Public Health
Seattle & King County

# SARS-CoV-2 Genome Sequencing and Variants in King County, WA

**November 1st, 2021**

## Key findings

- From January 2021 through October 2021, samples from 17,515 COVID-19 cases in King County (18% of all cases) have been sequenced. Of these, 39% (n = 6,927) of cases have had the Delta variant, 28% (n = 4,973) have had the Alpha variant, and 17% (n = 3,044) have had some other Variant of Concern.
- The volume of genome sequencing of COVID-19 cases in King County has significantly increased since the start of the pandemic. Around 30-40% of cases were sequenced in May through July 2021. Although the percent of cases sequenced has fallen to around 10-12% in August and September, the geographic and demographic characteristics of sequenced cases have been broadly similar to cases overall. This suggests current sequencing data provide a reasonable approximation of the distribution of SARS-CoV-2 variants among King County cases.
- Since at least March 2021, the majority of COVID-19 illness in King County was spread through one of four variants: Delta, Alpha, Gamma, and Epsilon.
- The most common variant has changed over time as some variants fade and new variants are identified. The current most common variant in King County is the Delta variant, making up 99.8% of sequenced cases in the last two weeks of complete data (September 27 – October 10).
- Three variants classified as Variants of Concern (VOC) – Beta, Delta, and Gamma – were associated with higher odds of hospitalization compared to earlier variants of SARS-CoV-2 in King County, when adjusted for vaccination, age group, race/ethnicity, and region. Gamma was also associated with higher adjusted odds of death from COVID-19.
- Vaccination appears to mitigate the effect of the Delta and Gamma variants on hospitalization. Fully vaccinated cases exposed to Delta and Gamma variants had lower odds of hospitalization than cases exposed to Delta and Gamma who were not fully vaccinated.
- In addition, fully vaccinated cases exposed to Delta had lower odds of hospitalization than cases exposed to earlier, non-VOC variants and who were not fully vaccinated (the most common scenario at the start of the year).

## Background

### *What is genome sequencing?*

As viruses replicate, their genetic material naturally changes. Genome sequencing is a laboratory method to read the genetic material of a viral specimen and look for these changes. When enough changes occur, the new version of the virus is called a "variant."[1] For public health, sequencing specimens from people with COVID-19 helps identify which variants of SARS-CoV-2, the virus that causes COVID-19, are spreading in our community, and whether particular variants are associated with changes that impact human health. Genome sequencing can also help public health officials identify cases that may be related, since cases with the same variant are more likely to be related than cases with different variants.

### *What is a variant of concern?*

Although many genetic changes in a virus have no discernable effect on virus behavior, some changes can alter how easily the virus spreads or the severity of the disease it causes. Variants of concern (VOC) are versions of the SARS-CoV-2 virus that the Centers for Disease Control and Prevention (CDC) or World Health Organization (WHO) consider concerning because of evidence of any of the following: increased transmission, more serious cases of disease, or reduced effectiveness of treatments, testing, or vaccines. The CDC and WHO also identify variants of interest (VOI), which are variants with genetic mutations that suggest a risk of higher transmissibility, severity, or resistance, but where the evidence is still very limited.[2] As new variants emerge and others fade, the variants classified as VOC and VOI may change. Table 1 summarizes the characteristics of current and past VOC (compared to the original SARS-CoV-2 variant).

**Table 1. Characteristics of Current and Past Variants of Concern[2]**

| Name | Lineage* | Rationale for monitoring | Earliest documented samples |
|---|---|---|---|
| Alpha | B.1.1.7 | - ~50% increased transmission<br>- Potential increased severity | U.K,<br>Sept. 2020 |
| Beta | B.1.351 | - ~50% increased transmission<br>- Some treatments significantly less effective<br>- Potential reduced protection from vaccine-induced or natural immune response | South Africa,<br>May 2020 |
| Delta | B.1.617.2 | - Increased transmission<br>- Potential increased severity<br>- Some treatments potentially less effective<br>- Potential reduced protection from vaccine-induced or natural immune response | India,<br>Oct. 2020 |
| Gamma | P.1 | - Some treatments significantly less effective<br>- Potential reduced protection from vaccine-induced or natural immune response | Brazil,<br>Nov. 2020 |
| Epsilon | B.1.427,<br>B.1.429 | - Early evidence suggested increased transmission, but treatments and vaccines were found to be effective | California,<br>May 2020 |

[1] https://www.cdc.gov/coronavirus/2019-ncov/variants/variant-surveillance.html, October 13, 2021.
[2] https://www.cdc.gov/coronavirus/2019-ncov/variants/variant-info.html#Concern, September 22, 2021.

| | | | |
|---|---|---|---|
| | | - De-escalated from a VOC to a VOI (Jun. 29) and further de-escalated out of VOI status (Aug. 17) as prevalence fell | |

*Lineage names are from the Pango lineage nomenclature.[3]

The variants classified as VOI differ between the CDC and WHO. All VOI are being monitored in King County, and key characteristics of all current VOI are summarized in Table 2 below. Recent terminology changes by the CDC have reclassified many VOC and VOI into a broader category of "Variants Being Monitored." For clarity in this report, which looks at variants since the start of the year, the earlier classifications of VOC and VOI continue to be used. For further information on these variants, see the CDC's variant information website. This report focuses on the current and past VOC present in King County.

**Table 2. Characteristics of Current Variants of Interest[4]**

| Name | Lineage* | Classified By | Rationale for monitoring | Earliest documented samples |
|---|---|---|---|---|
| Eta | B.1.525 | CDC, WHO | - Some treatments potentially less effective<br>- Potential reduced protection from vaccine-induced or natural immune response | Multiple countries, Dec. 2020 |
| Iota | B.1.526 | CDC, WHO | - Some treatments potentially less effective<br>- Potential reduced protection from vaccine-induced or natural immune response | New York, Nov. 2020 |
| Kappa | B.1.617.1 | CDC, WHO | - Some treatments potentially less effective<br>- Potential reduced protection from vaccine-induced or natural immune response | India, Oct. 2020 |
| *No name* | B.1.617.3 | CDC | - Some treatments potentially less effective<br>- Potential reduced protection from vaccine-induced or natural immune response | India, Oct. 2020 |
| Lambda | C.37 | WHO | - Potential increased transmission | Peru, Dec. 2020 |
| Mu | B.1.621 | WHO | - Some treatments potentially less effective<br>- Potential reduced protection from vaccine-induced or natural immune response | Colombia, Jan. 2021 |

*Lineage names used here are from the Pango lineage nomenclature.[5]

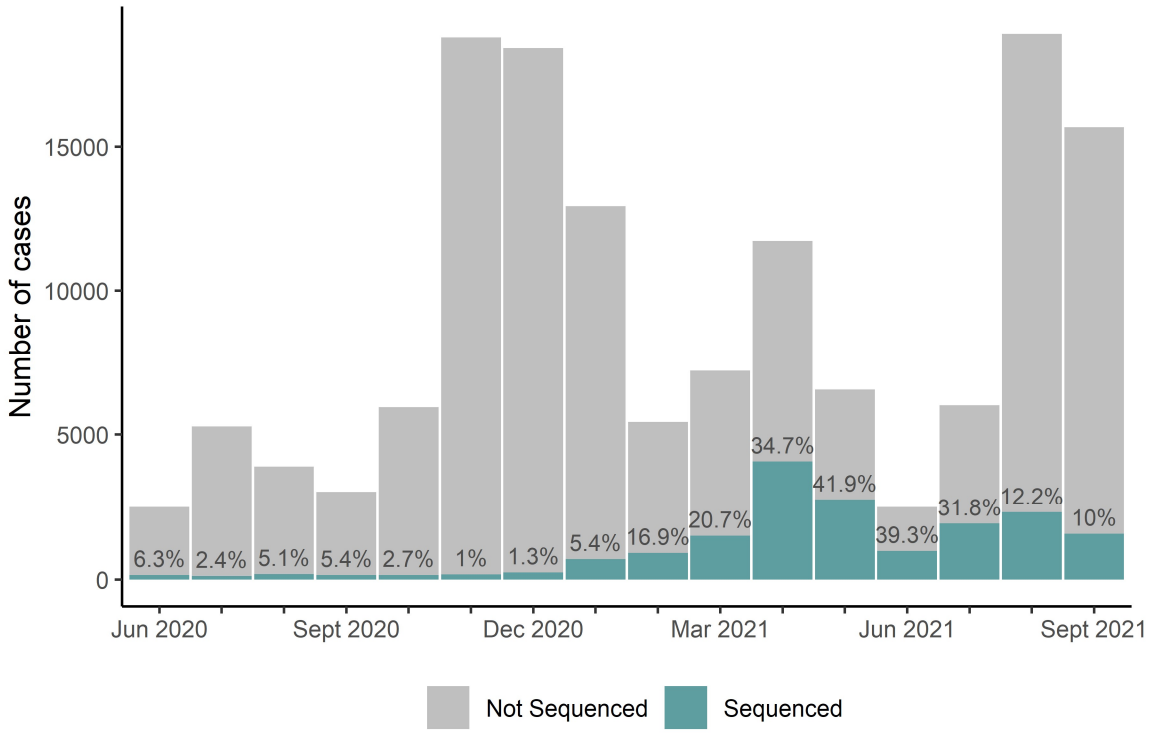
[3] https://cov-lineages.org/, August 3, 2021.
[4] https://www.cdc.gov/coronavirus/2019-ncov/variants/variant-info.html#Concern, September 22, 2021.
[5] https://cov-lineages.org/, August 3, 2021.

