

Manuscript title: Sequencing during times of change: Evaluating SARS-CoV-2 clinical samples during the transition from the Delta wave to Omicron wave in Chicago, USA

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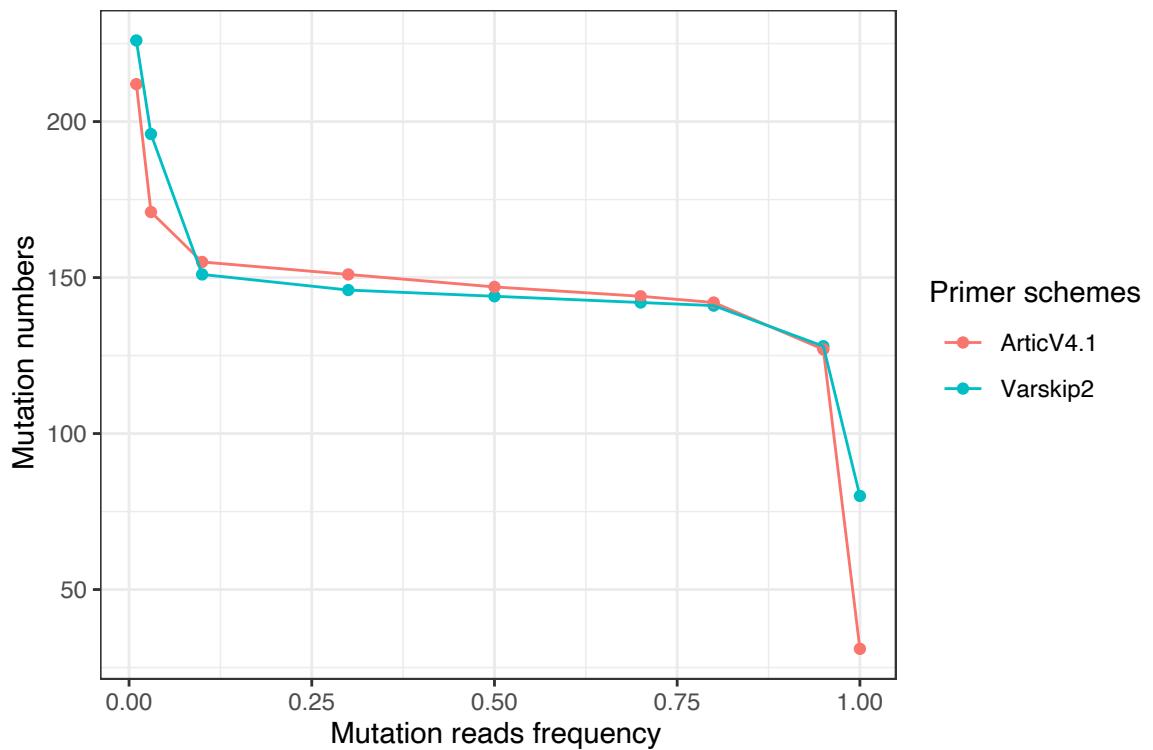


Figure S1. Mutation numbers identified at different reads frequencies in eight samples sequenced using both ArticV4.1 and Varskip2 primer schemes. Mutation numbers at reads frequency values of 0.01, 0.03, 0.1, 0.3, 0.5, 0.7, 0.8, 0.95 and 1 are plotted.

Varskip2 performance on Omicron samples (n=6)

