

Customer Name: **Telluride Wastewater Treatment Plant**  
 Internal Sample ID: **13155**

Account #: **40**  
 Internal Location ID: **n/a**

### Customer Provided Information:

Facility Name: **Telluride WWTP**  
 Sample Collection Date: **2/10/2021** to **2/10/2021**  
 Sampling Method: **Flow-proportional 24-hr composite**  
 Average influent flow over sample period (MGD): **0.73**

## Hyper Transmissible SARS-CoV-2 Variant in Sample del69-70 detected

### Hyper Transmissible Variant Quantification

*The UK Variant of the B.1.1.7 lineage accounts for an alarming increase in cases in parts of England. Viruses in this lineage have an unusually large number of mutations, particularly in the Spike protein, which is the part of the virus that binds human cells and initiates infection.*

*Our test does not test for every mutation present in the UK variant, instead we target 2 key mutations that have been previously described to have biological effects that drive the hyper-transmissibility of that UK variant. The presence of both of these mutations is a strong indicator that the UK variant or possibly another, related and yet to be defined hyper-transmissible variant is circulating within a community.*

#### Mutation: Spike Protein del69-70

*The deletion of amino acid residues 69 and 70 in the spike protein has been shown to cause a conformation change to the spike protein and enhance viral infectivity and virus fitness (1).*

<b>Percentage of detected viruses with variant mutation</b>	<b>0.746%</b>
Wuhan Viral Copies per Liter wastewater at del69-70 location:	117,278 copies/L
Mutated Viral Copies per Liter wastewater at del69-70 location:	875 copies/L

#### Mutation: Spike Protein N501Y

*Viruses containing the N501Y mutation demonstrate higher affinity for receptors found on human cells (2). This mutation, also found in the South African variant, has profound effects on infectivity and is potentially involved in immune system evasion (1).*

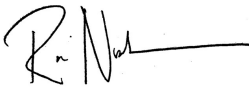
<b>Percentage of detected viruses with variant mutation</b>	<b>0.000%</b>
Wuhan ("wt") Viral Copies per L wastewater at N501Y location:	103,384 copies/L
Mutated Viral Copies per L wastewater at N501Y location:	0 copies/L

**Quality Control Data**

Metric	Pass Criteria	Measured	Pass or Fail
F+ Prophage Concentration (copies/L)	<i>Detection</i>	1.07E+08	<b>PASS</b>
Internal Process Control (% Viral Recovery)	>5%	27%	<b>PASS</b>
ddPCR Positive Control (Copies/Rxn)	>20	152	<b>PASS</b>
ddPCR Negative Control (Positive Droplets in NTC)	<1	0.00	<b>PASS</b>

**Data interpretation**

**We detected mutation del69-70 at a low frequency in this sample. We did not, however, detect the N501Y mutation which is a key signature of the B.1.1.7 lineage of hyper-transmissible variants. Because this mutation is known to drive a biological function, we advise continued monitoring.**

**X** 

Dr. Rose T. Nash  
 Laboratory Director, GT Molecular