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Pathogen Genomics Surveillance

TX SARS-CoV-2 Variant Surveillance Network

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Texas Department of State Health Services

October 30, 2023

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DISCLAIMER

The information presented today is based on current preliminary data and on CDC's recent guidance. Information is subject to change.

October 30, 2023

Texas SARS-CoV-2 Variant Surveillance Network Project

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- The Texas Department of State Health Services (DSHS), in partnership with The University of Texas Health Science Center at Houston School of Public Health (UTHealth SPH), has created a statewide SARS-CoV-2 variant surveillance monitoring network (Network).
- The Network is comprised of:
  - 8 Academic institutions
  - 1 Hospital System
  - 2 Commercial labs
  - 1 Public health lab
- Short-term goal: Increase SARS-CoV-2 sequencing capacity and analysis in Texas for electronic reporting of the data to DSHS.
- Long-term goals:
  - Establish the infrastructure & capacity for genomic surveillance and epidemiology with a statewide reach and local impact that could be applied to other emerging infectious disease pathogens.
  - Identify skills and develop training to build a pipeline of trained public health professionals to cover current workforce gaps & meet future public health needs.
- Initiated on 9/30/2021

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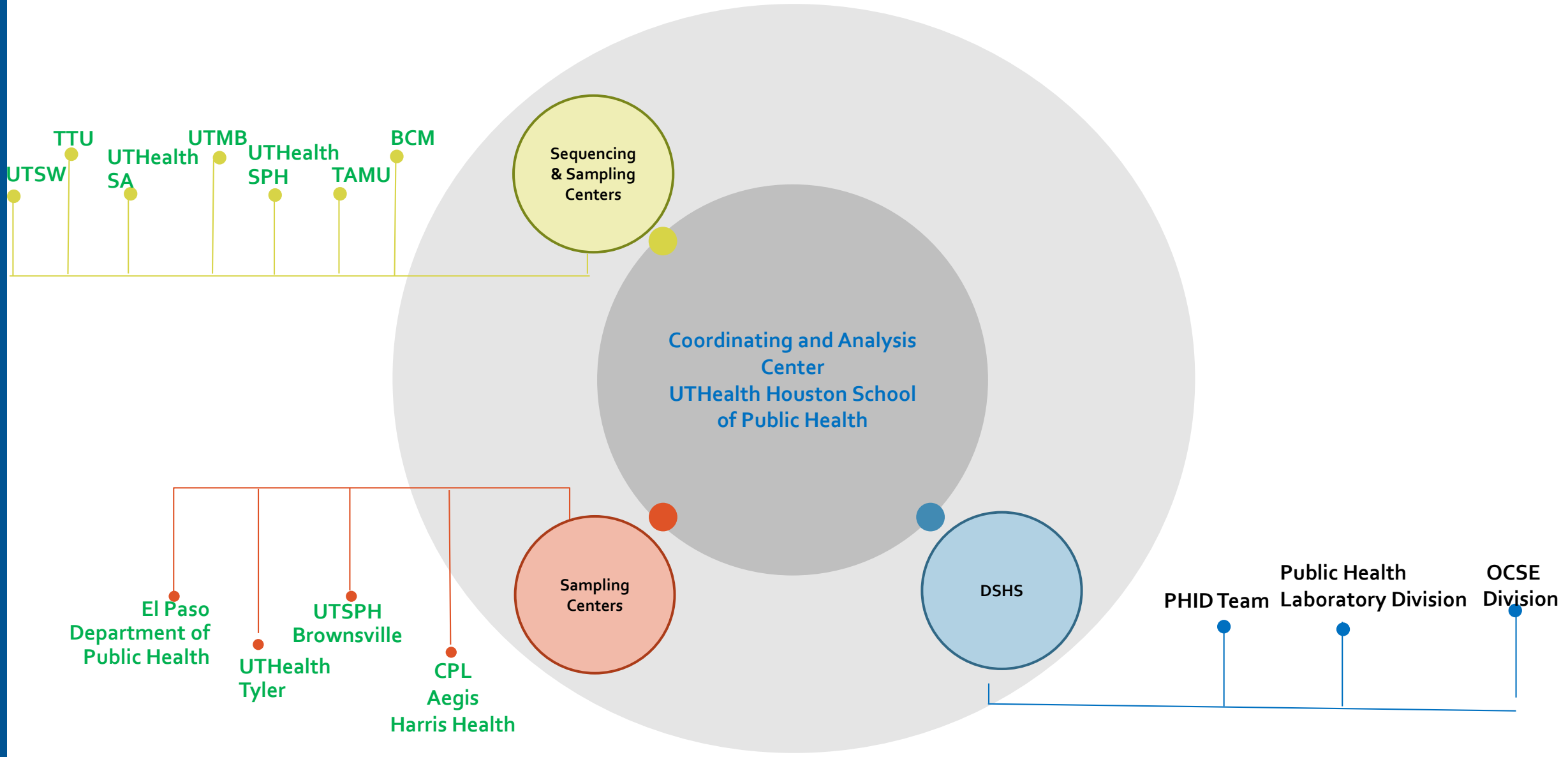
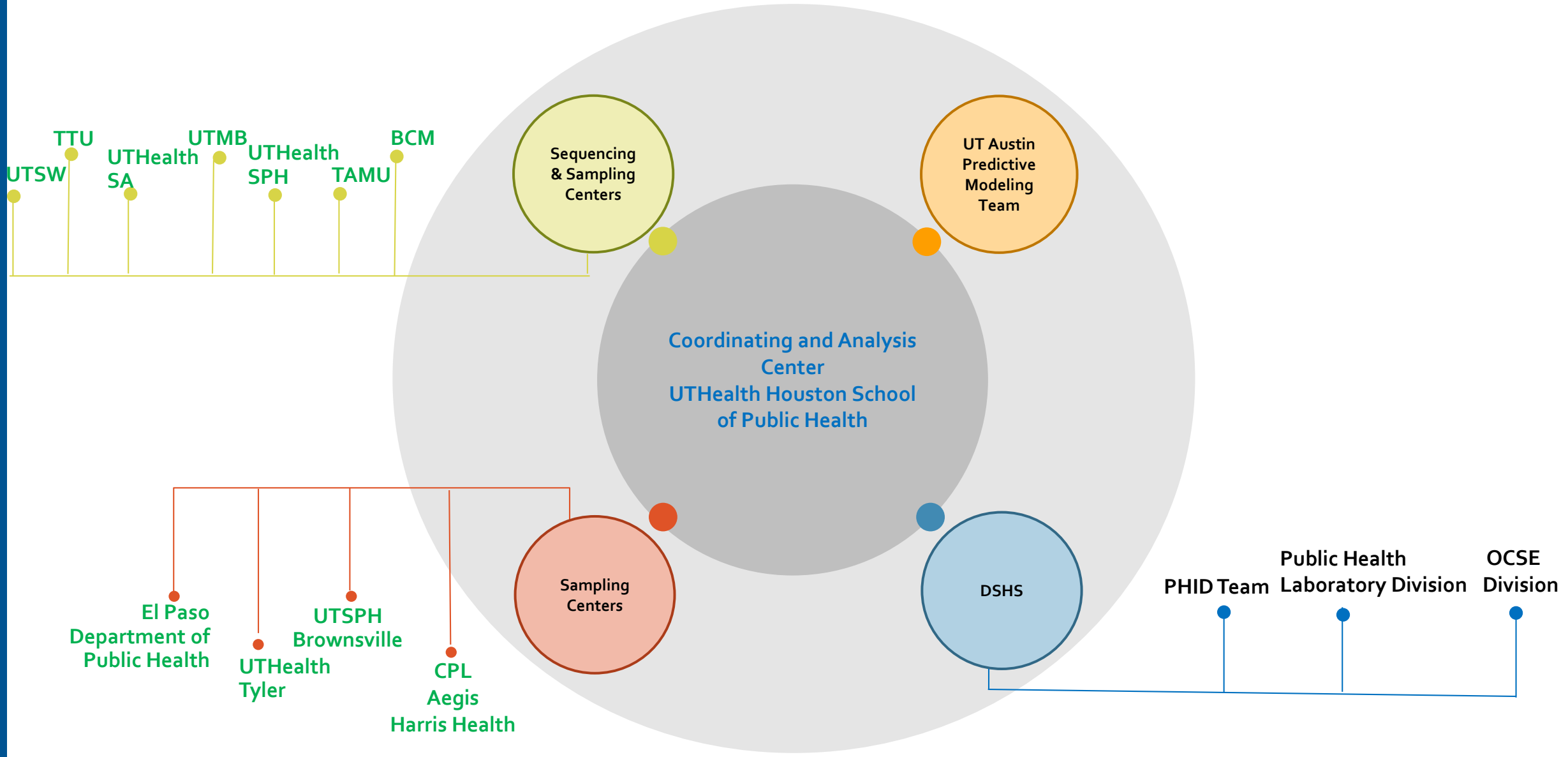
Network Project Structure