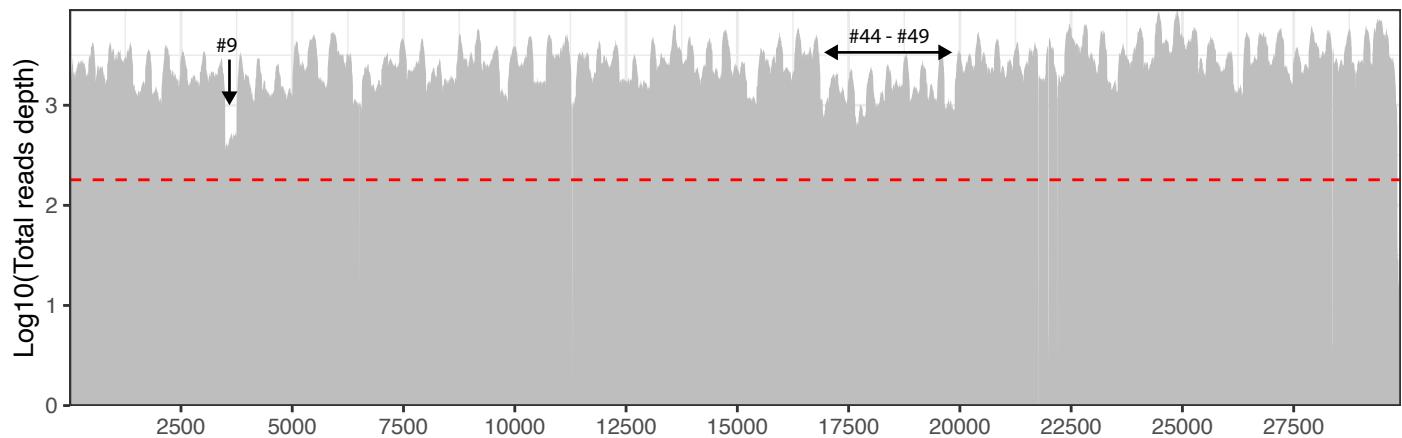


Figure S2. Summarized total reads depth across the genome for Omicron samples sequenced using the Varskip2 primer scheme (n=6). The X-axis represents genome positions. The Y-axis represents log10 transformed total reads depth. The relatively lower coverage amplicon regions (#9 and #44-#49) are indicated in arrows.

