1. PI Name: Dr. Stephanie Ceman.
2. Customer Name: Temirlan Shilikbay.
3. Date: 02/18/2021.
4. FOAPAL (on-campus customers only): 1-637605-584000-191100.

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| --- | --- | --- | --- | --- | --- |
| **Sample ID (this name will be used to name your fastq files). Use only letters, numbers and underscores.** | **Label on Tube**  **(we strongly suggest #1-xx)** | **Concentration (Qubit or Nanodrop?), ng/ul** | **Volume, ul** | **Total RNA (ng)** | **Final Pool #**  **(if we are mixing your libraries into multiple pools, designate that here)** |
| Del\_1 | 1-Del | 212.66 | 41.30 | 8782.86 |  |
| Del\_2 | 2-Del | 137.06 | 38.80 | 5317.93 |  |
| Del\_3 | 3-Del | 116.04 | 37.40 | 4339.90 |  |
| WT\_1 | 1-WT | 210.27 | 41.20 | 8663.12 |  |
| WT\_2 | 2-WT | 242.89 | 41.90 | 10177.09 |  |
| WT\_3 | 3-WT | 116.87 | 37.40 | 4370.94 |  |

1. Quality check of RNA: run an aliquot (~50 to 100ng) of the total RNA on a 1% agarose gel next to a DNA ladder and attach or embed the image here. This picture will be used to evaluate integrity of the total RNA as well as presence/absence of gDNA. Alternatively, run the total RNA on an RNA bioanalyzer chip and attach the .pdf file.

6) Sequencing options:

\*Number of lanes: 1.

\*Single or Paired-reads: Paired.

\*Read length: 150 nt.

\*Flowcell (MiSeq Nano, V2, V3, NovaSeq SP, S1, S2, S4): NovaSeq SP.