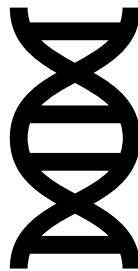
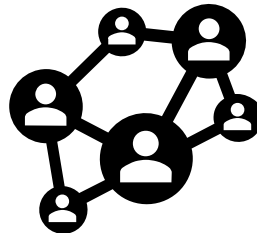


# Alaska COVID-19 Genomic Surveillance

Situation Report

17 August 2021



Prepared by the Alaska Sequencing Consortium\*,  
including Devin M. Drown<sup>1</sup>, Jayme Parker<sup>2</sup>, Lisa Smith<sup>2</sup>, Eric Bortz<sup>3</sup>, Jack Chen<sup>1,2</sup>

<sup>1</sup>Institute of Arctic Biology, University of Alaska Fairbanks, Fairbanks, AK 99775

<sup>2</sup>Alaska State Public Health Laboratories, Fairbanks, AK 99775

<sup>3</sup>Department of Biological Sciences, University of Alaska Anchorage, Anchorage, AK 99508

Correspondences: [dmdrown@alaska.edu](mailto:dmdrown@alaska.edu) [j.chen@alaska.edu](mailto:j.chen@alaska.edu) [jayme.parker@alaska.gov](mailto:jayme.parker@alaska.gov)

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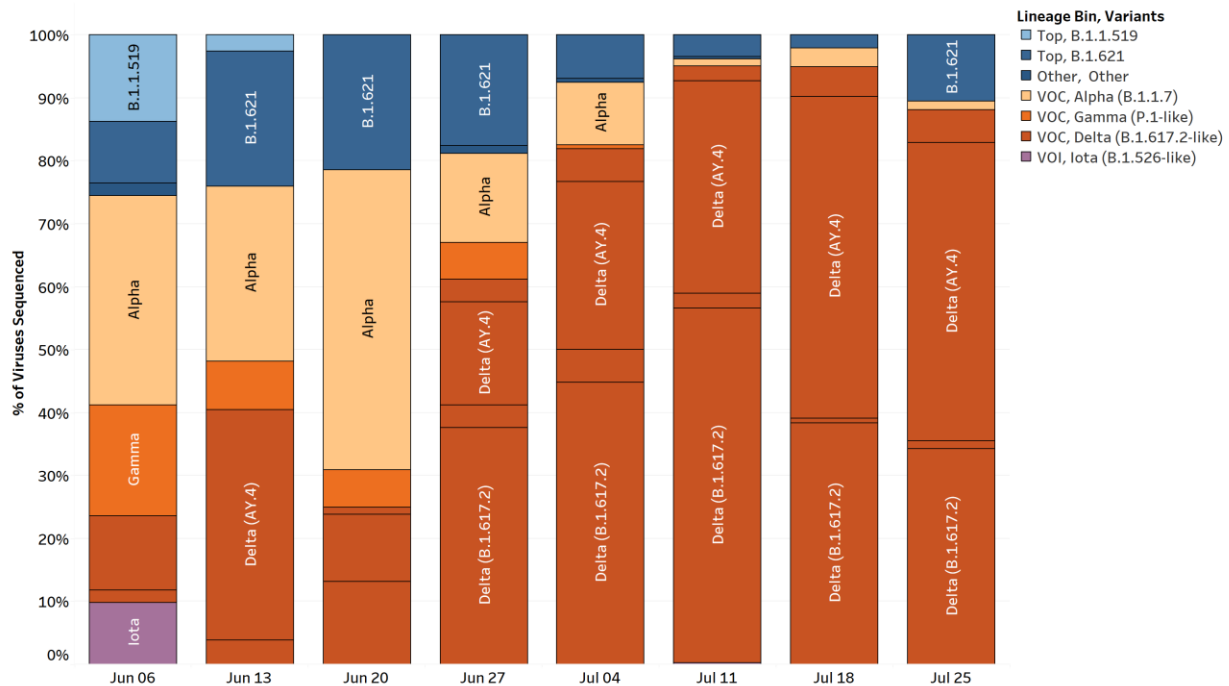
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## Executive Summary: Sequence Analysis of COVID-19 in Alaska