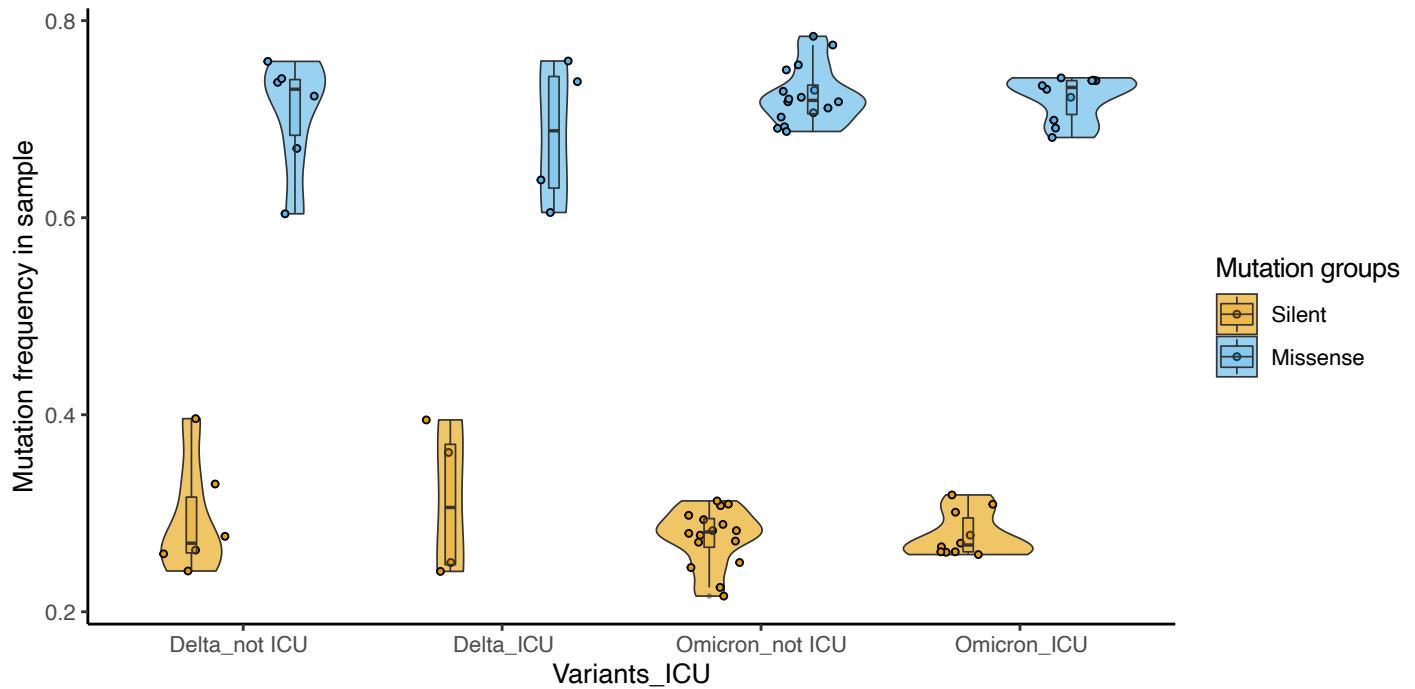


Figure S3. Silent and missense mutation frequencies in groups of variants (Delta or Omicron) and patient status (ICU/not-ICU). Silent mutations and missense mutations are represented in yellow and blue colors, respectively. The whiskers in the box plot represent for the 25th percentile, median and 75th percentile from the bottom to the top, respectively.

Table S1. Details of patient demographics (n=34), sample Ct values and lineages.

| Sample ID | Sex | Age | Sampling Date | Vaccinated | Immuno-suppressed* | Hospitalized** | Viral Load (Ct) | Lineage |
|-----------|-----|-----|---------------|------------|--------------------|----------------|-----------------|------------------|
| P1 | F | 62 | 05/26/21 | Yes | Yes | Yes/ICU | 21.1 | Alpha(B.1.1.7) |
| P2 | F | 67 | 08/05/21 | Yes | Yes | No | 23.6 | Delta(AY.110) |
| P3 | M | 52 | 11/03/21 | Yes | No | Yes | 24.5 | Delta(AY.39) |
| P4 | F | 54 | 11/03/21 | Yes | Yes | Yes/ICU | 22.0 | Delta(AY.25.1) |
| P5 | M | 53 | 11/24/21 | Yes | Yes | Yes | 20.4 | Delta(AY.42.1) |
| P6 | M | 38 | 11/25/21 | Yes | No | Yes | 18.4 | Delta(AY.3) |
| P7 | M | 52 | 12/07/21 | Yes | Yes | Yes/ICU | 26.3 | Delta(AY.117) |
| P8 | M | 30 | 12/15/21 | Yes | No | No | 28.1 | Omicron(BA.1) |
| P9 | M | 68 | 12/17/21 | Yes | Yes | Yes | 20.8 | Delta(AY.103) |
| P10 | M | 57 | 12/20/21 | Yes | Yes | Yes | 26.4 | Delta(AY.3) |
| P11 | F | 63 | 12/27/21 | Yes | Yes | Yes/ICU | 20.2 | Omicron(BA.1) |
| P12 | M | 49 | 12/29/21 | Yes | No | Yes | 23.8 | Omicron(BA.1.15) |
| P13 | F | 67 | 12/31/21 | Yes | Yes | Yes | 20.0 | Omicron(BA.1.15) |