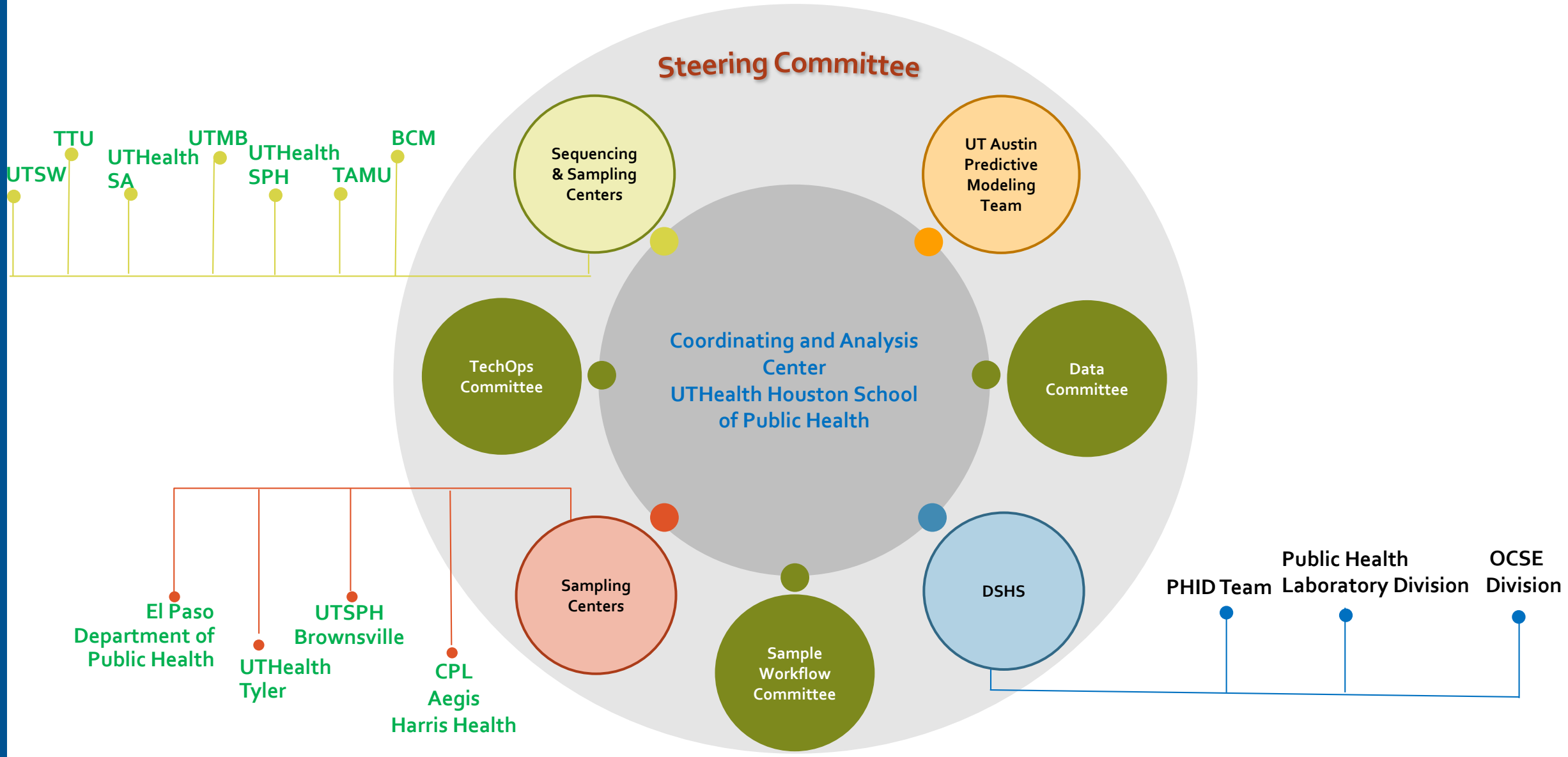
TXSCOV2 Network Project



TXSCOV2 Network Project



TXSCOV2 Network Project