- **Variant of Concern (VOC) Delta (B.1.617.2-like) accounts for almost all newly detected cases.** To date, we have detected 876 cases in multiple locations across the state. During the week beginning July 25, Delta represented 88% of sequenced cases in Alaska. According to data from the CDC, the proportion of cases attributed to Delta nationwide is estimated to be 97% for the two-week period ending Aug 7. ([CDC Variant Proportions website](#)).
- **Added designation for VOC Delta sub-lineages (B.1.617.2, AY.1-12):** We have added proportions of currently circulating sub-lineages of Delta. These lineages remain the Delta variant. Their designation does not imply any functional biological difference from B.1.617.2. In Alaska, we have detected the original lineage, B.1.617.2 (34%), as well as a significant proportion of AY.4 (47%). Sub-lineages AY.3 and AY.12 make up 6%.
- **VOC Alpha (B.1.1.7) proportion has appreciably declined.** To date, we have detected 450 cases across the state. During the week beginning July 25, Alpha represented less than 2% of sequenced cases in Alaska. This is a decline from early June when 33% of sequenced cases were Alpha. Alpha proportions have decreased nationwide and now represent 1% of cases.
- **No recent cases of VOC Beta (B.1.351) or VOC Gamma (P.1) detected.**
- **No recent cases of Variant of Interest (VOI) Epsilon (B.1.429/427), Eta (B.1.525), Iota (B.1.526), or Zeta (P.2) detected.**

## Recent Prevalence of Variants in Alaska



\*Estimated prevalence per week period beginning on the date. This estimate is based on genome sequencing from a non-targeted convenience sample of cases. This estimate excludes cases sequenced from targeted contact tracing.

## Variants of Concern/Interest

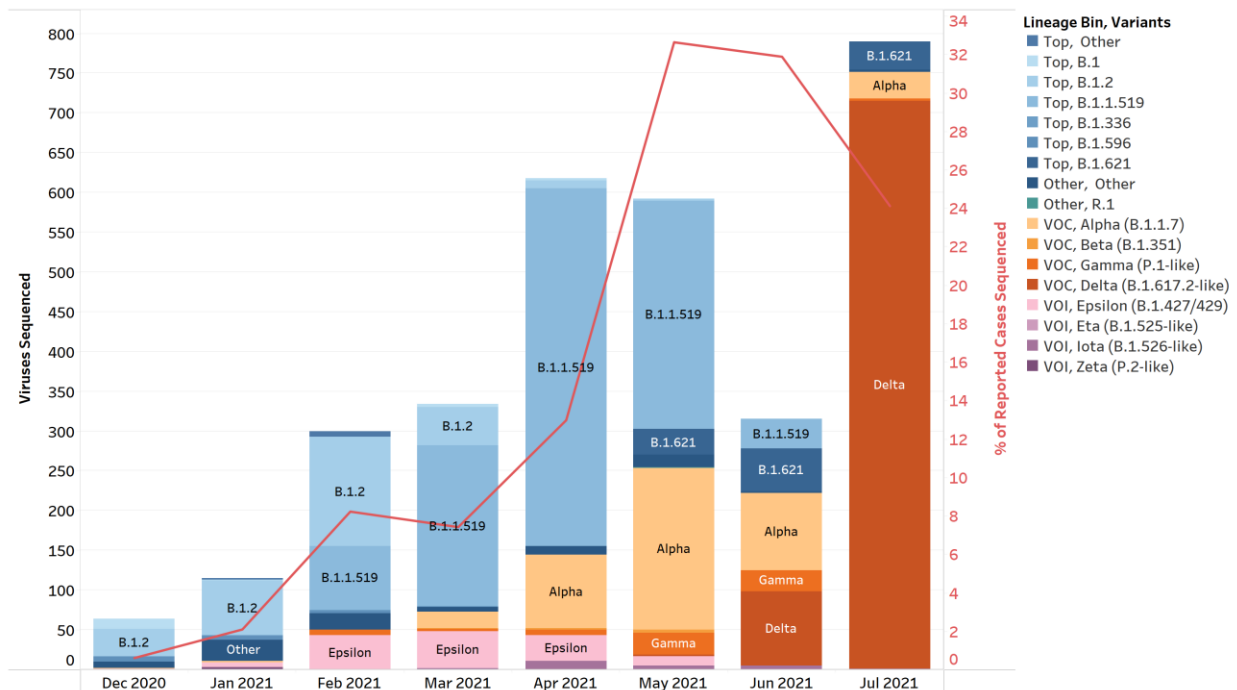
Name	Lineages	Cases Detected	Change from Previous Report*	First Identified in Alaska
VOC Alpha	B.1.1.7	450	+11	20 December 2020
VOC Beta	B.1.351	7	0	20 March 2021
VOC Gamma	P.1-like	74	+1	8 February 2021
VOC Delta	B.1.617.2-like	876	+299	30 May 2021
VOI Epsilon	B.1.427/429	140	+1	24 December 2020
VOI Eta	B.1.525	1	0	16 March 2021
VOI Iota	B.1.526	22	0	4 February 2021
VOI Zeta	P.2	4	0	27 January 2021

