

# Variant update

2022-10-03

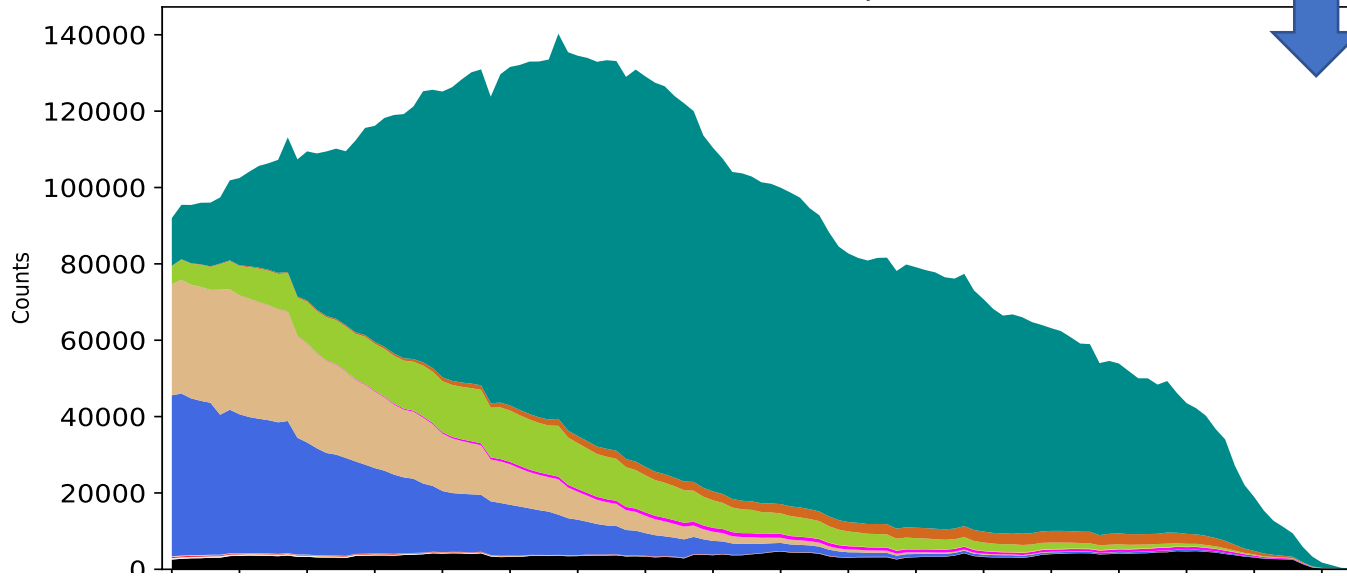
Bette Korber, James Theiler, Will Fischer, Hyejin Yoon

- i. Global transitions in major variants
- ii. BQ.1.1 notes
- iii. BA.2.75.2 and BA.5 sublineages, and the increasing frequency of Spike R346T in multiple lineages.