## Variants in King County

*When were VOC first identified in King County?*

- The first VOC detected in the county was the Epsilon variant on November 30, 2020. However, only around 1% of cases were sequenced in November 2020, so it is likely additional cases with VOC were present, but not identified.
- Sequencing capacity increased rapidly starting in January 2021. The proportion of cases sequenced rose from 1% in December 2021 to a peak of 41.9% in May 2021. In the more recent months of August and September, 12.2% and 10.0% of cases were sequenced, respectively.

**Figure 1. Percent of cases sequenced each month (by specimen collection date)**




*Which VOC are most common and what are the trends over time?*

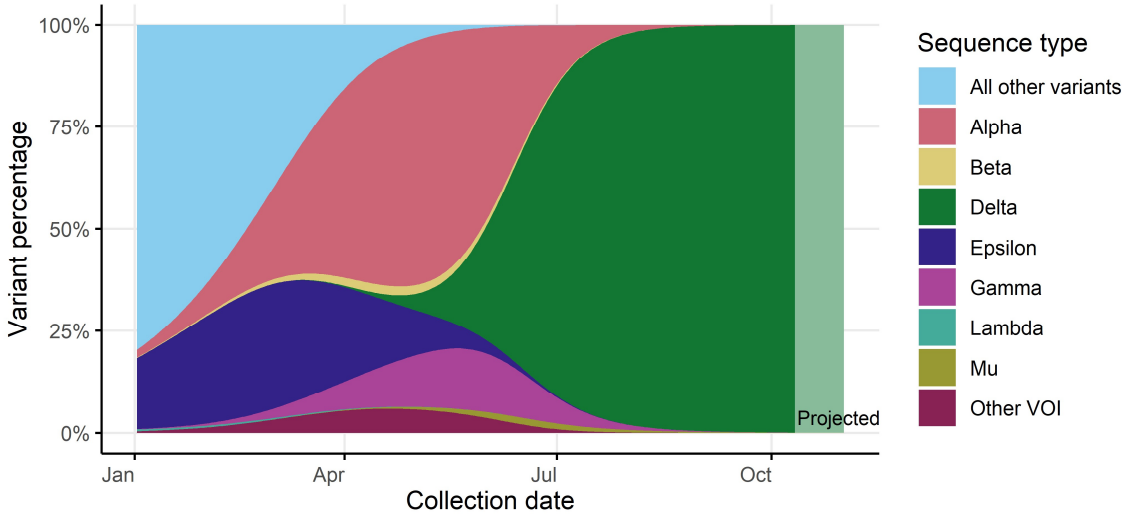
- The prevalence of each VOC has fluctuated significantly over time. In order to visualize the trends in prevalence of each variant over time, regardless of daily fluctuations in reporting, we used a multinomial logistic growth model to estimate the prevalence of each variant per day. This methodology is described further in the Technical Notes.[6] The estimated daily prevalence of each variant among all cases in the county throughout 2021 is shown in Figure 2.
- In early 2021, there was significant diversity in the variants circulating in King County, with no single variant making up the majority.
- Starting in February 2021, the Alpha variant grew increasingly prevalent, peaking in May 2021 when Alpha accounted for 63.7% of sequenced cases. During this time, overall diversity of

[6] See **Proportion model** in the Technical Notes

variants circulating in King County also decreased – with only a few variants accounting for nearly all cases.

- With the emergence of the Delta variant, the prevalence of the Alpha variant began to decline. Delta increased from 1.7% of sequences in April, when it was first detected, to 99.3% of sequences in September. The Delta variant became the most common variant due to its higher transmissibility relative to other existing variants. Following the shift from earlier variants to Delta, overall COVID-19 prevalence in King County also rose throughout July, likely due to a combination of factors, including the higher transmissibility of the Delta variant, as well as loosening of some restrictions and changes in behavior. Based on current trends, Delta will likely remain the dominant variant in future weeks.

**Figure 2. Estimated daily percentage of each variant among all cases in King County from January 1, 2021 to October 11, 2021**




*Since sequencing data from the most recent three weeks is incomplete, the most recent three weeks are projected based on trends up to that point and shown as a lighter region on the figure.

- The other three VOC (Epsilon, Beta, and Gamma) have been observed in the county at lower numbers than Alpha and Delta. The Epsilon variant was the most common variant in King County during March 2021. Since then, it has declined significantly and is only occasionally detected among new cases. The Gamma and Beta variants were never the dominant variants in the county, but they were more prevalent earlier in 2021 and have now also declined to very low levels.
- Since around 10-30% of cases are currently being sequenced (rather than **all** cases), it is possible that other, more rare variants are present in low numbers, but not being detected.
- Table 3 summarizes when each VOC was first identified in the county, when it was most recently detected, and the total number of cases to date.

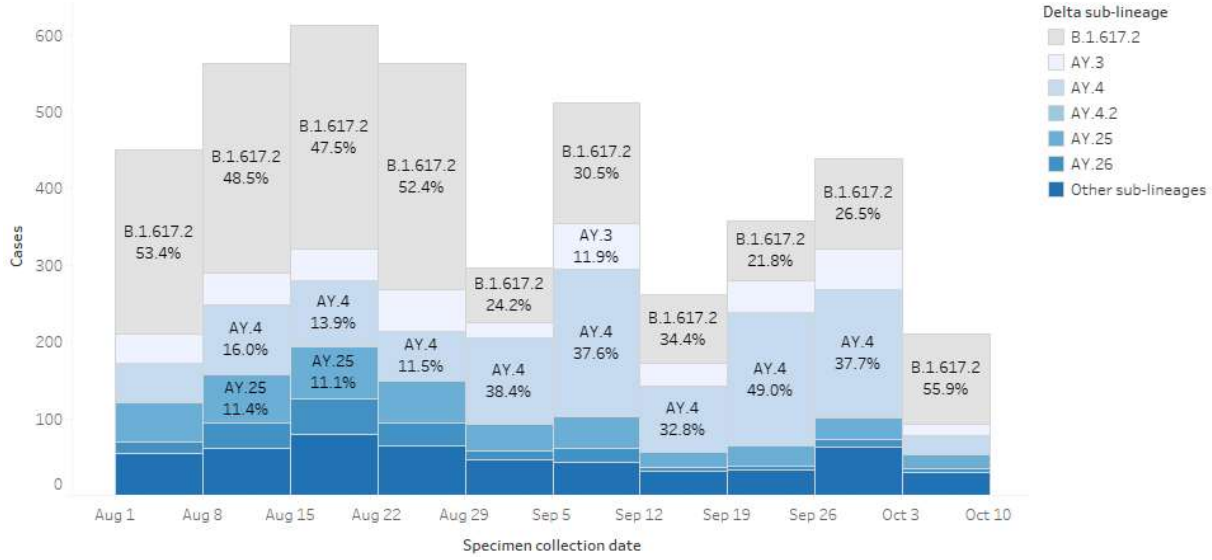
**Table 3. Summary of VOCs identified in King County to date (October 30, 2021)**

| VOC | First Detected | Most Recent Detected | Cases to Date |
|---|---|---|---|
| Epsilon | 2020-11-30 | 2021-09-18 | 1,824 |
| Alpha | 2021-01-08 | 2021-09-26 | 4,973 |
| Beta | 2021-02-18 | 2021-06-29 | 189 |
| Gamma | 2021-03-02 | 2021-08-19 | 1,031 |
| Delta | 2021-03-30 | 2021-10-26 | 6,927 |

*What new variants are currently emerging in King County?*

- In addition to VOC, all VOI are monitored to detect emerging risks. As of October 2021, there are no VOI circulating in significant numbers in King County.
- Sub-lineages of the Delta variant are also being monitored. Delta sub-lineages are versions of the initial Delta variant with slight genetic variations. As the global prevalence of Delta has increased, Delta sub-lineages have been designated to help identify geographic clusters of related cases within the increasingly large category of Delta cases and to track the continued evolution of Delta. The Delta sub-lineages do not necessarily have any functional or epidemiological differences from the original Delta variant and the WHO recommends treating all sub-lineages as the Delta variant. However, PHSKC is closely tracking cases at this level to detect if any noticeable differences arise. Globally, the Delta variant includes the initial lineage, B.1.617.2, and sub-lineages AY.1 through AY.111.[7]
- In the most recent two weeks of complete data in King County, the initial Delta lineage is the most common Delta sub-lineage (36.1%), followed by sub-lineage AY.4 (29.3%). Figure 3 shows the breakdown of sub-lineages among all recent Delta cases by week in the county.