\*Detected variants are identified from sequencing a combination of retrospective and contemporary SARS-CoV-2 positive specimens. Therefore, changes to the previous report do not always reflect recent collections but add to the overall understanding of variant proportions

## Table: Genomic Sequencing Effort in Alaska

	Samples
New Genomes released since last report	+339
Total Genomes released on GISAID	3492-3153

## Variants Identified in Alaska



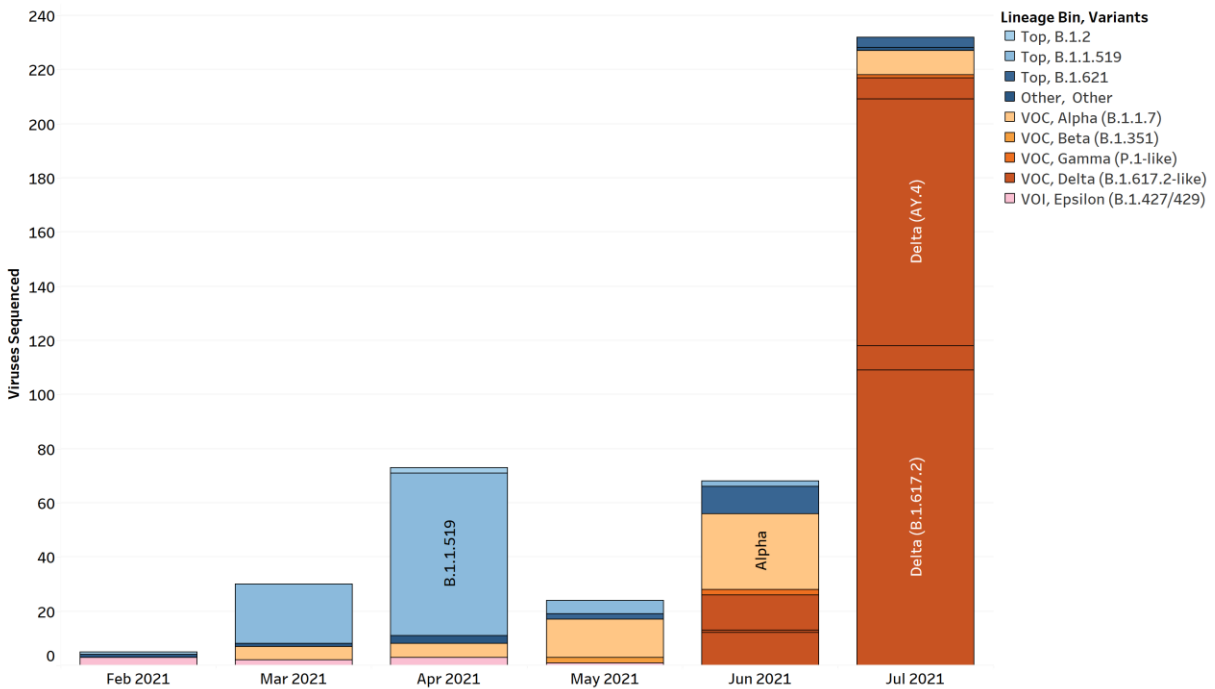
\*Note that SARS-CoV-2 genome sequencing may not be a random sample of all cases. This figure does not estimate the prevalence of the population.