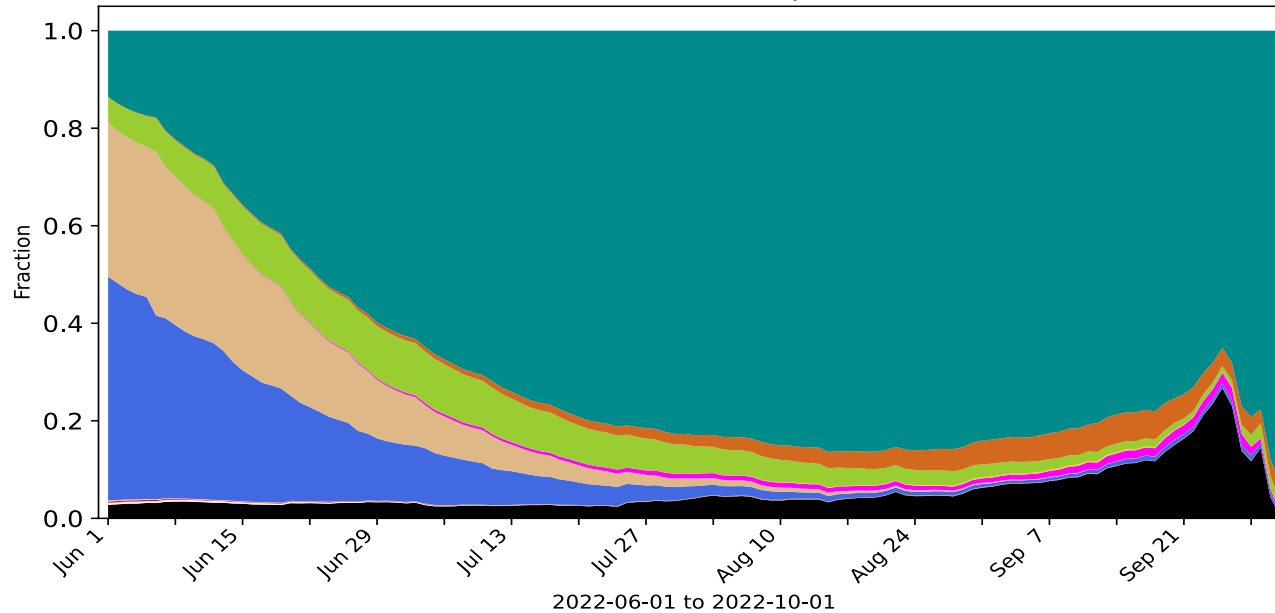
Limited recent sampled



Global: 1564676 sequences



Global: 1564676 sequences

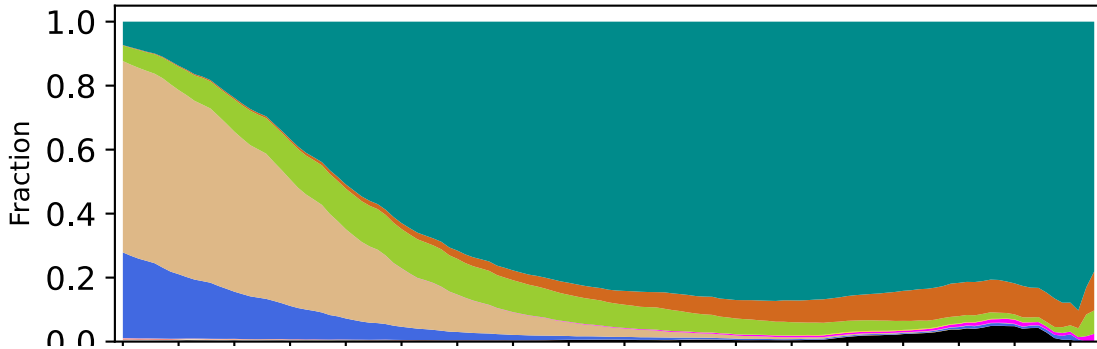


- Omicron\_BA.5/B[EFKTQUVWZ]/C[CDEF]
- Omicron\_BA.4.6
- Omicron\_BA.4
- Omicron\_BA.2.75.2/CA
- Omicron\_BA.2.75/B[LMNRY]/CB
- Omicron\_BA.2.12.1/BG
- Omicron\_BA.2/B[HJSP]
- Omicron\_BA.1.1/BC
- Omicron\_BA.1/BD
- Delta
- Iota
- Epsilon
- Mu
- Gamma
- Beta
- Alpha
- D614G
- Ancestral
- Recombinants
- Other