**Figure 3. Sub-lineage proportions among all Delta cases in King County in recent weeks**




[7] https://www.pango.network/new-ay-lineages/, September 17, 2021.

*How many cases with a VOC or VOI have been hospitalized or have died? Are VOCs and VOIs associated with greater odds of hospitalization and death than non-VOC/VOI variants?*

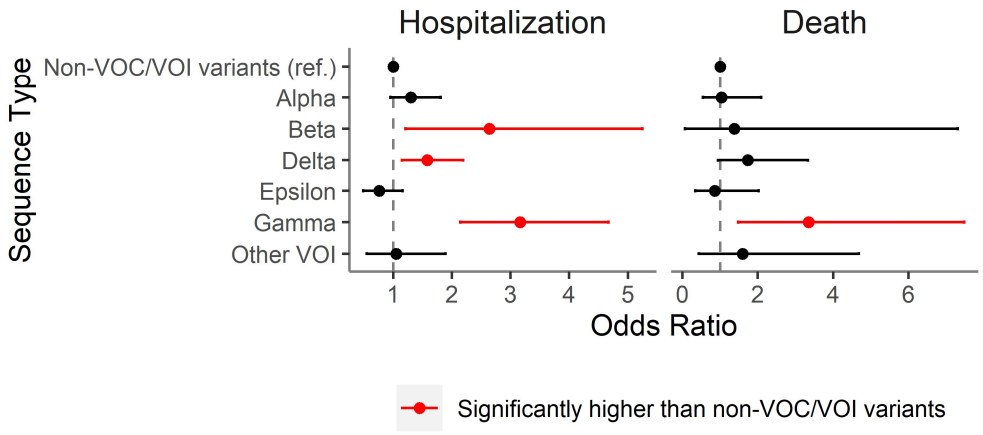
- To assess if odds of hospitalization and death differed by variant type, we compared the proportion of cases exposed to each variant who were hospitalized and who died. We used logistic regression models to estimate odds ratios and the percent hospitalized and percent died by variant type, adjusting for four factors that may affect the relationship between VOC exposure and risk of hospitalization and death. The four factors were vaccination status, age group, race/ethnicity, and region. These factors may be associated, directly or indirectly, with differences in exposure to specific VOCs, as well as differences in risk of hospitalization and death. More details about the model are in the Technical Notes.
- From January through October 2021, 1,975 cases had a variant that was not a VOC or VOI. Of those cases, 61 (3.1%) were hospitalized and 16 (0.8%) died. Among cases with the Alpha variant (n = 4,973), 137 (2.8%) were hospitalized and 23 (0.5%) died. Among cases with the Delta variant (n = 6,925), 190 (2.7%) were hospitalized and 51 (0.7%) died. Among cases with the Gamma variant (n = 1,030), 62 (6.0%) were hospitalized and 14 (1.4%) died.
- Compared to the cases exposed to variants that were not a VOC or VOI, cases exposed to the Delta, Gamma, and Beta variants had higher odds of hospitalization, after adjustment for vaccination status, age group, race/ethnicity, and region (Figure 4). Delta variant cases had 1.6 times higher odds of hospitalization (3.3% versus 2.2%), Gamma variant cases had 3.1 times higher odds (5.8% versus 2.2%), and Beta variant cases had 2.6 times higher odds (5.1% versus 2.2%). Cases exposed to the Alpha or Epsilon variant had similar odds of hospitalization as non-VOC/VOI cases.
- In terms of deaths, cases exposed to the Gamma variant had higher odds of death than cases exposed to non-VOC/VOIs, after adjustment for vaccination status, age group, race/ethnicity and region (Figure 4). Gamma variant cases had 2.9 times higher odds of death (1.8% versus 0.7%). Cases exposed to the Alpha, Beta, Delta, or Epsilon variant had similar odds of death as non-VOC/VOI cases.
- Comparisons of deaths by VOC should be interpreted more cautiously than hospitalizations because the number of deaths is relatively low, so small changes in the number of deaths can cause large changes in the comparisons between VOC.

**Table 4. Cases hospitalized and died of COVID-19 by type of variant, from January 1, 2021 to October 30, 2021**

| | | Hospitalizations | | | Deaths | | |
|---|---|---|---|---|---|---|---|
| Variant Type | Cases | Count | Unadjusted percent of cases | Adjusted[1] percent of cases | Count | Unadjusted percent of cases | Adjusted[1] percent of cases |
| **Non-VOC/VOI** | 1,975 | 61 | 3.1% | 2.2% | 16 | 0.8% | 0.7% |
| Alpha | 4,973 | 137 | 2.8% | 2.8% | 23 | 0.5% | 0.6% |
| Beta | 189 | 10 | 5.3% | 5.1% | 1 | 0.5% | 0.9% |
| Delta | 6,925 | 190 | 2.7% | 3.3% | 51 | 0.7% | 1.2% |
| Epsilon | 1,807 | 36 | 2.0% | 1.7% | 8 | 0.4% | 0.6% |
| Gamma | 1,030 | 62 | 6.0% | 5.8% | 14 | 1.4% | 1.8% |
| Other VOI | 616 | 14 | 2.3% | 2.3% | 4 | 0.6% | 1.1% |

*Red indicates statistically higher odds than non-VOC/VOI variants (the reference).
1. Adjusted for vaccination status, age group, race/ethnicity, and King County sub-region.

**Figure 4. Adjusted* odds ratio of hospitalization and death by type of variant**
*Adjusted for vaccination status, age group, race/ethnicity, and King County sub-region.




*How does vaccination modify the effect of VOCs on odds of hospitalization and death?*

- The risk of hospitalization or death from COVID-19 continues to be much lower for people who are fully vaccinated compared to people who are not fully vaccinated, regardless of the variant of exposure. In King County, since January 17, 2021, individuals who were fully vaccinated were 12 times less likely to be hospitalized than individuals who were not fully vaccinated and 14 times less likely to die, after adjusting for age. More information on the relative risk by vaccine status can be found on **PHSKC's COVID-19 Outcomes by Vaccination Status** dashboard.
- The effect of vaccination on odds of hospitalization and death by variant was analyzed by calculating the odds ratios of hospitalization and death in fully vaccinated and not fully

vaccinated individuals with each variant, compared to not fully vaccinated individuals with a non-VOC/VOI variant. The models were adjusted for age group, race/ethnicity, and region.

- This analysis was done on Delta, Gamma and Alpha variants since those variants either had higher odds of hospitalization and death than non-VOC/VOI variants, or in the case of Alpha, were one of the most frequent variants. Beta cases were excluded due to the small number of total cases.
- Not fully vaccinated cases exposed to the Delta variant had 1.7 times higher odds of hospitalization compared to not fully vaccinated cases exposed to non-VOC/VOI variants. Similarly, not fully vaccinated cases exposed to the Gamma variant had 2.9 times higher odds of hospitalization compared to not fully vaccinated cases exposed to non-VOC/VOI variants. Among cases exposed to the Alpha variant, individuals who were not fully vaccinated had similar odds of hospitalization as cases exposed to non-VOC/VOI variants.
- Vaccination reduced the effects of the Delta and Gamma variants on odds of hospitalization. Although among individuals who were not fully vaccinated, those exposed to the Delta and Gamma variants had higher odds of hospitalization compared to those exposed to non-VOC/VOI variants, we did not observe this relationship among fully vaccinated individuals. Fully vaccinated cases with the Delta variant had significantly *lower* odds of hospitalization compared to not fully vaccinated cases exposed to non-VOC/VOI variants (OR: 0.43; 95% CI: 0.24, 0.78). Similarly, there is no significant difference in odds of hospitalization between fully vaccinated individuals exposed to the Gamma variant and not fully vaccinated individuals exposed to non-VOC/VOI variants.
- We observed similar trends with deaths, but due to the relatively small number of deaths our estimates lack precision, which limits their interpretation.
- Figure 5 presents the odds ratios for hospitalization and death by variant and vaccination status, and Table 5 shows the counts, which were used to calculate the odds ratios.