## Table: Vaccine Breakthrough Investigation

<b>Patients under investigation for Vaccine Breakthrough (VB)</b>	1799
<b>Specimens submitted to SPHL for VB investigation</b>	708 (35.6%)
<b>Specimens fitting criteria for sequencing</b>	549
<b>Sequencing effort to assess VB</b>	525
<b>Successful virus lineage identifications</b>	437 (83.2%)
<b>Specimens in progress</b>	20+

Vaccine breakthrough refers to cases of COVID-19 which occur 14 or more days after receiving the second dose in a two-dose COVID-19 vaccine series or a single dose of a one-dose COVID-19 vaccine series. VBs may have a very low virus titer and are difficult to sequence.

## Identified Vaccine Breakthrough Lineages

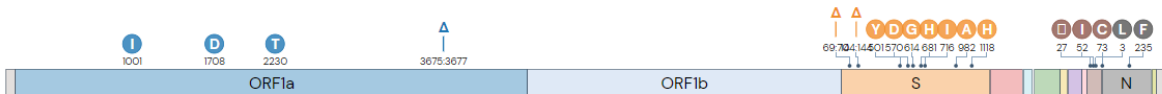


## Variants of Concern, Individual Lineage Reports

### Alpha - B.1.1.7

Alpha was first identified in the United Kingdom, also known as: Variant of Concern B.1.1.7, 202012/01, VOC-202012/01, 20B/501Y.V1, 20I/501Y.V1. This variant contains the N501Y mutation and a short deletion in the Spike (S) protein. This variant is concerning because it has shown to be significantly more transmissible (~50%) than the original SARS-CoV-2 lineage. Alpha does not appear to evade vaccine-induced neutralizing antibody responses. Alpha is still circulating in the US.

**In Alaska:** Alpha was detected in December 2020 in the Anchorage/Mat-Su region. Cases have been detected throughout Alaska.



### Beta - B.1.351

Beta (also known as: B.1.351, 20H/501Y.V2) was first identified in South Africa and is circulating in the US. The B.1.351 has both N501Y and E484K mutations in the Spike protein. This variant is concerning because it is significantly more transmissible (~50%) than the original SARS-CoV-2 lineages. Preliminary studies suggest Beta, like Gamma, may escape some vaccine-induced and naturally acquired antibody responses. However, as with all VOCs, the Pfizer, Moderna, and Johnson & Johnson/Janssen vaccines remain largely effective against this lineage.

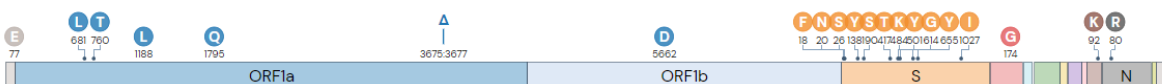
**In Alaska:** First identified in March 2021 in the Anchorage/Mat-Su region. Cases were detected in the Anchorage/Mat-Su and Southeast regions in May.



### Gamma - P.1

Gamma was first identified in Brazil, also known as: Variant of Concern P.1, B.1.1.28.1, 20J/501Y.V3. This variant contains three key mutations in the S gene: E484K, N501Y, and K417T. While preliminary studies suggest the Pfizer, Moderna, and Johnson & Johnson/Janssen vaccines currently deployed in Alaska may have reduced efficacy against Gamma, these vaccines remain largely effective against this lineage and demonstrate protection against serious illness, hospitalizations, and death. Recent analyses suggest that Gamma may be more transmissible with higher risk of severe disease, to some degree.

**In Alaska:** Gamma was identified in early February 2021 in the Anchorage/Mat-Su region. Cases have been detected throughout Alaska.

