

10x Submission Instructions for STUDY MADE 10x Libraries

Important: New project use the Next GEM – the newest version of the 10x chips and appropriate reagents and protocols. If you need your samples to be backwards compatible with a previously processed ones please inform the HTSF , make sure to include the kit version # on the submitted 10x manifest.

If you have any questions about processing please contact HTSF before proceeding.

10x Submissions for study made 10x libraries

- 1- When starting a study with 10x, make sure to contact the customer service group at the HTSF to update your study for 10x.
- 2- Submit via Tracseq as usual
- 3- Additionally, you will need to fill out the 10x Manifest for Study made Libraries with Index lists and Seq Submission Requirements. It can be found in the Forms and Guides Tab, Alternative Technology.
 - There are multiple tabs on this form:
 - 10xLib Manifest for Cell Ranger
 - Version-Cycle Length
 - 3 Primer Barcodes
 - ATAC Barcodes
 - VDJ barcodes
 - DNA barcodes
 - Genome –Exome Barcodes
 - Surface Barcodes
- 4- You need to fill out the first tab, 10xLib Manifest for Cell Ranger
 - a. List each library you are submitting (where you submit it as a library or part of a pool)
 - b. Direction are on the form as to what is required in each field.
 - c. Please indicate the % of each library in the pool (or wanting the pool, if HTSF will be pooling), we need to know this when we look at pool balancing
- 5- Email a copy of this manifest to the Customer Service group for attachment to the submission.
- 6- If HTSF is pooling your libraries, we will send the library QAQC for your approval before pooling.
- 7- HTSF will send QAQC for the Pool to be approved prior to sending to sequencing.
- 8- The doc will be used by the HTSF BioInformatics group when running the data through Cell Ranger