**Figure 5. Odds ratios of hospitalization and death by type of variant and vaccination status, from January 1, 2021 to October 30, 2021**

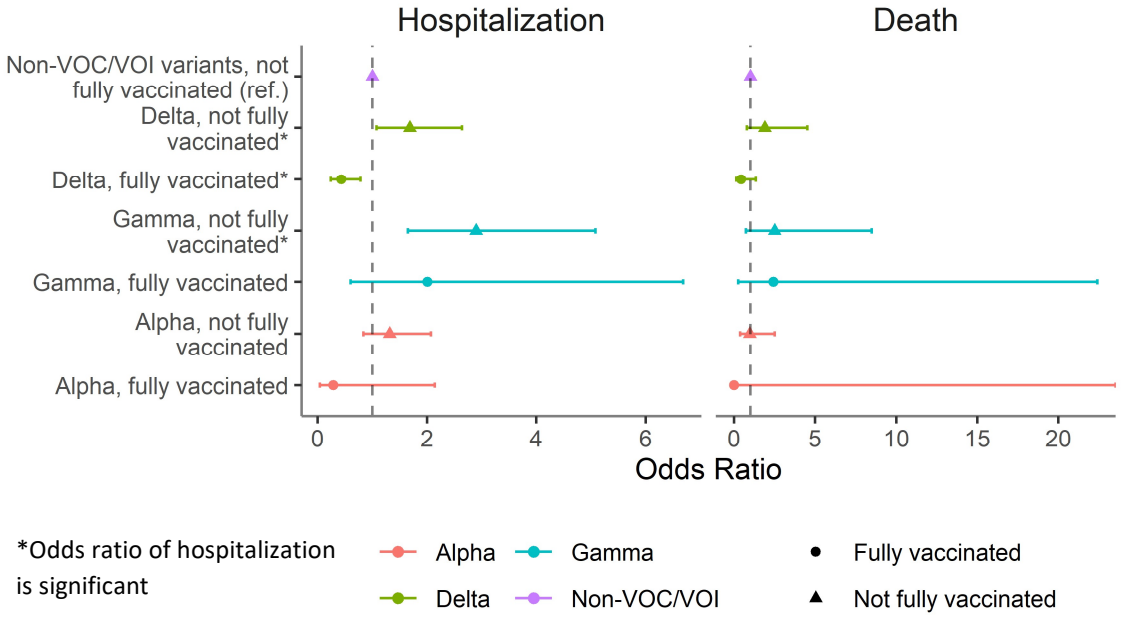


**Table 5. Cases, hospitalizations, and deaths from COVID-19 by type of variant and vaccination status, from January 1, 2021 to October 30, 2021**

| | Cases | | Hospitalizations | | Deaths | |
|---|---|---|---|---|---|---|
| Sequence Type | Fully Vaccinated | Not Fully Vaccinated | Fully Vaccinated | Not Fully Vaccinated | Fully Vaccinated | Not Fully Vaccinated |
| Non-VOC/VOI | 18 | 1,957 | 1 | 60 | 0 | 16 |
| Alpha | 175 | 4,798 | 3 | 134 | 2 | 21 |
| Beta | 7 | 182 | 0 | 10 | 0 | 1 |
| Delta | 2,581 | 4,344 | 41 | 149 | 12 | 39 |
| Epsilon | 52 | 1,755 | 3 | 33 | 0 | 8 |
| Gamma | 81 | 949 | 9 | 53 | 4 | 10 |
| Other VOI | 43 | 573 | 1 | 13 | 0 | 4 |

### *Limitations*

Sampling

- Only a portion of COVID-19 cases are sequenced. The conclusions drawn about overall trends in the county rely either on models, or on an assumption that sequenced cases are reasonably representative of all cases. Sequenced cases are likely a fairly representative sample of all cases because multiple labs, including the University of Washington (which performs the most sequencing for King County), are sequencing a random sample of all positive specimens of high enough quality from their testing facilities. However, PHSKC also requests sequencing for cases that are suspected vaccine breakthroughs or associated with notable outbreaks
- A table comparing characteristics of sequenced and unsequenced cases is included in the appendix. Though the two groups are broadly similar, a higher proportion of sequenced cases were under 50 years of age (82% compared to 76%) and Hispanic/Latinx (18% vs 15%), and a lower proportion of sequenced cases were hospitalized compared to unsequenced cases (2.9% vs 4.4%).

Timeliness

- Once a specimen is collected for a standard COVID-19 PCR test, the specimen may also be sequenced. Several labs in King County perform sequencing and upload de-identified results to an open-access genomic sequencing database called GISAID. Sequences are reviewed by the Washington Department of Health and linked to other testing and demographic data collected by the state.
- Currently the median time between when a specimen is collected and when it is sequenced and reported to PHSKC is 23 days (IQR: 17 to 90 days). This means more than half of samples sequenced take longer than three weeks to be reported. Because of the fast-changing nature of COVID-19 and genomic variants, the data presented in this report may not completely capture the prevalence and epidemiology of COVID-19 variants in King County as of today.

### *Directions for future work*

- Time since vaccination may play a role in the outcomes observed in different VOCs. However, it's difficult to compare across variants due to the similar timeline of when the vaccine rollout occurred and when variants shifted to be predominately Delta. As a result, almost all data on people who have been vaccinated for more than a few months is for the Delta variant, and there is very little similar data on other variants to compare it to. We are working on a separate analysis to better understand the impact of time since vaccination.

## Appendix

**Appendix Table 1. Comparison of characteristics of sequenced and unsequenced cases in 2021**

| | Sequenced | Unsequenced |
|---|---|---|
| Number of Cases | 17515 | 81396 |
| Age Group (%) | | |
| 0-9 years old | 1640 (9.4) | 7562 (9.3) |
| 10-19 years old | 2443 (13.9) | 9922 (12.2) |
| 20-29 years old | 4252 (24.3) | 17073 (21.0) |
| 30-39 years old | 3594 (20.5) | 15927 (19.6) |
| 40-49 years old | 2404 (13.7) | 11772 (14.5) |
| 50-59 years old | 1722 (9.8) | 9337 (11.5) |
| 60-69 years old | 948 (5.4) | 5827 (7.2) |
| 70-79 years old | 336 (1.9) | 2567 (3.2) |
| 80+ years old | 175 (1.0) | 1376 (1.7) |
| Unknown | 1 (0.0) | 33 (0.0) |
| Race/Ethnicity (%) | | |
| American Indian / Alaska Native, not Hispanic | 156 (0.9) | 690 (0.8) |
| Asian, not Hispanic | 2144 (12.2) | 9219 (11.3) |
| Black, not Hispanic | 1745 (10.0) | 7441 (9.1) |
| Hispanic or Latino, Any Race | 3096 (17.7) | 11792 (14.5) |
| Native Hawaiian / Pacific Islander, not Hispanic | 447 (2.6) | 2097 (2.6) |
| Other or Multi-Racial, not Hispanic | 1063 (6.1) | 4703 (5.8) |
| Unknown | 1955 (11.2) | 9959 (12.2) |
| White, not Hispanic | 6909 (39.4) | 35495 (43.6) |
| Region (%) | | |
| Auburn, Kent, and Federal Way | 4200 (24.0) | 20326 (25.0) |
| Bellevue, Issaquah and Mercer Island | 1483 (8.5) | 5698 (7.0) |
| Burien, Renton, Tukwila and SeaTac | 2325 (13.3) | 13014 (16.0) |
| Central Seattle | 1588 (9.1) | 6560 (8.1) |
| East King County | 582 (3.3) | 4085 (5.0) |
| Kirkland, Redmond, Bothell, and Woodinville | 1079 (6.2) | 5936 (7.3) |
| North Seattle and Shoreline | 2369 (13.5) | 7687 (9.4) |
| Not Geocoded | 790 (4.5) | 3684 (4.5) |
| South East King County | 1435 (8.2) | 7338 (9.0) |
| Vashon Island | 12 (0.1) | 104 (0.1) |
| West Seattle, South Seattle, Delridge and Highline | 1652 (9.4) | 6964 (8.6) |
| Hospitalizations (%) | 510 (2.9) | 3571 (4.4) |
| Deaths (%) | 117 (0.7) | 587 (0.7) |

# Technical Notes

## Proportion model

To estimate trends in the prevalence of each variant over time, we ran a multinomial logistic growth model on all sequenced samples from King County residents collected from January 1, 2021 through October 11, 2021. The percentage of cases represented by each variant was estimated by day. The model was used to smooth out daily fluctuations in counts of each variant and to estimate the prevalence of each variant in the most recent three weeks, since data reporting is highly incomplete during this time period. Thank you to the Institute for Disease Modeling (IDM) for sharing this methodology with PHSKC.

## Hospitalization and death percentages and odds ratios

We used logistic regression models to estimate odds ratios and the percent hospitalized and percent died by variant type, adjusting for four factors that may affect the relationship between VOC exposure and risk of hospitalization and death. One logistic regression model was used for hospitalizations and one model for deaths. Cases before 2021 were excluded because sequencing data before 2021 is highly incomplete. The reference category was variants that were not a VOC or VOI.

