., 2020c](#)).
- Mutations in the SARS-CoV-2 RBD identified by genome sequencing also include N439K, V483A, and V367F ([Tables S3](#) and [S4](#)), but the affected residues are not within the epitopes of the COV21 Fab(s) ([Figures 6A](#) and [6B](#)) or the C105 Fab ([Figure 6C](#)), and residue 483 is disordered in unliganded S protein structures ([Walls et al., 2020](#); [Wrapp et al., 2020](#)).