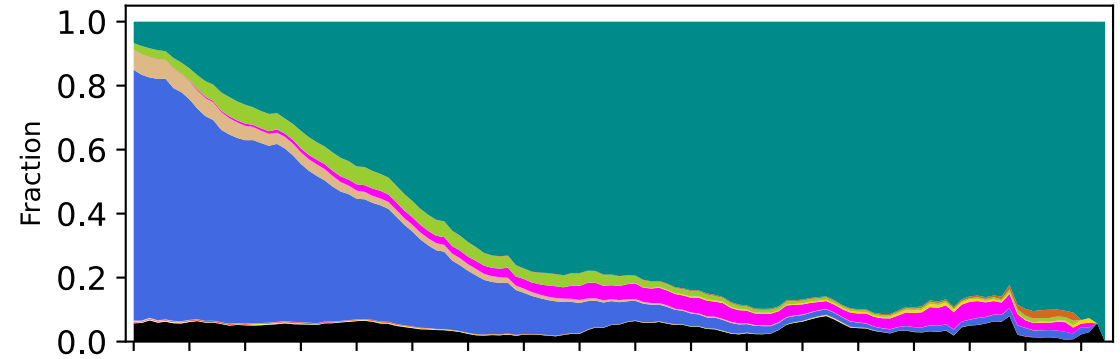


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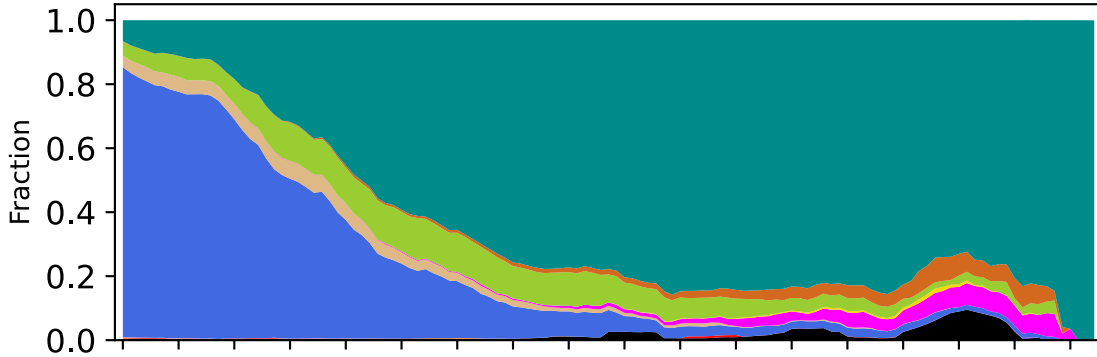
North-America: 616523 sequences