The four factors we adjusted for were vaccination status, age group, race/ethnicity, and King County sub-region (aggregate health reporting area). Vaccination status was dichotomized as fully vaccinated and not fully vaccinated, where fully vaccinated was defined as at least 14 days after completion of a 2-dose mRNA vaccine series (Pfizer or Moderna) or a single dose of the Johnson & Johnson/Janssen vaccine. These factors may be associated, directly or indirectly, with differences in exposure to specific VOCs as well as differences in risk of hospitalization and death. These factors may be related to VOC exposure and risk of hospitalization and death through indirect pathways. For example, individuals in different racial/ethnic groups may have had differences in which variants they were exposed to because of differences in the prevalence of each VOC in the communities they lived in or settings they congregated in. Racial/ethnic differences in risk of hospitalization and death may be due to issues related to structural and institutional racism, which affect health care access and utilization, and other social determinants of health.

Adjustment for these variables allows us to more accurately compare variants by estimating how many hospitalizations and deaths would have occurred if each variant infected groups of people with the same age, race/ethnicity, vaccination, and regional distribution.

## Effect modification of the VOC and risk of hospitalization and death relationship by vaccination status

To determine if vaccination modified the effect of VOCs on the odds of hospitalization and death, we used logistic regression models similar to the ones described above, but with vaccination status as an effect modifier instead. The purpose of this report is to describe the spread and impact of VOCs in the county; the impact of VOCs on hospitalizations compares fully vaccinated cases exposed to VOCs to cases representing the most common scenario at the start of the year: cases who were not fully vaccinated and exposed to earlier, non-VOC/VOI variants. By defining this group as the reference group, the odds ratios can be interpreted as whether the odds of hospitalization are higher or lower following

exposure to a given VOC with a given vaccination status compared to the typical situation at the start of the year. We analyzed the Alpha, Delta, and Gamma variants in comparison to that reference group. Beta cases were excluded due to the small number of total cases. In addition to including vaccination status as an effect modifier, the regressions adjusted for age group, race/ethnicity, and King County sub-region. A similar analysis including samples from all Washington state residents was conduction by the Washington Department of Health. Methodological details and results from that study have been previously published elsewhere (Parades MI, Lunn MS, Famulare M, Frisbie LA, Painter I et al. 2021. Associations between SARS-CoV-2 variants and risk of COVID-19 hospitalization among confirmed cases in Washington State: a retrospective cohort study. medRxiv doi: 10.1101/2021.09.29.21264272).

## Data sources

The following datasets were used to produce this report.

1. Genetic sequencing and electronic lab reporting data provided by the Washington Department of Health through the Washington Disease Reporting System (WDRS), including whether sequencing was performed, lineage if determined to be a VOC, specimen collection date, and PCR testing results. Demographic information on all individuals tested for COVID-19 and information on hospitalizations and deaths were also available through this dataset.
2. Genetic sequencing data provided by the public genome sequencing database, GISAID. GISAID accession numbers provided by the Washington Department of Health enabled us to link the additional sequencing data in GISAID, namely lineages beyond those designated as VOC, to the testing and demographic data from WDRS.
3. COVID-19 vaccination data from the Washington Immunization Information System, including dose date, dose number, and manufacturer. These data were linked to the demographic and testing data from WDRS based on a probabilistic match on first name, last name, and date of birth. Vaccine breakthroughs were defined as a positive test 14 or more days after final vaccine dose, in alignment with the definition from the CDC.

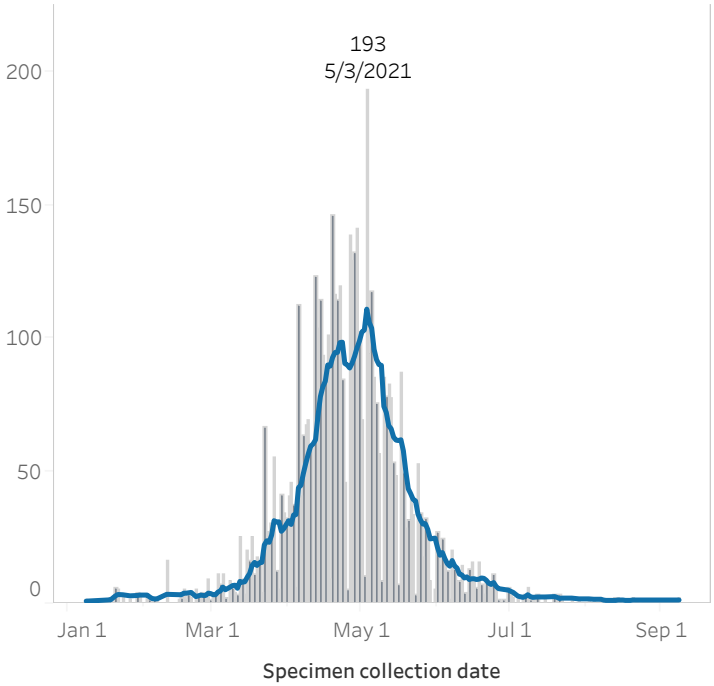
## Summaries by variant of concern

# COVID-19 Alpha variant cases in King County

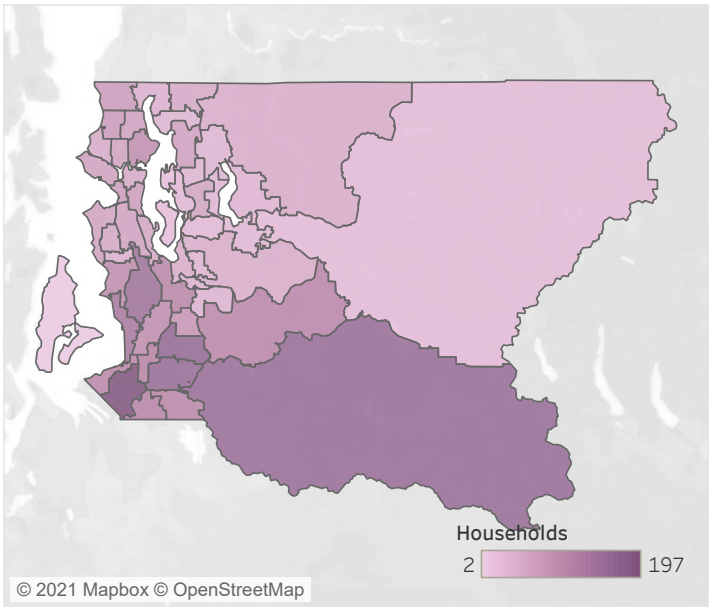
All data is through October 21, 2021 (a three week delay).

| | Cases | % of Sequenced Cases | Hospital-izations | % of Hospitalizations | Deaths | % of Deaths | Fully Vaccinated Cases |
|---|---|---|---|---|---|---|---|
| **Overall (in 2021)** | 4,972 | 24.2% | 137 | 2.8% | 23 | 0.5% | 175 |
| **Most recent 14 days** | No cases with the Alpha variant detected in the most recent 14 days. | | | | | | |

### Daily case count and 7-day moving average

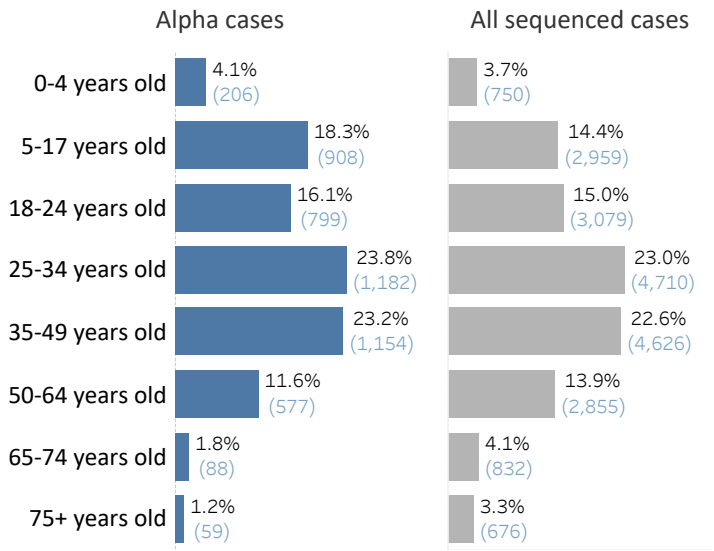



### Households with a Alpha variant case

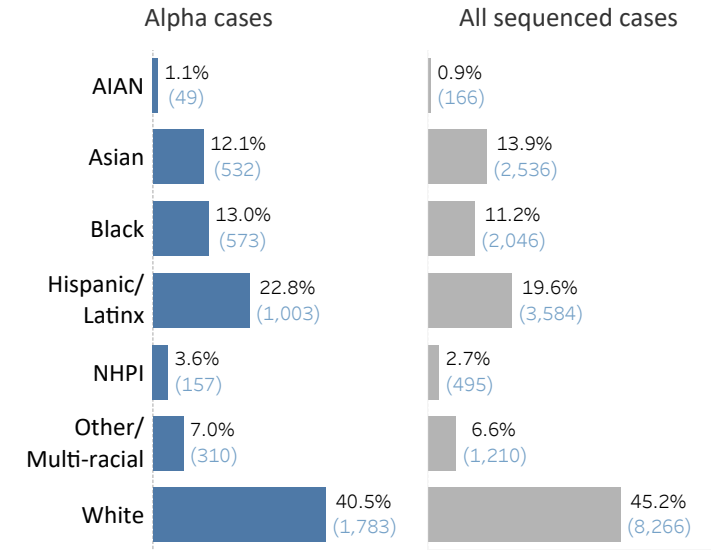



*Household defined as all cases that share a distinct residential address.