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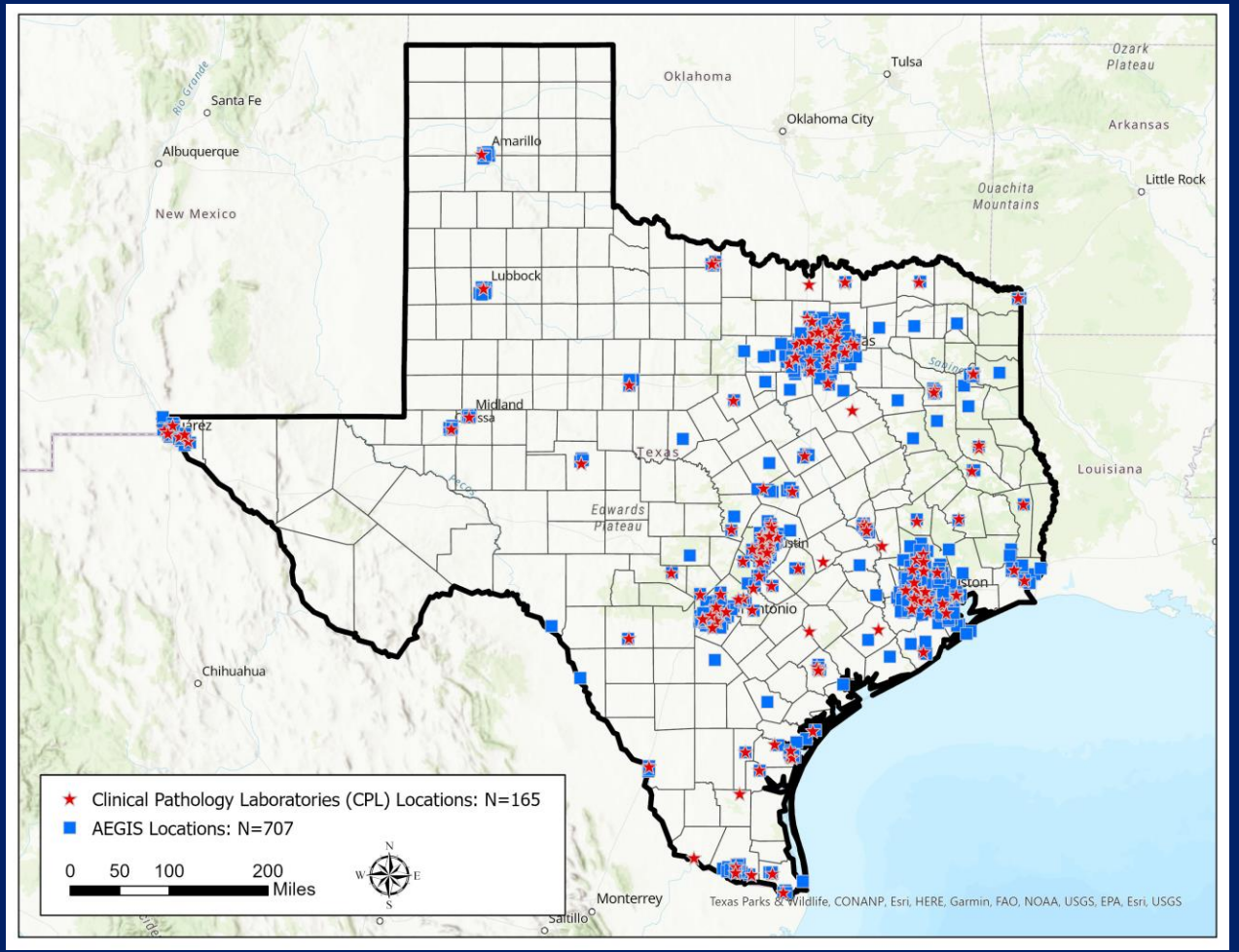
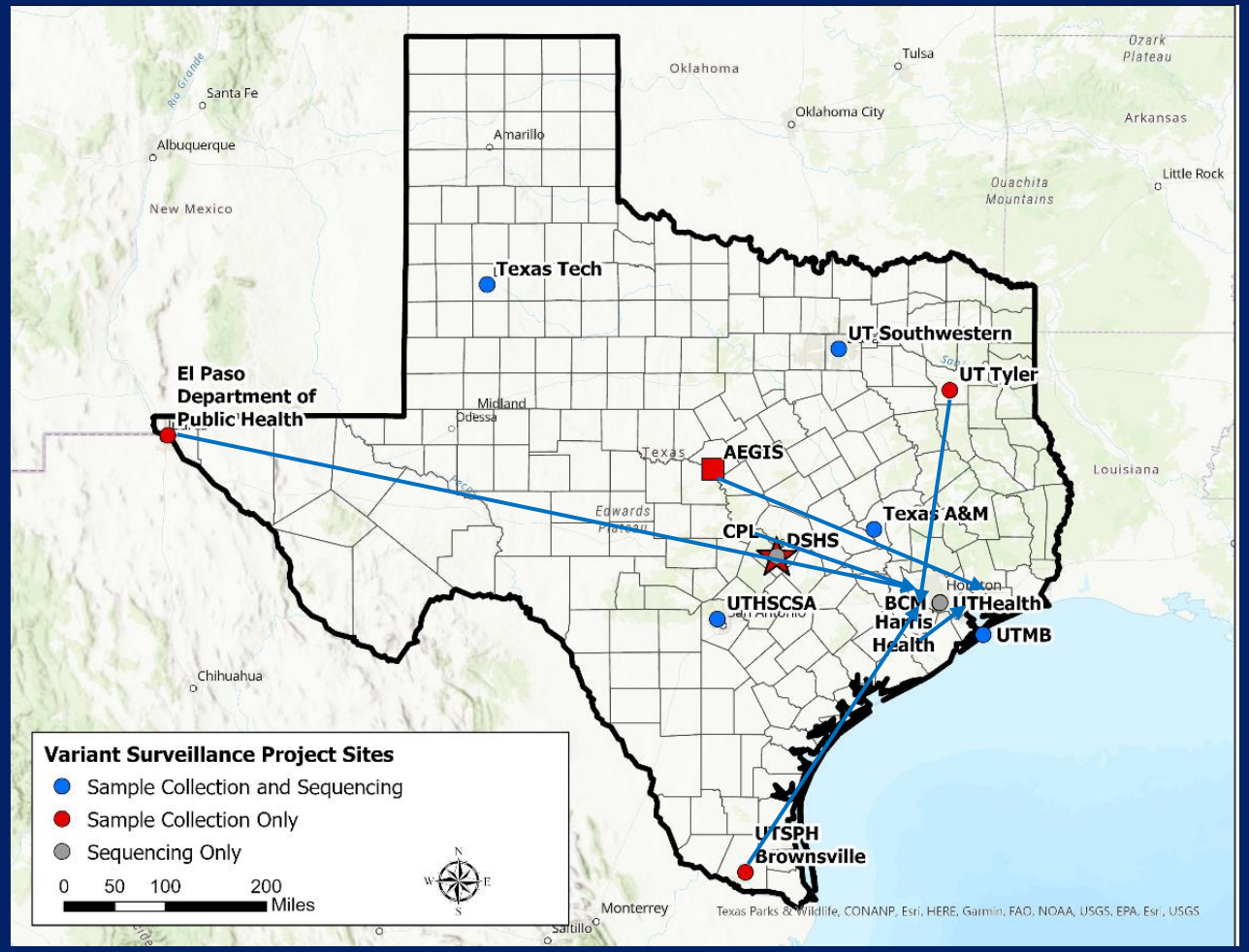
Network Participating Laboratories