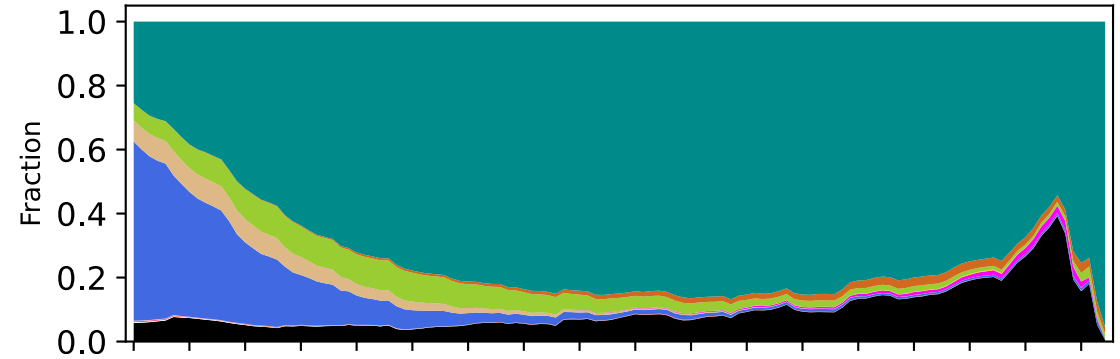
Asia: 239963 sequences



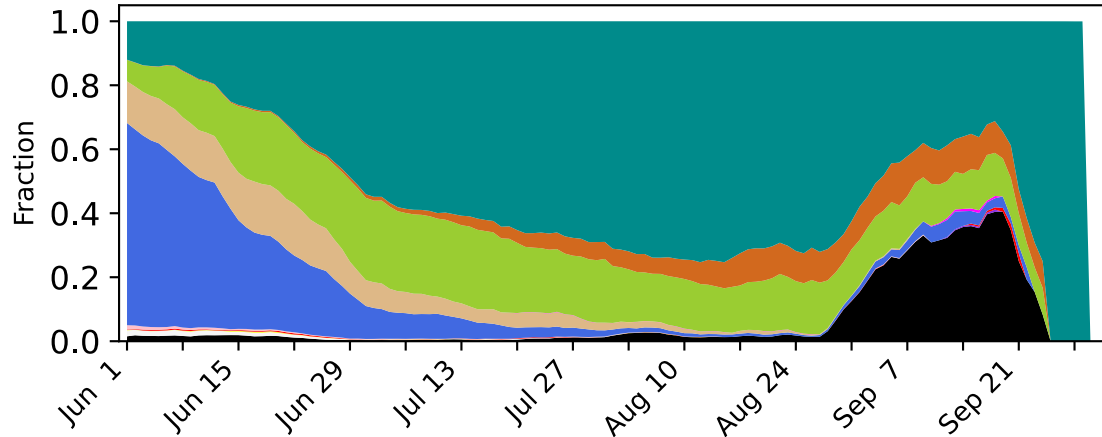
Oceania: 43987 sequences



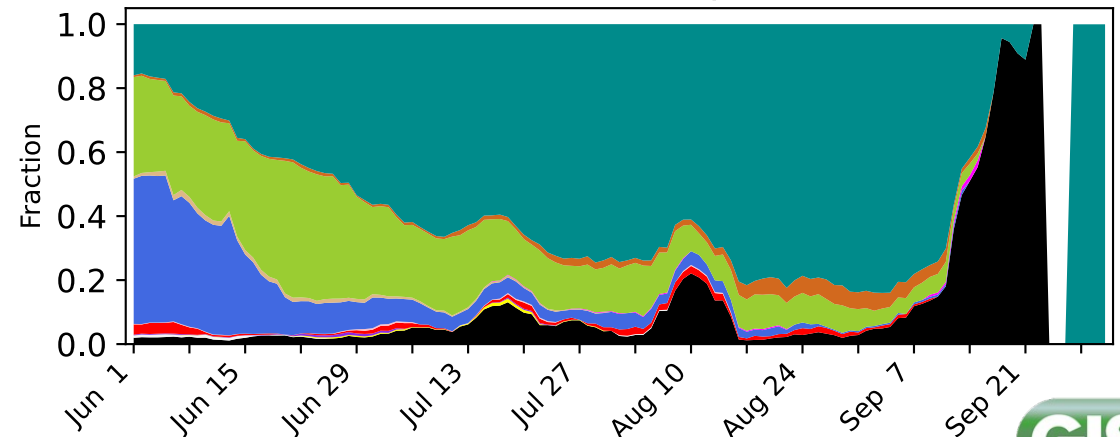
Europe: 608660 sequences



South-America: 44957 sequences



Africa: 10586 sequences



2022-06-01 to 2022-10-01

2022-06-01 to 2022-10-01



# Isotonic Regression Results

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Last data update: Sep 30, 2022

Position: SPIKE 346 T  
 Assumption: Test amino acid form is increasing over time  
 Correlated variant: Do not consider. Include all sequences  
 Range of dates: 2022-07-02 - 2022-09-30

Pango lineage designation in GISAID : BA.5, BA.5.1, BA.5.1.1, BA.5.1.10, BA.5.1.11, BA.5.1.12, BA.5.1.13, BA.5.1.14, BA.5.1.2, BA.5.1.3, BA.5.1.4, BA.5.1.5, BA.5.1.6, BA.5.1.7, BA.5.1.8, BA.5.1.9, BA.5.10, BA.5.2, BA.5.2.1, BA.5.2.2, BA.5.2.3, BA.5.2.4, BA.5.2.5, BA.5.2.6, BA.5.2.7, BA.5.3, BA.5.3.1, BA.5.3.2, BA.5.3.3, BA.5.3.4, BA.5.5, BA.5.5.1, BA.5.6, BA.5.6.1, BA.5.6.2, BA.5.7, BA.5.8, BA.5.9, BE.1, BE.1.1, BE.1.2, BE.2, BE.3, BF.1, BF.1.1, BF.10, BF.11, BF.12, BF.13, BF.14, BF.15, BF.2, BF.3, BF.3.1, BF.4, BF.5, BF.6, BF.7, BF.8, BF.9, BK.1

Hosts: Human Countries where BA.5+R346T was found more than 10x

[Download plots and data](#)