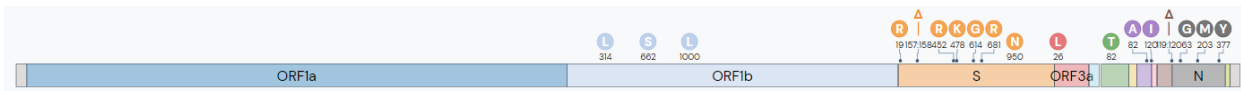


### Delta - B.1.617.2-like

Delta was first identified in India in late 2020, also known as: Variant of Concern B.1.617.2, 20A/S:478K. The Delta variant has become widespread over the last number of months and B.1.617.2 is the predominant lineage in many countries worldwide. In addition to B.1.617.2, Delta also contains lineages AY.1 – AY.12. The AY lineages break up B.1.617.2-like viruses into smaller related clusters that can be tracked separately. These lineages remain classified as the Delta variant and their designation as AY does not imply any functional biological difference from B.1.617.2.

Delta contains key mutations in the S gene: K417N, T478K, L452R, N501Y, P681R, and others of unknown significance. The spectrum of mutations in Delta evades binding of neutralizing antibodies induced by natural infection or vaccines to a measurable extent. This variant has significantly increased transmissibility. It is currently unclear whether Delta is associated with increased severity of infection. According to CDC data, Delta is currently driving case numbers and COVID-19 hospitalizations in the US, particularly among unvaccinated individuals.

**In Alaska:** Delta was identified in late May 2021 in the Anchorage/Mat-Su region. Cases have now been detected in many additional locations in Alaska. Delta VOC has predominated the surge of cases in July-August 2021 in Alaska. In Alaska, we have the original B.1.617.2 as well as a significant proportion of AY.4. AY.3 and AY.12 make up 6% of sequenced cases.



## Variants of Interest, Individual Lineage Reports

### Epsilon - B.1.429 & B.1.427

Epsilon, includes B.1.429 and a related B.1.427 lineages, were first identified in California and known as: CA VUI1. The prevalence of these VOI grew in California from initial observations in summer 2020 and has spread to many other states. Research suggests an increased transmission (~20%). Deescalated from a VOC on June 29, 2021 due to the significant decrease in the proportion of B.1.429 lineage viruses circulating nationally and available data indicating that vaccines and treatments are effective against this variant. This variant is characterized by the L452R mutation in the S gene and is genetically like B.1.351 but lacks several key mutations.

**In Alaska:** These variants have been detected across Alaska beginning in December 2020. This VOI has not been detected in Alaska since May 2021.

### Iota - B.1.526

Iota (also known as B.1.526) was first identified in New York and has begun circulating in other parts of the US. Little is known about this variant, but some genomes contain the E484K mutation in the Spike protein.

**In Alaska:** The B.1.526 variant was identified in February 2021, in the Anchorage-Mat Su region. Cases have been detected throughout Alaska.

### Eta - B.1.525

Eta (also known as B.1.525) is circulating in New York and has begun circulating in other parts of the US. Little is known about this variant. The genomes contain the E484K, Q677H, and F888L mutations in the Spike protein.

**In Alaska:** The B.1.525 variant was identified in March 2021, in the Gulf Coast region. This VOI has not been detected recently in Alaska.

### Zeta - P.2

Zeta was first identified in Brazil and is also known as: P.2 or B.1.1.28.2. Little is known about this variant beyond that its prevalence grew in Brazil. This variant contains the E484K mutation in the Spike protein but lacks many key mutations in other variants of concern.