Texas SARS-CoV-2 Variant Surveillance Network
Participating Laboratories





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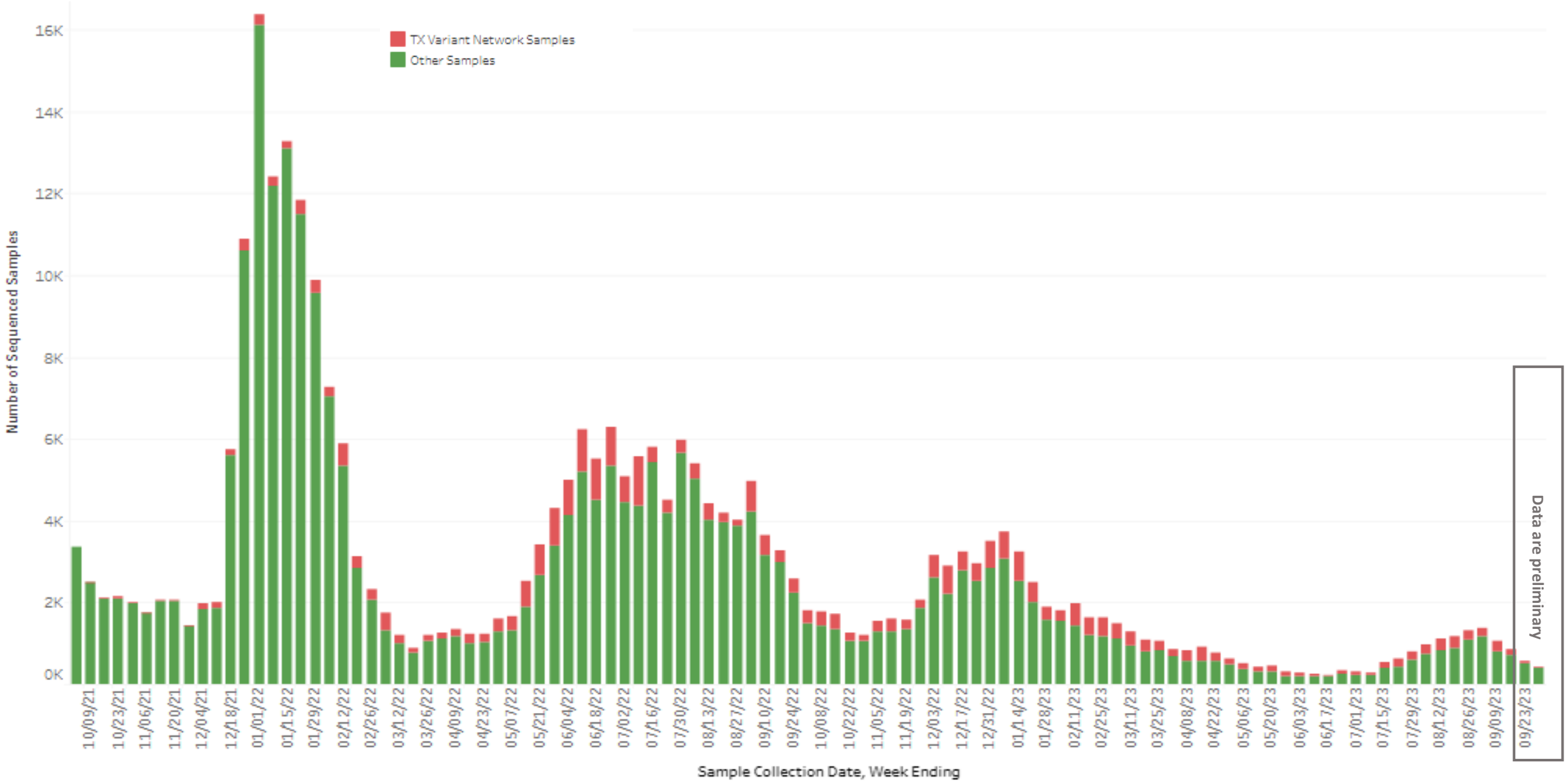