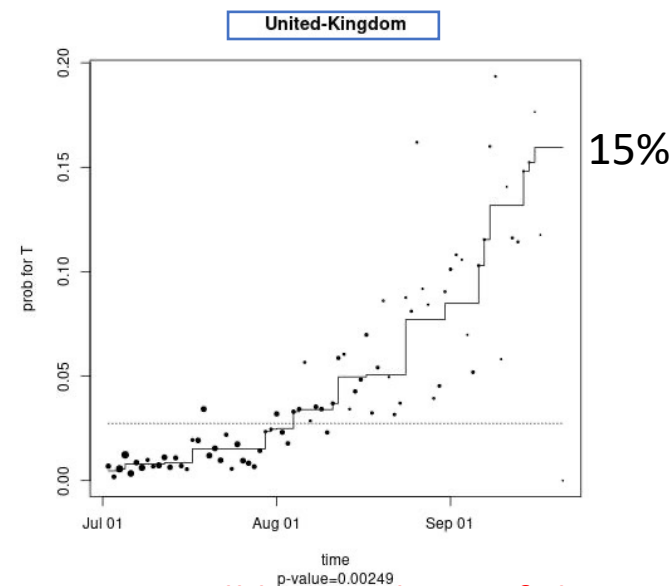
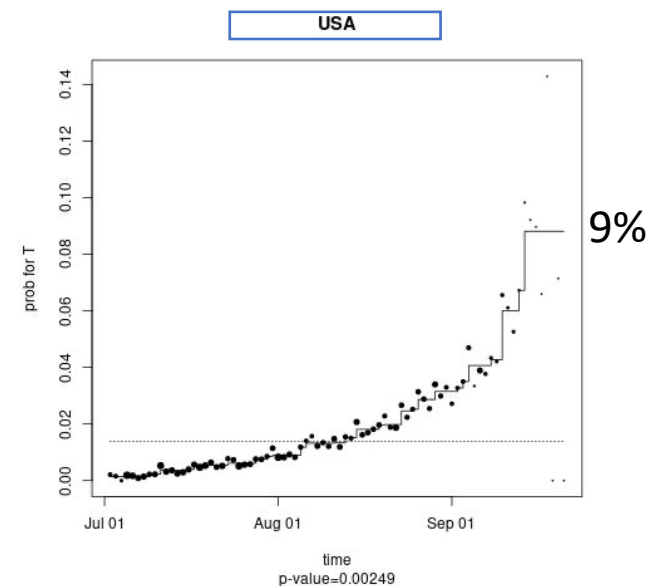
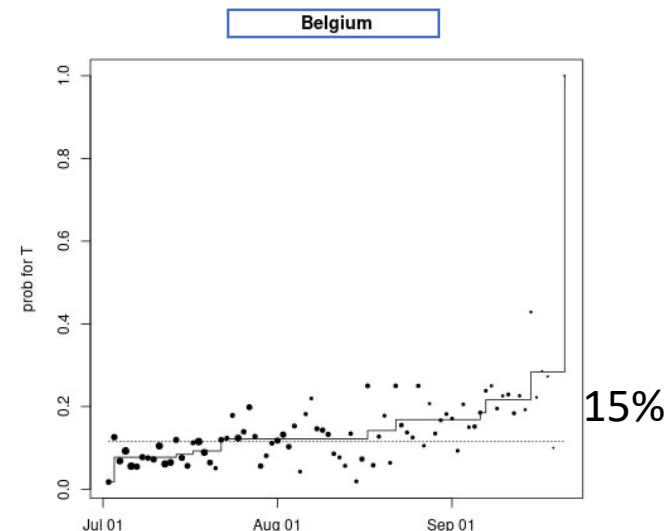
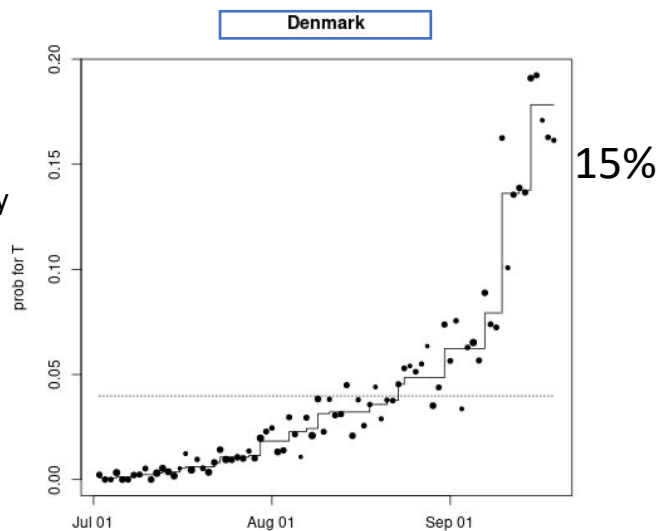
P < 0.05 indicates significantly increasing in frequency