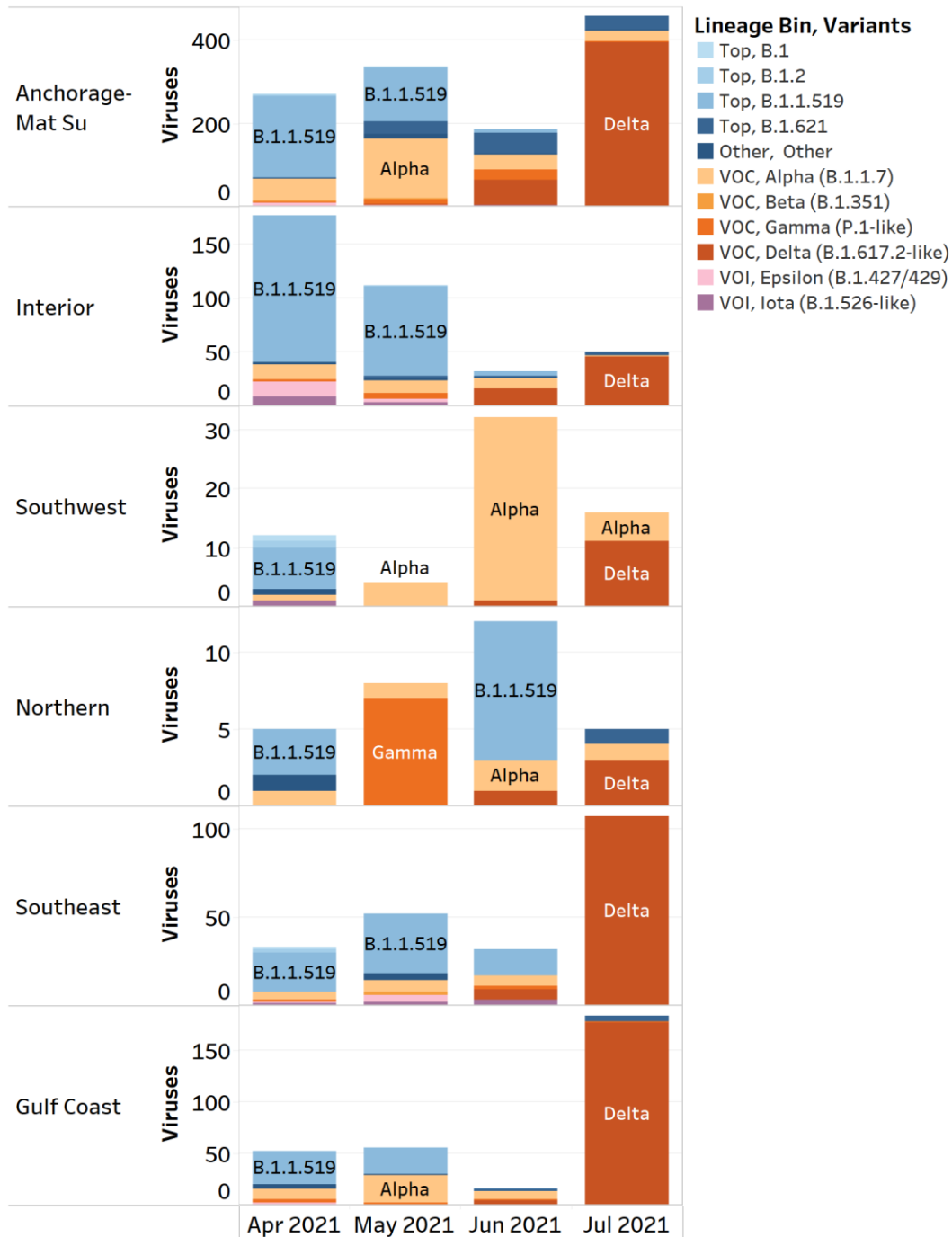
**In Alaska:** The P.2 variant was identified in January 2021, in the Southwest Alaska region. This VOI has not been detected recently in Alaska.



## Lineages in Alaska

### Lineages by Alaska Location

The graphs below indicate the number of genomes sequenced from Alaska cases per month within economic regions (map below). Colors and labels indicate PANGO lineages label the sections. Note that vertical axis ranges are independent across regions.



## Additional Resources

**CDC COVID-19 National Genomic Surveillance Dashboard** - <https://www.cdc.gov/coronavirus/2019-ncov/cases-updates/variant-surveillance/genomic-surveillance-dashboard.html>

**SARS-CoV-2 (hCoV-19) Mutation Situation Reports** - <https://outbreak.info/situation-reports>

**Nextstrain SARS-CoV-2 resources** - <https://nextstrain.org/sars-cov-2/>

**CoVariants** - <https://covariants.org/>

**PANGO Lineage Reports** - [https://cov-lineages.org/global\\_report.html](https://cov-lineages.org/global_report.html)

Locations within Alaska are grouped by Economic Region as seen below.