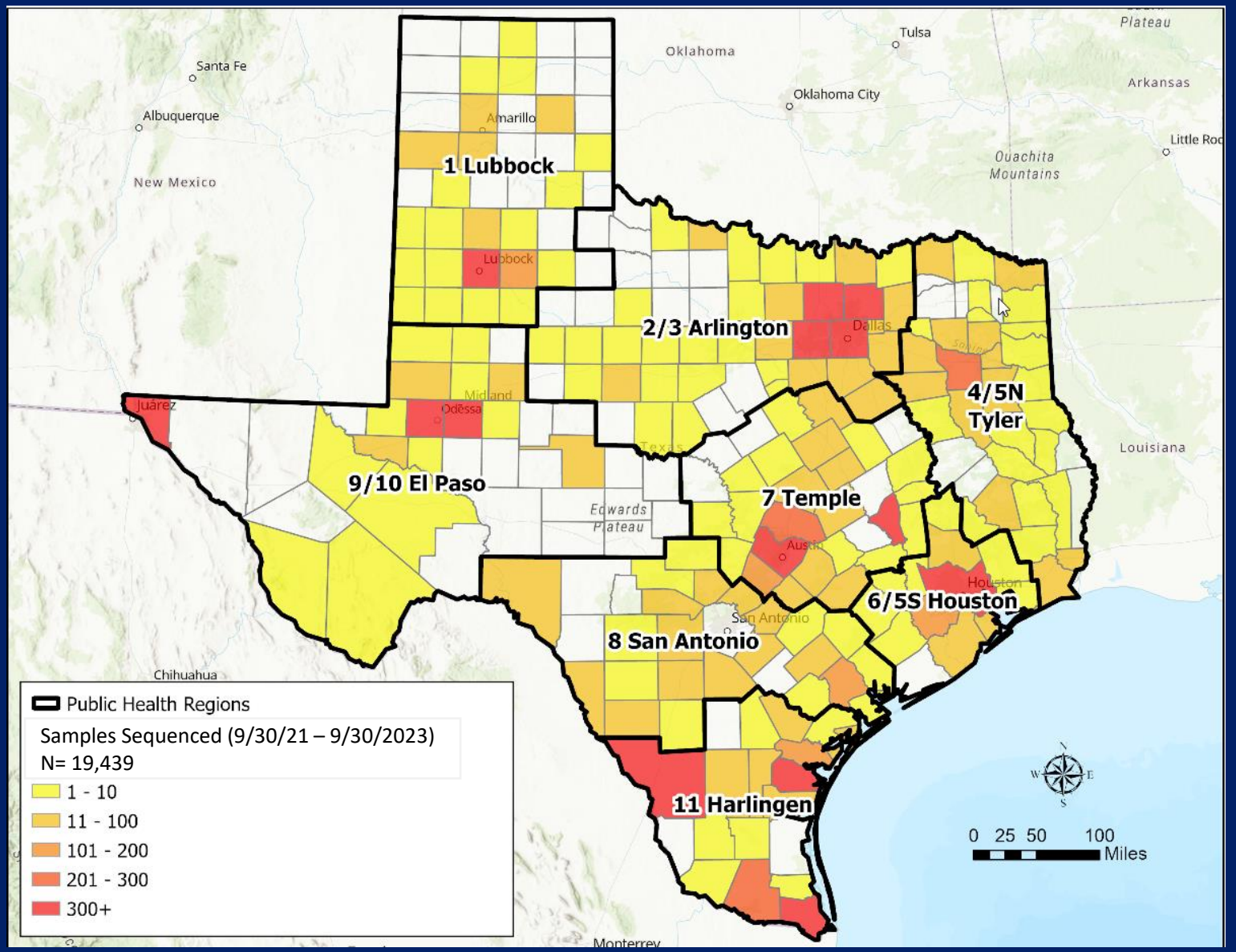
Network Project Findings

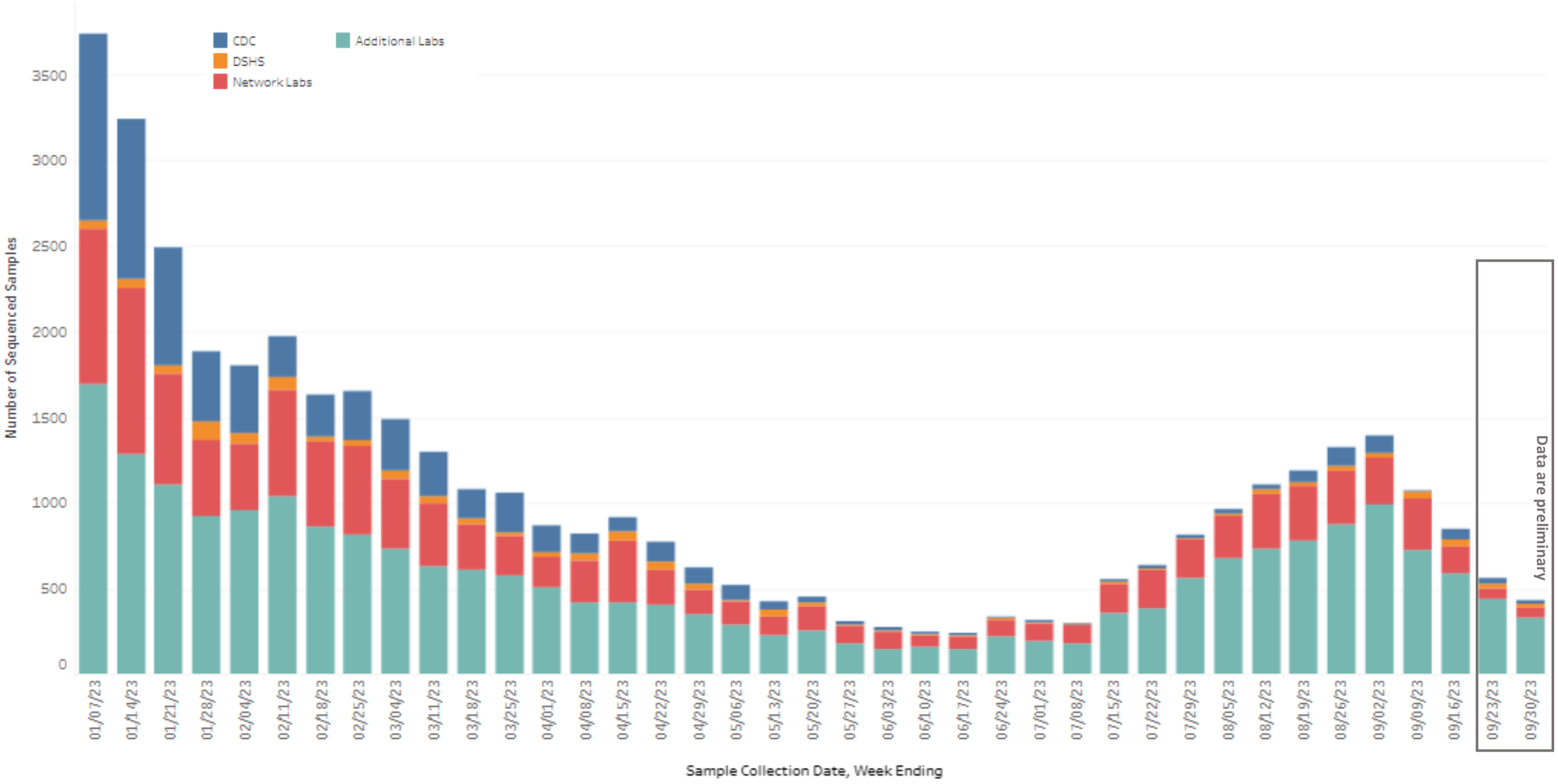
Texas SARS-CoV-2 Whole Genome Sequencing by Sample Collection Week (9/30/2021 - 09/30/2023)