Country level	# T	# Others	Total	T/Total (%)	# days	Time window	p-val
Australia	82	11842	11924	0.69	80	79	0.00249
Austria	75	2250	2325	3.23	68	81	0.00249
Belgium	788	6056	6844	11.51	81	81	0.00249
Brazil	43	4002	4045	1.06	53	61	0.28607
Cambodia	10	255	265	3.77	71	77	0.00249
Canada	353	24565	24918	1.42	80	79	0.00249
Costa-Rica	106	760	866	12.24	79	80	0.00249
Czech-Republic	18	594	612	2.94	67	69	0.00249
Denmark	1304	31465	32769	3.98	80	79	0.00249
Finland	15	1730	1745	0.86	57	60	0.01741
France	507	22864	23371	2.17	80	79	0.00249
Germany	515	24714	25229	2.04	80	79	0.00249
Iceland	38	912	950	4.00	73	80	0.00249
India	11	898	909	1.21	51	60	0.00249
Indonesia	40	4407	4447	0.90	73	74	0.00249
Ireland	20	1227	1247	1.60	73	72	0.00249
Israel	146	13149	13295	1.10	64	66	0.00249
Italy	92	4463	4555	2.02	80	80	0.00249
Japan	101	60820	60921	0.17	80	80	0.00249
Luxembourg	205	4747	4952	4.14	72	71	0.00249
Mexico	11	4804	4815	0.23	64	64	0.00249
Netherlands	334	6508	6842	4.88	80	79	0.00249
Norway	29	1531	1560	1.86	65	65	0.00249
Poland	25	1471	1496	1.67	73	79	0.00249
Portugal	55	2314	2369	2.32	69	68	0.00249
Reunion	12	679	691	1.74	51	71	0.00249
Russia	18	2763	2781	0.65	55	70	0.40547
Singapore	39	2267	2306	1.69	75	74	0.00249
Slovakia	31	2396	2427	1.28	68	67	0.00498
Slovenia	25	1149	1174	2.13	61	64	0.43781
South-Africa	37	292	329	11.25	64	68	0.00249
South-Korea	47	7385	7432	0.63	74	74	0.64925
Spain	73	6350	6423	1.14	79	78	0.00249
Sweden	170	4343	4513	3.77	79	78	0.00249
Switzerland	91	3328	3419	2.66	78	77	0.00249
USA	2878	204526	207404	1.39	82	81	0.00249
United-Kingdom	932	33113	34045	2.74	79	81	0.00249

## Many BA.5s now carry R346T, scattered in multiple Pango BA.5 sublineages that are spreading globally since August



Fraction of BA.5+S R346T relative to all other BA.5's, 4 examples where it is most common:



BQ.1.1 will be a subset of these...

# BQ.1.1 Spike sequences

## cov-lineages.org

BQ.1.1:

BA.5+ Spike R346T, K444T and N460K

[Of note BA.2.75 also carries N460K, and now many of the BA.2.75 also carry R346T, which has been rapidly outgrowing baseline BA.2.75.]