| P14-1 | M | 70 | 12/31/21 | Yes | Yes | Yes/ICU | 27.7 | Delta(AY.103) |
| P14-2 | | | 01/10/22 | | | Yes/ICU | 26.1 | Delta(AY.103) |
| P15 | F | 30 | 01/01/22 | Yes | Yes | Yes | 33.1 | Omicron(BA.1.1) |
| P16-1 | M | 78 | 01/04/22 | Yes | Yes | No | 24.5 | Omicron(BA.1) |
| P16-2 | | | 01/18/22 | | | Yes/ICU | 26.8 | Omicron(BA.1) |
| P17 | M | 66 | 01/05/22 | Yes | Yes | Yes/ICU | 22.4 | Omicron(BA.1) |
| P18 | M | 58 | 01/05/22 | Yes | No | No | 30.6 | Omicron(BA.1) |
| P19 | M | 59 | 01/06/22 | Yes | Yes | No | 21.5 | Omicron(BA.1) |
| P20 | F | 52 | 01/07/22 | Yes | No | No | 23.6 | Omicron(BA.1.1) |
| P21 | F | 61 | 01/09/22 | Yes | Yes | No | 29.7 | Omicron(BA.1) |
| P22 | F | 53 | 01/10/22 | Yes | Yes | Yes | 25.4 | Omicron(BA.1) |
| P23 | F | 67 | 01/13/22 | Yes | No | Yes | 29.2 | Omicron(BA.1.1) |
| P24 | F | 67 | 01/13/22 | Yes | Yes | Yes/ICU | 19.0 | Omicron(BA.1.1) |
| P25 | F | 64 | 01/13/22 | Yes | Yes | Yes/ICU | 27.3 | Omicron(BA.1) |
| P26 | M | 62 | 01/14/22 | No | Yes | Yes | 26.9 | Omicron(BA.1.15) |
| P27 | F | 65 | 01/14/22 | Yes | Yes | Yes/ICU | 22.2 | Omicron(BA.1) |
| P28 | M | 71 | 01/15/22 | Yes | Yes | Yes/ICU | 19.8 | Omicron(BA.1) |
| P29-1 | F | 62 | 01/15/22 | Yes | Yes | No | 27.3 | Omicron(BA.1.1) |
| P29-2 | | | 02/01/22 | | | Yes/ICU | 28.6 | Omicron(BA.1.1) |
| P30 | M | 79 | 01/18/22 | Yes | Yes | Yes | 17.8 | Omicron(BA.1) |
| P31 | M | 52 | 01/18/22 | Yes | Yes | Yes/ICU | 22.0 | Omicron(BA.1) |
| P32 | M | 48 | 01/20/22 | Yes | Yes | Yes/ICU | 22.6 | Omicron(BA.1.1) |
| P33 | M | 41 | 01/24/22 | Yes | Yes | Yes | 24.5 | Omicron(BA.1) |
| P34 | M | 40 | 01/31/22 | Yes | Yes | Yes | 25.5 | Omicron(BA.1) |

