

Customer Name: **Telluride**
 Internal Sample ID: **GT12562**

Account #: **1037**
 Internal Location ID: **100007**

Customer Provided Information:

Facility Name: **Influent**
 Sample Collection Date: **1/06/2021 12:00AM** to **1/06/2021 11:00PM**
 Sampling Method: **Flow-proportional 24-hr composite**
 Average influent flow over sample period (MGD): **0.689**

SARS-CoV-2 in Sample

DETECTED

Viral Copies per Liter of Wastewater (recovery adjusted) **2,769,920** **copies/L**

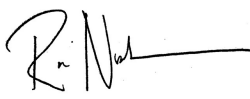
Quality Control Data

Metric	Pass Criteria	Measured	Pass or Fail
F+ Prophage Concentration (copies/L)	<i>Detection</i>	9.32E+07	PASS
Internal Process Control (% Viral Recovery)	>5%	10%	PASS
ddPCR Positive Control (Copies/Rxn)	>20	2940	PASS
ddPCR Negative Control (Positive Droplets in NTC)	<1	0	PASS

Notes on Methodology

The GT Molecular method utilizes an internal process control which is a bovine coronavirus that we spike into every sample at a known concentration. By measuring the concentration of this spiked virus control following sample processing, we can adjust the concentration of SARS-CoV-2 to account for any loss of the virus during processing. While this is best practice for determining an accurate measurement, most other groups are not yet doing this. *We advise against comparing concentrations to other groups using different method due to differences in viral recovery from method to method and batch to batch.*

Your non-recovery adjusted SARS-CoV-2 concentration was **264,396** **copies/L**.

X 
 Dr. Rose T. Nash
 Laboratory Director, GT Molecular