SARS-CoV-2 Positive Samples Sequenced by the Network Labs by Texas County (9/30/2021 – 9/30/2023)



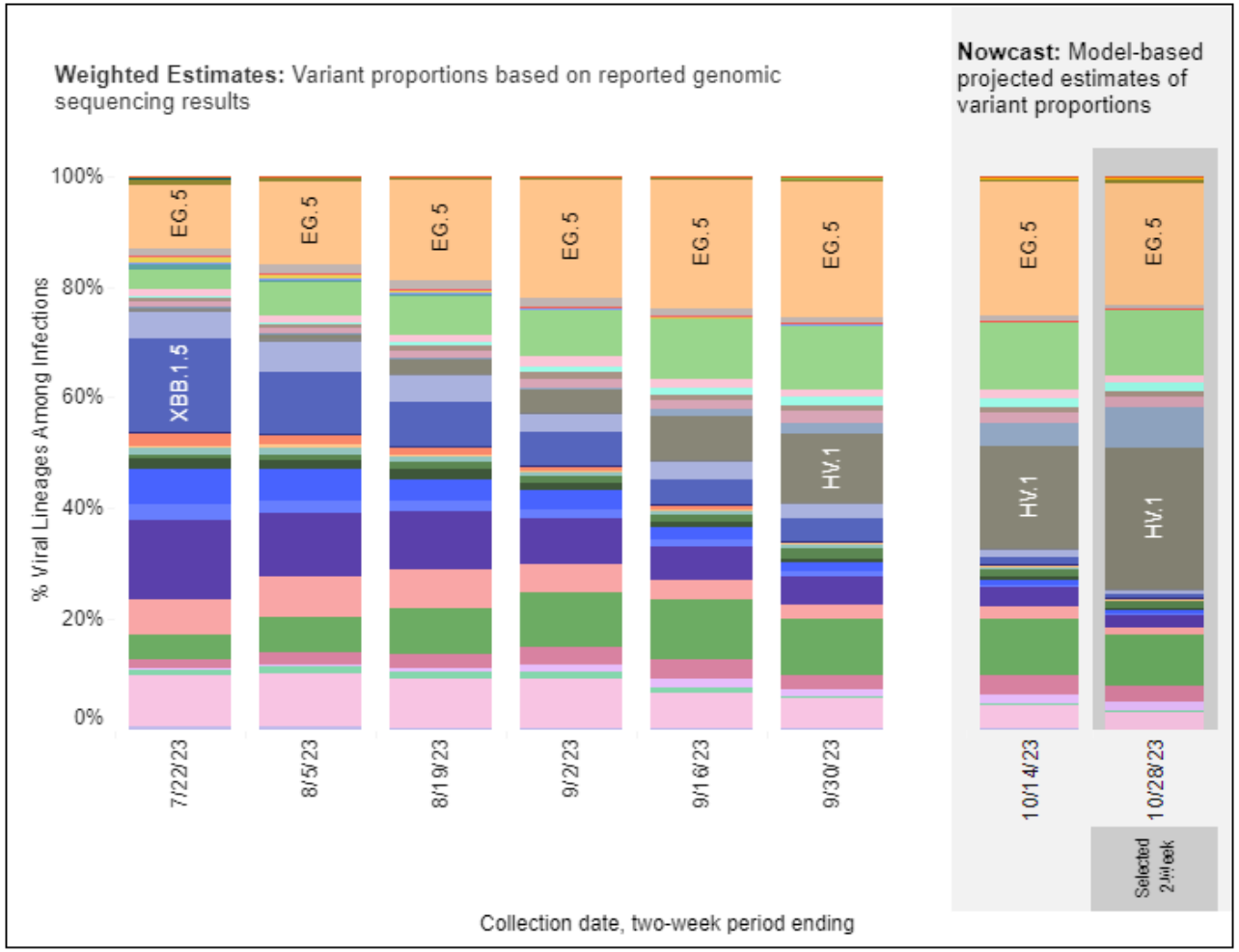
Texas SARS-CoV-2 Whole Genome Sequencing by Sample Collection Week, by Reporting Lab (01/01/2023 - 09/30/2023)



SARS-CoV-2 Variant Proportions – U.S.