* Immunosuppression due to multiple myeloma, solid organ transplant, systemic lupus erythematosus, or chronic lymphoid leukemia.

** P18, P19 and P21 were asymptomatic infections admitted for non-COVID reasons, therefore were considered as not hospitalized for COVID in this study.

Table S2. Private mutations identified from the 37 samples by Nextclade. Nucleic acid changes in the first 50 bp and last 100 bp length of the reference genome are not included as these are affected a lot by low coverage and high rate of sequencing and/or mapping errors.

| Patients | Variants | Lineages | Labeled private mutations | Unlabeled private mutations | Numbers of labeled private mutations | Numbers of unlabeled private mutations |
|----------|----------|----------|-----------------------------|---|--------------------------------------|--|
| P1 | Alpha | B.1.1.7 | C2395T,C7851T,T150 96C | C4206T,C7299T,C10138T,C11750T,C1981 3T | 3 | 5 |
| P2 | Delta | AY.110 | | C13326T,C19154T,A27397G,G27415A,T2 7504A,C28744T | 0 | 6 |
| P3 | Delta | AY.39 | | C2509T,C3619T,C12084T,A16006G,C2244 4T,T23725G,G25855C,C26111T | 0 | 8 |
| P4 | Delta | AY.25.1 | | C7200T,T8764C,C13620T,G29425A | 0 | 4 |
| P5 | Delta | AY.3 | | C3695T,C4012T,C7162T,G7246T,A11782 G,C12073T,C12513T,T13701C,C15141T,C 24374T,G27390T,G27589T,C28313T | 0 | 13 |
| P6 | Delta | AY.3 | | C1479T,C9073T,G10533A,A10994G,C189 12T,G18948T,C21145T,C22480T,C26936T | 0 | 9 |
| P7 | Delta | AY.117 | | C3315T,G10642A,C22432T,C27304T | 0 | 4 |
| P8 | Omicron | BA.1 | C28472T | C10543T,C11950T,A21137G,T23332C,C29 144T | 1 | 5 |
| P9 | Delta | AY.103 | C18744T | A259G,C4900T,G6671A,C14688T,C14925 T,G19684T,C21910T,G23401T,G26828A, G27260T,C28236T | 1 | 11 |
| P10 | Delta | AY.3 | | A1622T,C5565T,T5566A,C5730T,C6681T, G21055A,C22624T,G24390T,A27663G,G2 9734T,G29742T | 0 | 11 |
| P11 | Omicron | BA.1 | | A8590G | 0 | 1 |
| P12 | Omicron | BA.1.15 | | C25777T | 0 | 1 |
| P14-1 | Delta | AY.103 | C9891T | C664T,C2842T,T6661C,C12890T,T14448C, A22780T,G22899T,A23013T,C24034T,G2 7967A,G29422A | 1 | 11 |
| P14-2 | Delta | AY.103 | C9891T | C664T,C2842T,T6661C,C12890T,T14448C, A22780T,G22899T,A23013T,C24034T,G2 7967A,G29422A | 1 | 10 |
| P15 | Omicron | BA.1.1 | C21595T | | 1 | 0 |
| P16-1 | Omicron | BA.1 | C28472T | C6361T,C11950T | 1 | 2 |
| P16-2 | Omicron | BA.1 | C28472T | C6361T,C11950T | 1 | 2 |
| P17 | Omicron | BA.1 | C28472T | T6152C,A6293G,A7930G,G8371A,G1153 4A,C11950T | 1 | 6 |
| P18 | Omicron | BA.1 | C28472T | C11950T,C17898T,C25515T | 1 | 3 |
| P19 | Omicron | BA.1 | | C25714T | 0 | 1 |
| P20 | Omicron | BA.1.1 | C21595T | C18788T | 1 | 1 |
| P21 | Omicron | BA.1 | C28472T | A7981G,C11950T,T22685A,T22686A | 1 | 4 |
| P22 | Omicron | BA.1 | C28472T | C11950T | 1 | 1 |
| P24 | Omicron | BA.1.1 | C21595T | | 1 | 0 |
| P25 | Omicron | BA.1 | C28472T | C11950T,C22224T | 1 | 2 |
| P26 | Omicron | BA.1.15 | | G14268A,C19572T | 0 | 2 |
| P27 | Omicron | BA.1 | C28472T,A28877T,G 28878C | C4406T,C11950T,C26447T | 3 | 3 |
| P28 | Omicron | BA.1 | C28472T | C11950T | 1 | 1 |
| P29-1 | Omicron | BA.1.1 | C21595T | C676T,A22005C,C24334A | 1 | 3 |
| P29-2 | Omicron | BA.1.1 | C4965T,C21595T,G2 3012A | T168C,C676T,G4985A,C12784T,A22005C, G23282A,C24334A | 3 | 7 |
| P30 | Omicron | BA.1 | C28472T | A6625T,C9207A,C11950T,C17135T | 1 | 4 |
| P31 | Omicron | BA.1 | C28472T | G3122T,C11950T,T28642C | 1 | 3 |
| P32 | Omicron | BA.1.1 | C21595T | C15928T,T27569C | 1 | 2 |
| P33 | Omicron | BA.1 | C28472T | C3923T,C11950T | 1 | 2 |
| P34 | Omicron | BA.1 | C28472T | C11950T,C17402A,G19851A | 1 | 3 |

Table S3. Variant-specific mutation list for detection of potential recombination events¹⁻³.