### Age




### Race/Ethnicity

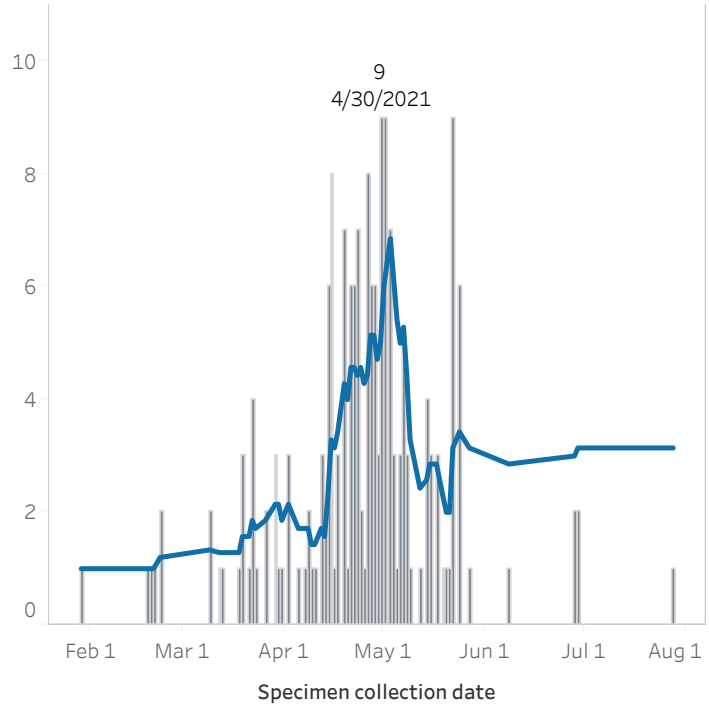


# COVID-19 Beta variant cases in King County

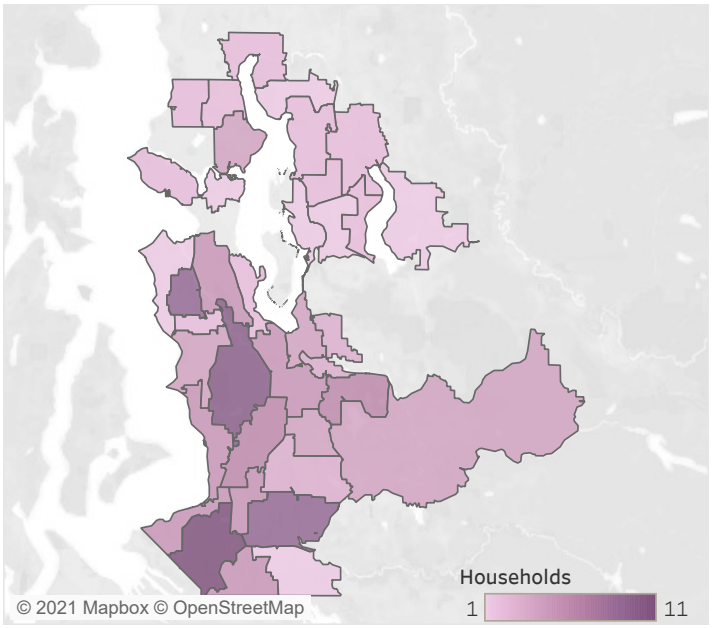
All data is through October 21, 2021 (a three week delay).

| | Cases | % of Sequenced Cases | Hospital-izations | % of Hospitalizations | Deaths | % of Deaths | Fully Vaccinated Cases |
|---|---|---|---|---|---|---|---|
| **Overall (in 2021)** | 189 | 0.9% | 10 | 5.3% | 1 | 0.5% | 7 |
| **Most recent 14 days** | No cases with the Beta variant detected in the most recent 14 days. | | | | | | |

## Daily case count and 7-day moving average

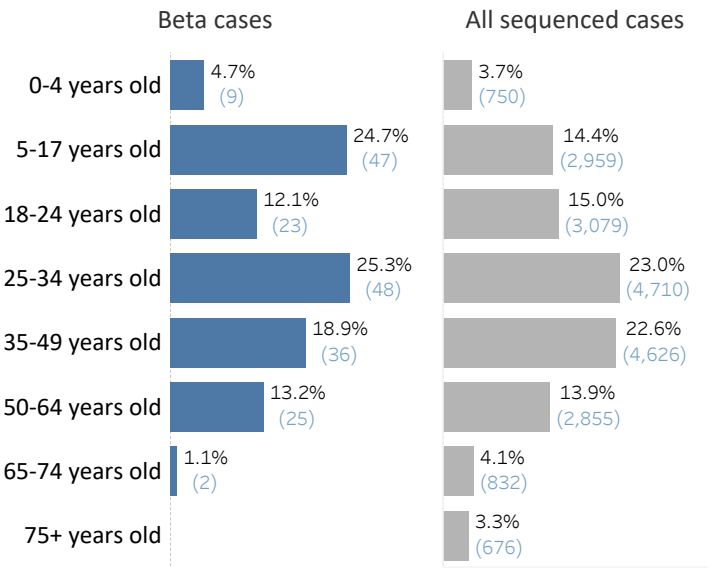



## Households with a Beta variant case

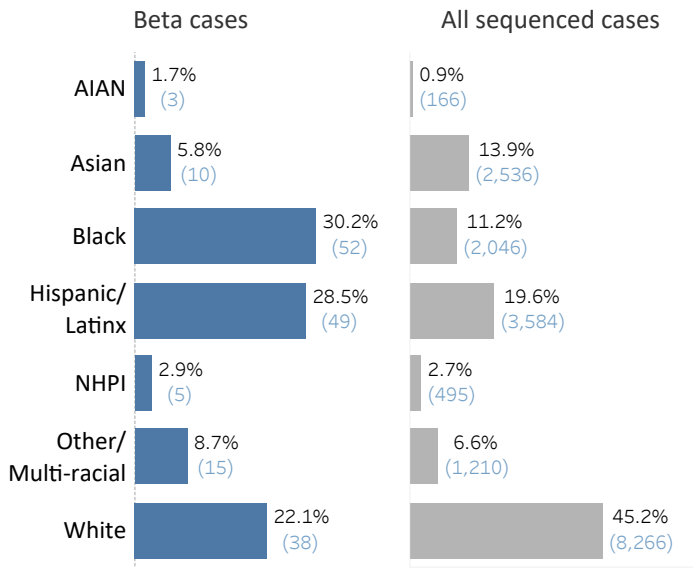



*Household defined as all cases that share a distinct residential address.