The BQ.1.1 label in GISAID is pending, but it is a subset of BE.1.1; 320 of these have the full BQ.1.1 set with +[R346T,K444T,N460K]

From the sublineage of BQ.1:

<https://cov-lineages.org/lineage.html?lineage=BQ.1>

Alias of B.1.1.529.5.3.1.1.1.1.1, found globally, defining mutations ORF1b:N1191S and S:R346T, from issue #993

# BA.2.75 variants relative to a BA.2 baseline

Pango	Lineage Count	Form count	Form%	Form
BA.2.75	1612	247	15.3%	0 +[K147E,W152R,F157L,I210V,G257S,G339H,G446S,N460K]-[G339D,Q493R] (consensus)
BA.2.75	1612	239	14.8%	2 +[K147E,W152R,F157L,I210V,G257S,G339H,R346T,G446S,N460K,F486S]-[G339D,Q493R]
BA.2.75	1612	236	14.6%	1 +[K147E,W152R,F157L,I210V,G257S,G339H,K356T,G446S,N460K]-[G339D,Q493R]
BA.2.75	1612	86	5.3%	3 +[K147E,W152R,F157L,I210V,G257S,G339H,R346T,G446S,N460K,F486S,D1199N]-[G339D,Q493R]
BA.2.75	1612	41	2.5%	3 +[K147E,W152R,F157L,I210V,G257S,G339H,R346T,K356T,G446S,N460K,F490S]-[G339D,Q493R]
BA.2.75.1	457	294	64.3%	0 +[K147E,W152R,F157L,I210V,G257S,G339H,G446S,N460K,D574V]-[G339D,Q493R] (consensus)
BA.2.75.1	457	9	2.0%	1 +[K147E,W152R,F157L,I210V,G257S,G339H,G446S,N460K,D574V,T761I]-[G339D,Q493R]
BA.2.75.1	457	8	1.8%	1 +[K147E,W152R,F157L,I210V,G257S,G339H,G446S,N460K,D574V,T1117I]-[G339D,Q493R]
BA.2.75.1	457	5	1.1%	1 +[K147E,W152R,F157L,I210V,G257S,G339H,G446T,N460K,D574V]-[G339D,Q493R]
BA.2.75.1	457	5	1.1%	2 +[K147E,W152R,F157L,I210V,R214L,G219D,G257S,G339H,G446S,N460K,D574V]-[G339D,Q493R]
BA.2.75.2	394	286	72.6%	0 +[K147E,W152R,F157L,I210V,G257S,G339H,R346T,G446S,N460K,F486S,D1199N]-[G339D,Q493R] (consensus)
BA.2.75.2	394	10	2.5%	2 +[K147E,W152R,F157L,I210V,G257S,G339H,R346T,G446S,L452R,N460K,F486S,T604I,D1199N]-[G339D,Q493R]
BA.2.75.2	394	9	2.3%	1 +[K147E,W152R,F157L,I210V,G257S,G339H,R346T,G446S,N460K,F486S]-[G339D,Q493R]
BA.2.75.2	394	5	1.3%	1 +[K147E,W152R,F157L,I210V,G339H,R346T,G446S,N460K,F486S,D1199N]-[G339D,Q493R]
BA.2.75.2	394	5	1.3%	1 +[L5F,K147E,W152R,F157L,I210V,G257S,G339H,R346T,G446S,N460K,F486S,D1199N]-[G339D,Q493R]
BA.2.75.5	18	11	61.1%	0 +[K147E,W152R,F157L,I210V,G257S,G339H,K356T,G446S,N460K]-[G339D,Q493R] (consensus)
BA.2.75.5	18	3	16.7%	2 +[K147E,W152R,F157L,I210V,G257S,G339H,R346T,K356T,G446S,N460K,F490S]-[G339D,Q493R]
BA.2.75.5	18	1	5.6%	1 +[K147E,W152R,F157L,I210V,G257S,K356T,G446S,N460K]-[G339D,Q493R]
BA.2.75.5	18	1	5.6%	5 +[I210V,G257S,G339H,K356T,G446S,N460K,A1020V]-[G142D,G339D,Q493R]
BA.2.75.5	18	1	5.6%	1 +[K147E,W152R,F157L,I210V,G257S,G339H,K356T,G446S,N460K,F490S]-[G339D,Q493R]
BA.2.75.3	13	2	15.4%	0 +[K147E,W152R,F157L,I210V,G257S,G339H,R346T,G446S,N460K,F486S]-[G339D,Q493R] (consensus)
BA.2.75.3	13	2	15.4%	1 +[K147E,W152R,F157L,I210V,G257S,G339H,G446S,N460K,F486S]-[G339D,Q493R]
BA.2.75.3	13	1	7.7%	5 +[K147G,W152R,F157L,K182E,I210V,G257S,G339H,R346T,G446S,N460K,F486S,F490S,T883I]-[G142D,G339D,Q493R]
BA.2.75.3	13	1	7.7%	3 +[K147E,W152R,F157L,I210V,G339H,R346T,G446S,N460K,F486S,F490S]-[G142D,G339D,Q493R]
BA.2.75.3	13	1	7.7%	1 +[K147E,W152R,F157L,I210V,G257S,G339H,R346T,G446S,N460K,T478I,F486S]-[G339D,T478K,Q493R]
BA.2.75.4	3	1	33.3%	0 +[K147E,W152R,F157L,I210V,G257S,G339H,G446S,L452R,N460K,C1247Y]-[G339D,Q493R]
BA.2.75.4	3	1	33.3%	1 +[K147E,W152R,F157L,I210V,G257S,G339H,G446S,L452R,N460K]-[G339D,Q493R] (consensus)
BA.2.75.4	3	1	33.3%	3 +[K147E,W152R,F157L,I210V,G257S,G339H,K444T,G446S,L452R,N460K,D574V]-[G339D,Q493R]
BL.1	313	154	49.2%	0 +[K147E,W152R,F157L,I210V,G257S,G339H,R346T,G446S,N460K,D574V]-[G339D,Q493R] (consensus)
BL.1	313	23	7.3%	6 +[K147E,W152R,F157L,I210V,G257S,G339H,R346T,G446S,N460K,F486S]-[L24-,P25-,P26-,A27S,G339D,Q493R]
BL.1	313	21	6.7%	7 +[K147E,W152R,F157L,I210V,G257S,G339H,R346T,G446S,N460K,F486S,D1199N]-[L24-,P25-,P26-,A27S,G339D,Q493R]
BL.1	313	11	3.5%	1 +[K147E,W152R,F157L,I210V,D215G,G257S,G339H,R346T,G446S,N460K,D574V]-[G339D,Q493R]
BL.1	313	8	2.6%	1 +[K147E,W152R,F157L,I210V,G257S,G339H,R346T,G446S,N460K,D574V,D614S]-[G339D,Q493R,D614G]