| Genomic position | Nucleic acid change | gene | Index for lineage | Used for Delta v.s. Omicron | Used for BA.1 v.s. BA.2 |
|------------------|---------------------|--------|--------------------------|-----------------------------|-------------------------|
| 670 | T670G | ORF1ab | BA.2, BA.3 | yes | yes |
| 2790 | C2790T | ORF1ab | BA.2 | yes | yes |
| 2832 | A2832G | ORF1ab | BA.1, BA.1.1 | yes | yes |
| 4184 | G4184A | ORF1ab | BA.2, BA.3 | yes | yes |
| 6402 | C6402T | ORF1ab | Delta | yes | |
| 7124 | C7124T | ORF1ab | Delta | yes | |
| 8393 | G8393A | ORF1ab | BA.1, BA.1.1 | yes | yes |
| 9053 | G9053T | ORF1ab | Delta | yes | |
| 9344 | C9344T | ORF1ab | BA.2 | yes | yes |
| 9534 | C9534T | ORF1ab | BA.2, BA.3 | yes | yes |
| 9866 | C9866T | ORF1ab | BA.2 | yes | yes |
| 10449 | C10449A | ORF1ab | BA.1, BA.1.1, BA.2, BA.3 | yes | |
| 11201 | A11201G | ORF1ab | Delta | yes | |
| 11235 | C11235T | ORF1ab | BA.3 | yes | |
| 11287 | G11287T | ORF1ab | BA.1, BA.1.1, BA.2 | yes | |
| 11288 | del11288_11296 | ORF1ab | BA.1, BA.1.1, BA.2, BA.3 | yes | |
| 11537 | A11537G | ORF1ab | BA.1, BA.1.1 | yes | yes |
| 15451 | G15451A | ORF1ab | Delta | yes | |
| 16466 | C16466T | ORF1ab | Delta | yes | |
| 17410 | C17410T | ORF1ab | BA.2 | yes | yes |
| 18163 | A18163G | ORF1ab | BA.1, BA.1.1, BA.2, BA.3 | yes | |
| 19220 | C19220T | ORF1ab | Delta | yes | |
| 19955 | C19955T | ORF1ab | BA.2 | yes | yes |
| 21618 | C21618T | S | BA.2 | yes | yes |
| 21618 | C21618G | S | Delta | yes | |
| 22578 | G22578A | S | BA.1, BA.1.1, BA.2, BA.3 | yes | |
| 22599 | G22599A | S | BA.1.1 | yes | yes |
| 22674 | C22674T | S | BA.2, BA.3 | yes | yes |
| 22679 | T22679C | S | BA.1, BA.1.1, BA.2, BA.3 | yes | |
| 22686 | C22686T | S | BA.1, BA.1.1, BA.2, BA.3 | yes | |
| 22688 | A22688G | S | BA.2 | yes | yes |
| 22775 | G22775A | S | BA.2, BA.3 | yes | yes |
| 22786 | A22786C | S | BA.2 | yes | yes |
| 22882 | T22882G | S | BA.1, BA.1.1, BA.2, BA.3 | yes | |
| 22898 | G22898A | S | BA.1, BA.1.1, BA.3 | yes | |
| 22917 | T22917G | S | Delta | yes | |
| 23013 | A23013C | S | BA.1, BA.1.1, BA.2, BA.3 | yes | |
| 23040 | A23040G | S | BA.1, BA.1.1, BA.2, BA.3 | yes | |
| 23048 | G23048A | S | BA.1, BA.1.1 | yes | yes |
| 23055 | A23055G | S | BA.1, BA.1.1, BA.2, BA.3 | yes | |
| 23063 | A23063T | S | BA.1, BA.1.1, BA.2, BA.3 | yes | |
| 23075 | T23075C | S | BA.1, BA.1.1, BA.2, BA.3 | yes | |
| 23525 | C23525T | S | BA.1, BA.1.1, BA.2, BA.3 | yes | |
| 23599 | T23599G | S | BA.1, BA.1.1, BA.2, BA.3 | yes | |
| 23604 | C23604A | S | BA.1, BA.1.1, BA.2, BA.3 | yes | |
| 23604 | C23604G | S | Delta | yes | |
| 23854 | C23854A | S | BA.1, BA.1.1, BA.2, BA.3 | yes | |
| 23948 | G23948T | S | BA.1, BA.1.1, BA.2, BA.3 | yes | |
| 24410 | G24410A | S | Delta | yes | |
| 24424 | A24424T | S | BA.1, BA.1.1, BA.2, BA.3 | yes | |
| 24469 | T24469A | S | BA.1, BA.1.1, BA.2, BA.3 | yes | |
| 24503 | C24503T | S | BA.1, BA.1.1 | yes | yes |
| 25469 | C25469T | ORF3a | Delta | yes | |
| 26270 | C26270T | E | BA.1, BA.1.1, BA.2, BA.3 | yes | |
| 26530 | A26530G | M | BA.1, BA.1.1 | yes | yes |
| 26577 | C26577G | M | BA.1, BA.1.1, BA.2, BA.3 | yes | |
| 26709 | G26709A | M | BA.1, BA.1.1, BA.2, BA.3 | yes | |
| 26767 | T26767C | M | Delta | yes | |
| 27638 | T27638C | ORF7ab | Delta | yes | |
| 27752 | C27752T | ORF7ab | Delta | yes | |
| 28311 | C28311T | N | BA.1, BA.1.1, BA.2, BA.3 | yes | |
| 28362 | del28362_28370 | N | BA.1, BA.1.1, BA.2, BA.3 | yes | |
| 28461 | A28461G | N | Delta | yes | |
| 28881 | G28881A | N | BA.1, BA.1.1, BA.2, BA.3 | yes | |
| 28881 | G28881T | N | Delta | yes | |
| 28882 | G28882A | N | BA.1, BA.1.1, BA.2, BA.3 | yes | |
| 28883 | G28883C | N | BA.1, BA.1.1, BA.2, BA.3 | yes | |
| 29510 | A29510C | N | BA.2, BA.3 | yes | yes |
| 22673, 22674 | T22673C, C22674T | S | BA.1, BA.1.1 | yes | yes |