## Age




## Race/Ethnicity

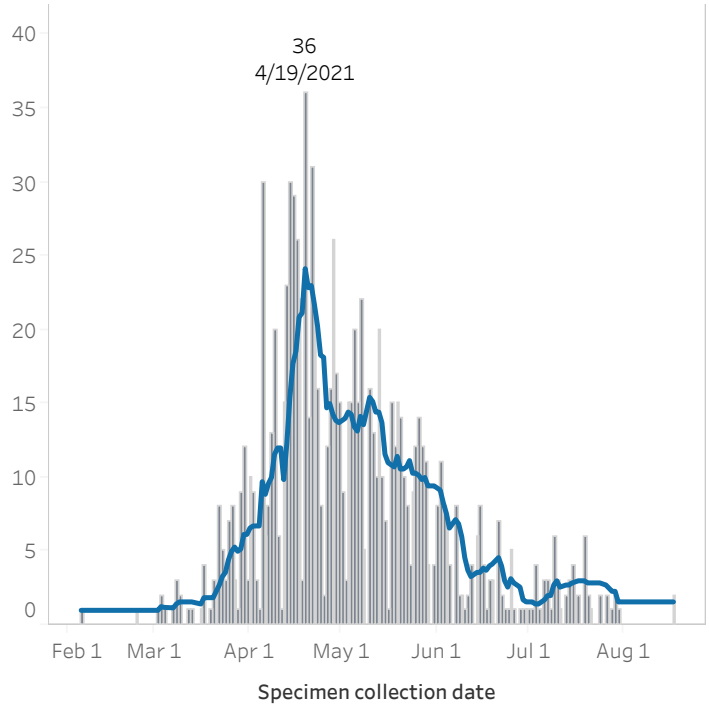


# COVID-19 Gamma variant cases in King County

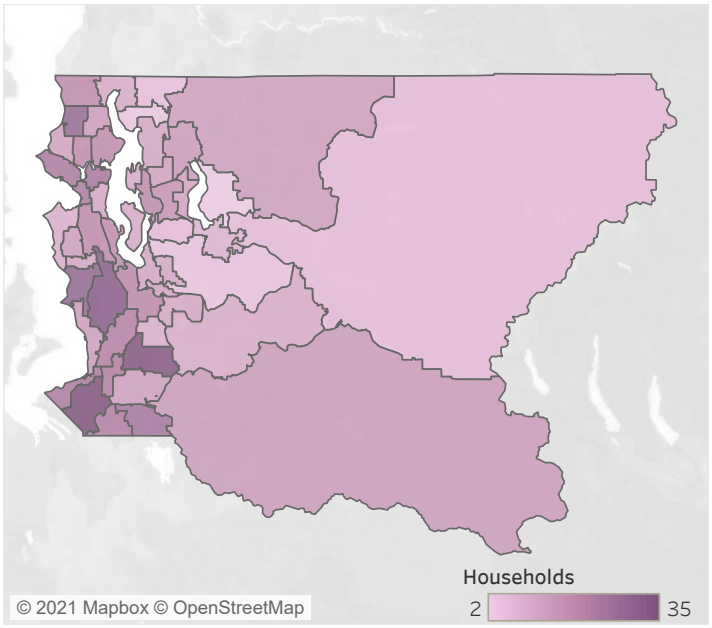
All data is through October 21, 2021 (a three week delay).

| | Cases | % of Sequenced Cases | Hospital-izations | % of Hospitalizations | Deaths | % of Deaths | Fully Vaccinated Cases |
|---|---|---|---|---|---|---|---|
| **Overall (in 2021)** | 1,031 | 5.0% | 62 | 6.0% | 14 | 1.4% | 81 |
| **Most recent 14 days** | No cases with the Gamma variant detected in the most recent 14 days. | | | | | | |

## Daily case count and 7-day moving average

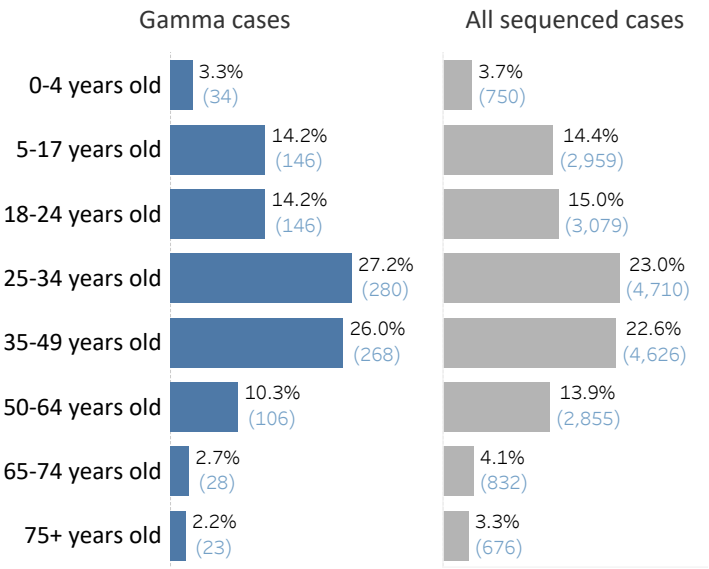



## Households with a Gamma variant case

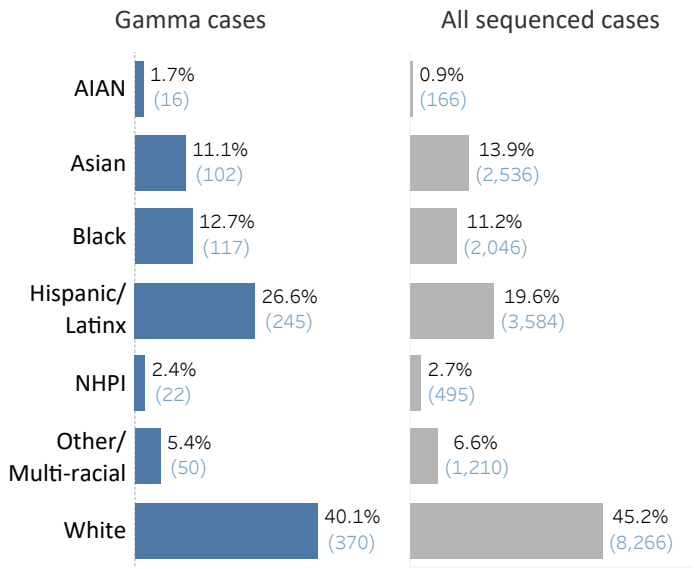



*Household defined as all cases that share a distinct residential address.

## Age




## Race/Ethnicity

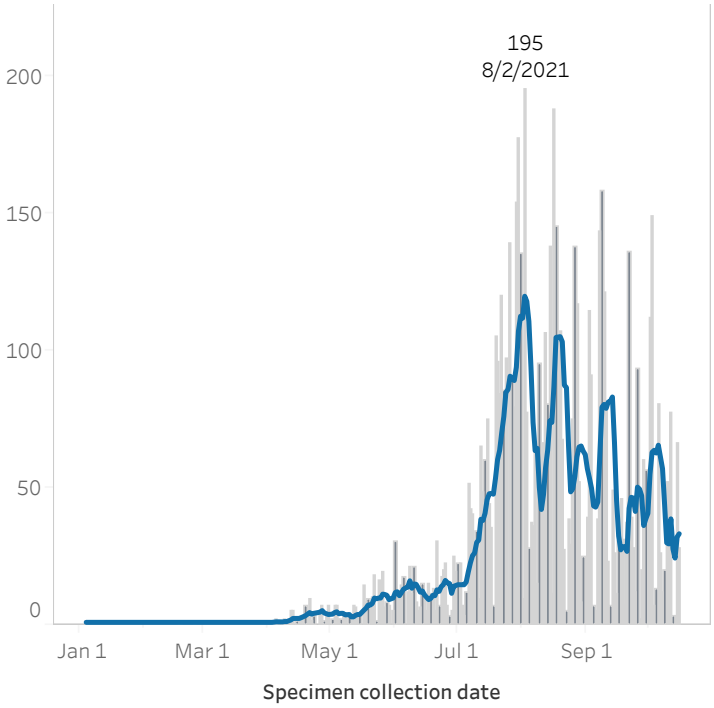


# COVID-19 Delta variant cases in King County

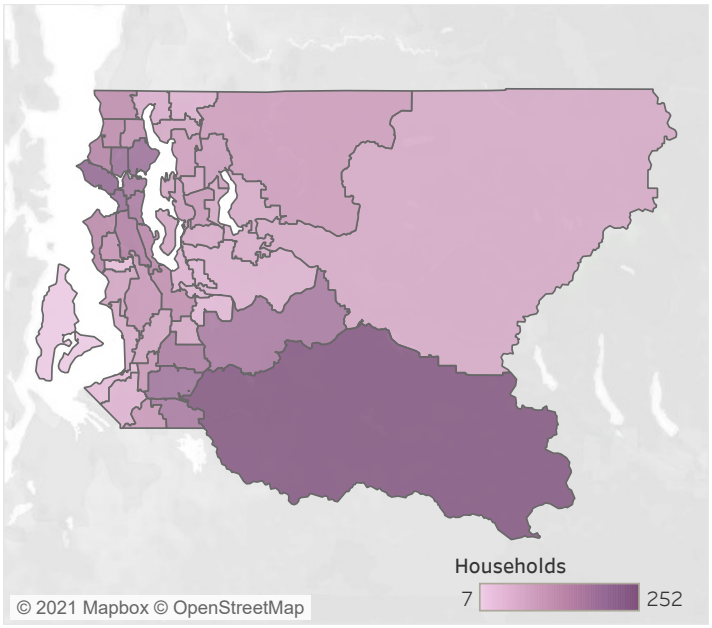
All data is through October 21, 2021 (a three week delay).

| | Cases | % of Sequenced Cases | Hospital-izations | % of Hospitalizations | Deaths | % of Deaths | Fully Vaccinated Cases |
|---|---|---|---|---|---|---|---|
| **Overall (in 2021)** | 6,923 | 33.7% | 190 | 2.7% | 52 | 0.8% | 2,580 |
| **Most recent 14 days** | 265 | 100.0% | 13 | 4.9% | 2 | 0.8% | 111 |