Weighted and Nowcast Estimates in United States for 2-Week Periods in 7/9/2023 – 10/28/2023

Hover over (or tap in mobile) **any lineage of interest** to see the amount of uncertainty in that lineage's estimate.



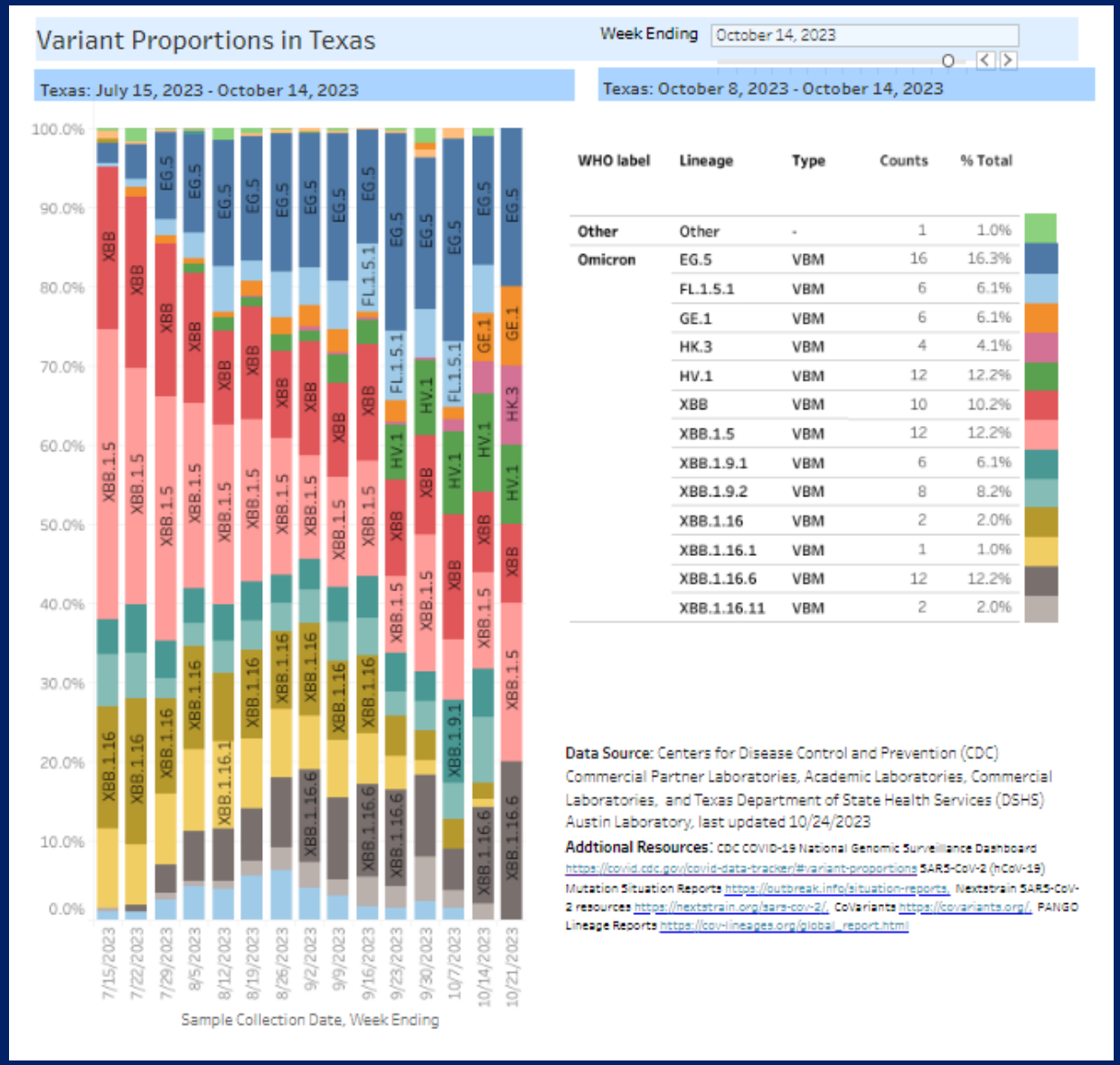
Nowcast Estimates in United States for 10/15/2023 – 10/28/2023

USA

WHO label	Lineage #	%Total	95%PI
Omicron	HV.1	25.2%	22.7-27.9%
	EG.5	21.9%	19.6-24.3%
	FL.1.5.1	12.0%	9.8-14.6%
	XBB.1.16.6	9.2%	8.0-10.5%
	HK.3	7.5%	5.6-9.9%
	XBB.1.16.11	3.1%	2.4-4.0%
	XBB.2.3	3.0%	2.5-3.6%
	XBB.1.16	2.2%	1.8-2.7%
	HF.1	1.8%	1.1-3.0%
	GK.1.1	1.8%	1.3-2.6%
	XBB.1.16.15	1.5%	1.1-2.2%
	XBB.1.16.1	1.4%	1.1-1.8%
	XBB.1.5.70	1.3%	0.8-2.1%
	GE.1	1.1%	0.8-1.5%
	XBB	1.1%	0.8-1.4%
	GK.2	0.9%	0.6-1.2%
	CH.1.1	0.8%	0.5-1.3%
	EG.6.1	0.7%	0.5-1.0%
	XBB.1.5	0.6%	0.5-0.8%
	XBB.1.9.1	0.5%	0.4-0.7%
	BA.2	0.5%	0.2-0.9%
	XBB.1.42.2	0.3%	0.2-0.6%
	XBB.1.5.72	0.3%	0.2-0.4%
	XBB.1.5.68	0.3%	0.2-0.5%
	XBB.1.9.2	0.3%	0.2-0.4%
	XBB.1.5.10	0.2%	0.1-0.2%
	XBB.2.3.8	0.1%	0.1-0.2%
	XBB.1.5.59	0.1%	0.1-0.2%
	FD.1.1	0.1%	0.0-0.1%
	FE.1.1	0.0%	0.0-0.0%
	EU.1.1	0.0%	0.0-0.0%
	XBB.1.5.1	0.0%	0.0-0.0%
	BQ.1	0.0%	0.0-0.0%
	B.1.1.529	0.0%	0.0-0.0%
Other	Other*	0.0%	0.0-0.1%

