**Introduction**

This report provides a summary of the human viruses detected in wastewater from various sites throughout Texas. The work is supported by funding to the Texas Epidemic Public Health Institute (TEPHI) as part of the 87th legislative session (Bill SB1780). Virus levels are monitored by two distinct methods, comprehensive deep sequencing (CDS) and quantitative polymerase chain reaction (PCR). The Methods section provides an overview of some of the technical elements of these procedures. The report was generated by members of the TEPHI Wastewater Consortium. The Principal Investigators of the consortium are scientists at Baylor College of Medicine and the University of Texas Public Health system.

**Report Interpretation, Disclaimers, and Definitions.**

1. This report is an aggregate of viral shedding in community wastewater and does not represent individual tests or diagnoses.
2. Absolute viral levels are difficult to measure, vary by viral species, and are impacted by many factors, including number of people infected, the stability of the virus over time, the composition of wastewater from a given site, and the detection method itself. However, the relative changes of the viral signal may be used as an approximate gauge of viral trends in space and time.
3. Data in this report should not substitute the need for individual testing. Instead, it can be used as one piece of information in filling population-level gaps in the behavior of viruses at the various sites.
4. The report data is interactive. Simply mouse-over the table heading or graphs to rank order information or attain more granularity.
5. Sequencing data output is in reads per kilobase of transcript per million reads mapped (RPKM). This is the number of reads of a given viral sequence from a sample. Generally, the higher this number, the more of that sequence and hence the more virus present. PCR data output is in genome copies. Generally, the more genomes present, the more virus there was in the sample.
6. Both data sets represent the moving average.
7. Change from baseline values represent the fraction of signal that has increased or decreased since the last sampling period.
8. Percent covered represents the fraction of the genome detected in the sequencing data.
9. Accession number is the unique identifier for that genome in NCBI.