BA.2.75 listing from 2022-10-01  
BL.1 added 2022-10-03

R346T  
Mutations associated with R346T



The [set] after the minus sign means a mutation found in most BA.2 relative to the Wuhan reference reverts to ancestral or is further mutated in the sequence.

Most of the BA.2.75s now carries R346T, scattered in multiple Pango sublineages that are spreading globally since August

### Isotonic Regression Results cov.lanl.gov

Last data update: Oct 3,

Position: SPIKE 346 T

Assumption: Test amino acid form is increasing over time

Correlated variant: Do not consider. Include all sequences

Range of dates: 2022-07-05 - 2022-10-03

Pango lineage designation in GISAID : BA.2.75, BA.2.75.1, BA.2.75.2, BA.2.75.3, BA.2.75.4, BA.2.75.5, BL.1

Hosts: Human

[Download plots and data](#)

Countries where BA.2.75+R346T was found more than 10x

Country level

	# T	# Others	Total	T/Total (%)	# days	Time window	p-val
Australia	170	223	393	43.26	70	78	0.00249
Austria	133	84	217	61.29	29	70	0.00249
Belgium	17	29	46	36.96	35	62	0.00498
Canada	64	155	219	29.22	69	76	0.00249
France	31	25	56	55.36	24	70	0.00249
Germany	18	21	39	46.15	29	60	0.02239
India	222	590	812	27.34	72	72	0.00249
Israel	43	46	89	48.31	43	75	0.00249
Japan	36	115	151	23.84	54	70	0.00249
Netherlands	21	13	34	61.76	24	50	0.14677
Singapore	211	244	455	46.37	62	71	0.00249
South-Korea	22	33	55	40.00	37	65	0.00498
Switzerland	20	14	34	58.82	23	61	0.00249
USA	361	444	805	44.84	78	82	0.00249
United-Kingdom	96	82	178	53.93	57	81	0.00249

P < 0.05 indicates significantly increasing in frequency

The frequency of Spike BA.2.75+R346T relative to other all other BA.2.75's