Table S4. Welch's t-test results for comparison of silent and missense mutation frequencies in available Omicron and Delta samples.

| Mutation type | Group 1 | Group 2 | Group 1 sample numbers | Group 2 sample numbers | statistic | df | p-value | significance |
|---------------|-----------------|-----------------|------------------------|------------------------|------------|-----------|---------|-----------------|
| Silent | Delta_not_ICU | Delta_ICU | 6 | 4 | -0.3869703 | 5.219775 | 0.714 | not significant |
| Silent | Delta_not_ICU | Omicron_not_ICU | 6 | 16 | 0.7485096 | 5.939187 | 0.483 | not significant |
| Silent | Delta_not_ICU | Omicron_ICU | 6 | 10 | 0.6418841 | 5.927932 | 0.545 | not significant |
| Silent | Delta_ICU | Omicron_not_ICU | 4 | 16 | 0.9155498 | 3.207296 | 0.423 | not significant |
| Silent | Delta_ICU | Omicron_ICU | 4 | 10 | 0.848647 | 3.206737 | 0.455 | not significant |
| Silent | Omicron_not_ICU | Omicron_ICU | 16 | 10 | -0.260579 | 22.501685 | 0.797 | not significant |
| Missense | Delta_not_ICU | Delta_ICU | 6 | 4 | 0.4650685 | 5.382407 | 0.66 | not significant |
| Missense | Delta_not_ICU | Omicron_not_ICU | 6 | 16 | -0.7485096 | 5.939187 | 0.483 | not significant |
| Missense | Delta_not_ICU | Omicron_ICU | 6 | 10 | -0.6418841 | 5.927932 | 0.545 | not significant |
| Missense | Delta_ICU | Omicron_not_ICU | 4 | 16 | -1.0287225 | 3.224352 | 0.375 | not significant |
| Missense | Delta_ICU | Omicron_ICU | 4 | 10 | -0.959252 | 3.223701 | 0.404 | not significant |
| Missense | Omicron_not_ICU | Omicron_ICU | 16 | 10 | 0.260579 | 22.501685 | 0.797 | not significant |

Reference

1. Bolze, A.; White, S.; Basler, T.; Rossi, A.D.; Roychoudhury, P.; Greninger, A.L.; Hayashibara, K.; Wyman, D.; Kil, E.; Dai, H.; et al. Evidence for SARS-CoV-2 Delta and Omicron Co-Infections and Recombination. medRxiv 2022, 2022.03.09.22272113.
2. Abbas, Q.; Kusakin, A.; Sharrouf, K.; Jyakhwo, S.; Komissarov, A.S. Follow-up Investigation and Detailed Mutational Characterization of the SARS-CoV-2 Omicron Variant Lineages (BA.1, BA.2, BA.3 and BA.1.1). bioRxiv 2022, 2022.02.25.481941, doi:10.1101/2022.02.25.481941.
3. Proposal to split B.1.1.529 to incorporate a newly characterised sibling lineage. Available online: <https://github.com/cov-lineages/pango-designation/issues/361> (accessed on 20 April 2022)