## Daily case count and 7-day moving average

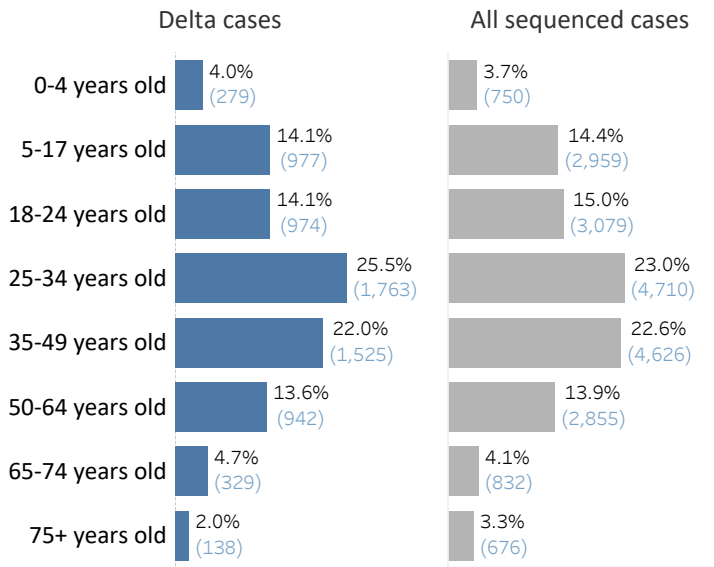



## Households with a Delta variant case

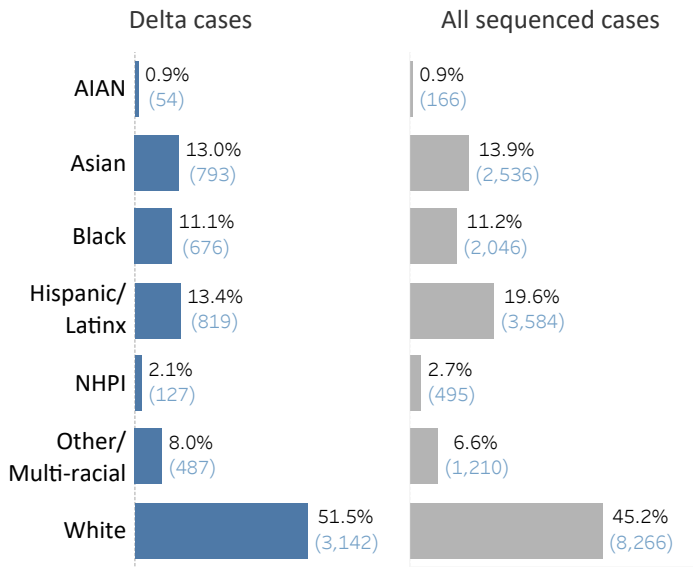



*Household defined as all cases that share a distinct residential address.

## Age




## Race/Ethnicity

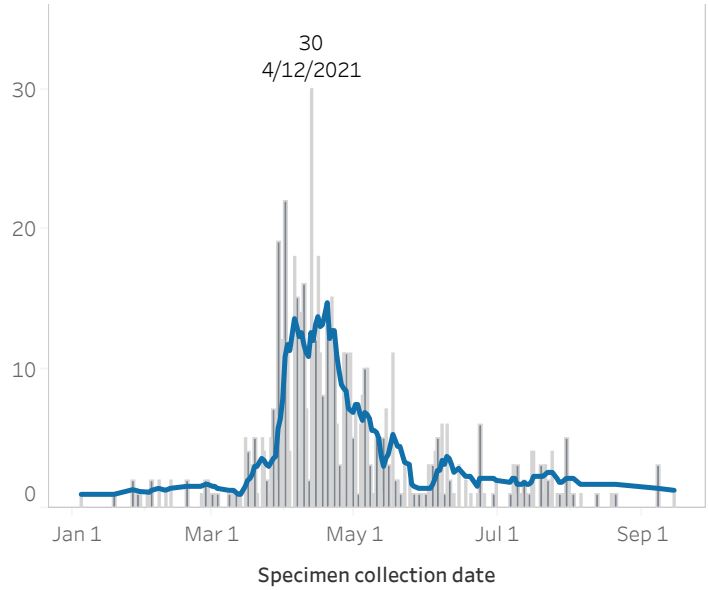


# COVID-19 VOI cases in King County

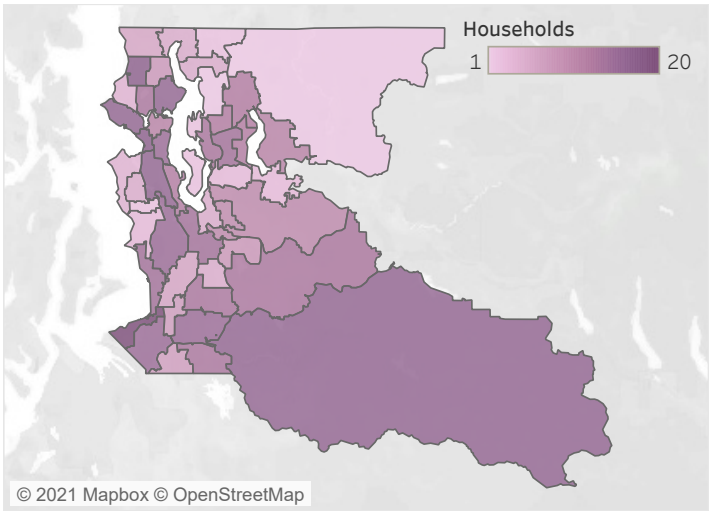
All data is through October 21, 2021 (a three week delay).

| | Variant | Cases | % of Sequenced Cases | Hospital-izations | % of Hospital izations | Deaths | % of Deaths | Fully Vaccinated Cases |
|---|---|---|---|---|---|---|---|---|
| Overall (in 2021) | B.1.617.3 | 1 | 0.0% | 0 | 0.0% | 0 | 0.0% | 0 |
| | Eta (B.1.525) | 32 | 0.2% | 0 | 0.0% | 0 | 0.0% | 1 |
| | Iota (B.1.526) | 436 | 2.1% | 9 | 2.1% | 3 | 0.7% | 15 |
| | Kappa (B.1.617.1) | 37 | 0.2% | 1 | 2.7% | 0 | 0.0% | 1 |
| | Lambda (C.37) | 16 | 0.1% | 1 | 6.3% | 0 | 0.0% | 0 |
| | Mu (B.1.621) | 80 | 0.4% | 4 | 5.0% | 1 | 1.3% | 26 |
| Most recent 14 days | No cases with a VOI detected in the most recent 14 days. | | | | | | | |

## Daily case count and 7-day moving average

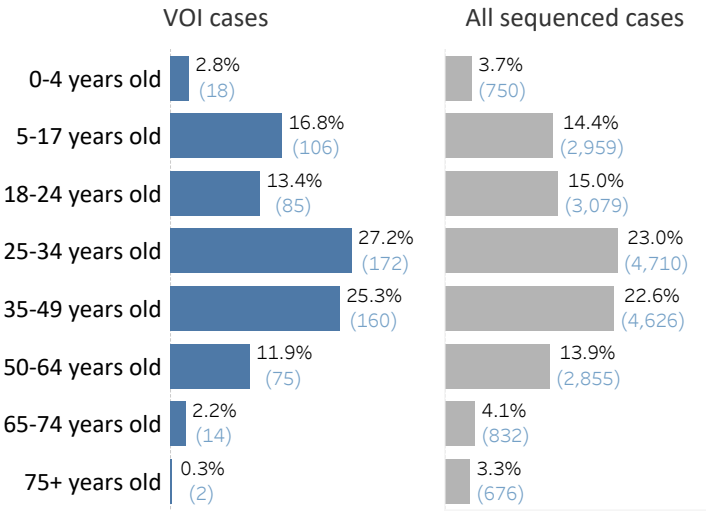


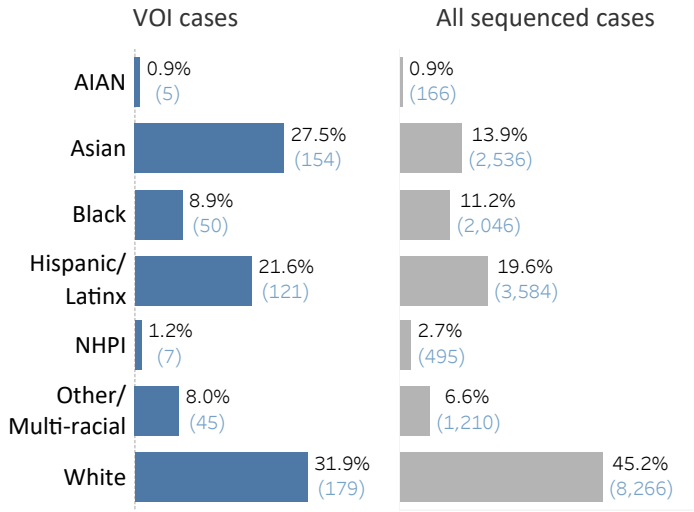

## Households with a VOI case




*Household defined as all cases that share a distinct residential address.

## Age




## Race/Ethnicity