CEL-Seq2 sample requirements

Bulk CEL-Seq2 is a high-throughput low-input 3'-mRNA-seq method. The protocol involves barcoding of samples by reverse transcription using an oligo dT primer, pooling of samples and subsequent molecular reactions for linear amplification and preparation for Illumina sequencing. For references see (Hashimshony, T., Senderovich, N., Avital, G. et al. CEL-Seq2: sensitive highly-multiplexed single-cell RNA-Seq. Genome Biol 17, 77 (2016)).

Please read carefully and follow the instructions below for RNA submission:

- Measure RNA concentration with Qubit or NanoDrop. The samples should be diluted to a concentration of 10 ng/µl and submitted with at least 20 ul (for samples outside the recommended concentration and/or volume, please contact us).
  Please note that NanoDrop is reliable only if RNA concentration is >20ng/µl (if lower – use Qubit).
- TapeStation should be performed to test RNA integrity (recommended RIN>5).
- Samples should be submitted in PCR strips (preferably with attached caps) as follows:
  - Write the sample number (not name) on the side and on the top of the tube. In the matching electronic sample submission form, write the number + a meaningful name (this name will be used as the sample name in your fastq files). Ensure that the number on the tube is identical to the serial number of the sample in the electronic Sample Submission Form.
  - Arrange samples in the correct order in a box. We cannot accept samples in plastic bags or randomly placed on ice. Mark the box with your name and date.
- Fill out the RNA Submission Form and send it together with TapeStation results to linde@technion.ac.il.

Recommendations-

It is recommended to use column-based kit (such as Qiagen) for RNA extraction.