Source: CDC COVID Data Tracker: Variant Proportions, accessed 10/27/2023

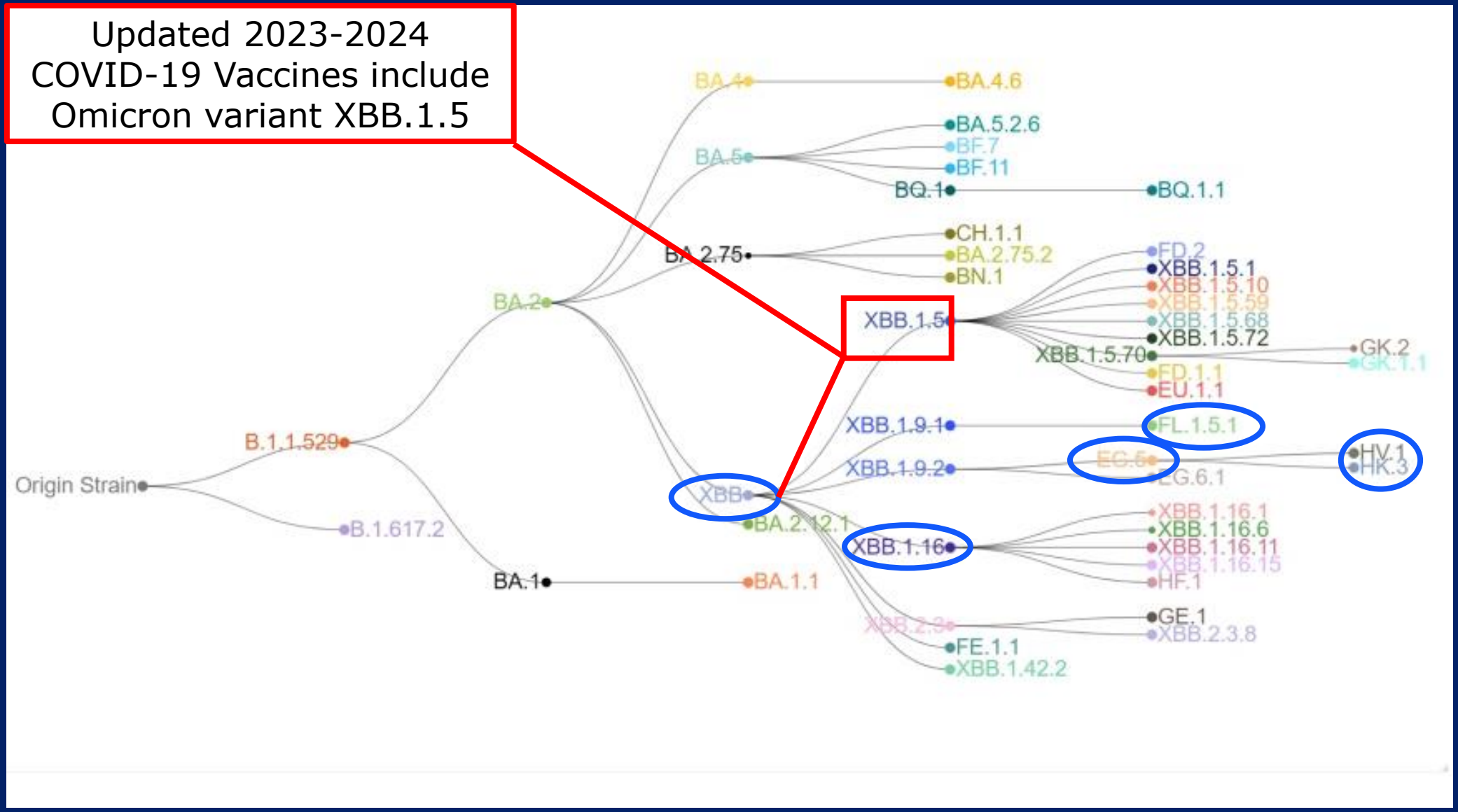
SARS-CoV-2 Variant Proportions - Texas



Source: https://www.dshs.texas.gov/covid-19-coronavirus-disease/sars-cov-2-variants-and-genomic-surveillance-Texas, accessed 10/27/2023

SARS-CoV-2 Lineages

Updated 2023-2024 COVID-19 Vaccines include Omicron variant XBB.1.5



Available at: CDC COVID Data Tracker: Variant Proportions accessed October 24, 2023

SARS-CoV-2 Variant BA.2.86

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- BA.2.86 is a newly designated variant of SARS-CoV-2 that has several additional mutations compared with previously detected Omicron variants.
  - Closely related to BA.2, the dominant Omicron lineage in early 2022.
  - Over 30 amino acid changes in the Spike region compared with the more recently circulating XBB.1.5.
  - This number of genetic differences is roughly of the same magnitude as seen between the initial Omicron variant (BA.1) and previous variants, such as Delta (B.1.617.2).
- As of October 23, 2023, the Centers for Disease Control and Prevention reported detection of the variant in 32 countries, including the United States.
- As of October 25, 2023, one case of BA.2.86 has been detected in Texas Public Health Region 6/5S in August, but the case was a Maryland resident.

Available at: Early Detection and Surveillance of the SARS-CoV-2 Variant BA.2.86 — Worldwide, July–October 2023 | MMWR (cdc.gov), accessed October 26, 2023

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Network Project Overall Accomplishments

Overall Network Accomplishments

- Increased the infrastructure and capacity for genomic surveillance and epidemiology statewide and electronic reporting of the data to DSHS.
  - Flexible infrastructure set-up to allow for regional varying needs
  - Ability to monitor circulating/emerging variants at regional/local levels
- Identified needs/skills and developed training to build a pipeline of trained public health workforce to meet future public health needs.
  - Developed 6 Genomic Epidemiology training modules in collaboration with UT Austin Center Biomedical Research Support
  - Conducted 6 live with on-demand access training sessions with a total of 426 attendees
  - 4 additional training modules are in development

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*Former DSHS

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Thank you