**Filling Out a Manifest:** part II

**KEY POINTS for filling out manifest**

1. **Never modify the manifest you download from TracSeq**. This manifest will interact with a number of databases when you upload it to TracSeq and when processing your samples. The manifest will not upload and/ or function as intended if you modify header, move columns, add or delete columns and add/ or delete rows
2. Use drop down menus when available
	1. Click on box below header, arrow will appear at the right for drop down selection
	2. Databases like things exactly as they expect so many fields are preset with selections
3. Do not “pull down” through the table on excel. It is additive. Either use the fill feature or copy and paste.
4. Use correct study name
	1. It has been agreed on previously
	2. It is referenced in the subject line of emails
5. The person filling out the manifest should be the name in the “SubmitterName” field
6. Funding Account Number field
	1. this is the account number that will be billed at UNC
		1. A different account number can be listed for different submissions
		2. We request to keep to same funding account for each manifest submission
	2. HTSF Internal account
		1. Please use the account number previously assigned, contact us if you do not remember the number
7. Naming a Sample or Pool
	1. Sample Name between 5-10 characters long
	2. ID cannot start with a Zero
	3. Use both alpha + numeric
	4. ONLY use hyphens

\*Do not use period, brackets, and special characters

* 1. Do not use generic names: i.e.- “sample1” or “PoolA”
	2. Use of “POOL” or “PL” in a pool name is helpful
1. External Code Field
	1. use this field to track other necessary info for your sample.
	2. The Sample ID and the external code are linked and visible at all times for the lab and with your final data
	3. There is a mix of 25 alpha or numeric in this field
2. Each line on the manifest will be a new sample
	1. DNA/RNA: each line is a single sample
	2. Libraries which the HTSF will pool:
		1. Each line will be a single sample
		2. “librarypool” field – answer **“no”**
		3. “poolname” field – enter the name you wish to be used. List will the same name for each library you want in the pool
	3. Libraries a study has pooled :
		1. Each line will be a single sample
		2. “librarypool” field – answer **“** **yes”**
		3. “poolname” field – enter the name you wish to be used. List will the same name for each library you want in the pool
3. Sample Data fields (Conc., Vol., A260/280, A260/230, RIN, Ave fragment size)
	1. ALWAYS enter conc and volume for a sample
	2. A260/280, A260/230 – please enter these fields
	3. RIN – only for RNA samples
		1. If you do not know this there will be a small fee for the HTSF to determine it
	4. Ave Fragment Size – this is required for all libraries and pools that are submitted to the HTSF
	5. For unknown fields, enter 9999 – this will indicate to us you do not know the values
4. DUAL BARCODES- list a dual barcodes separated with a hyphen in 5’ then 3’ order
	1. Index Number field = 5’ index#**-**3’index#
	2. NT Sequence field = 5’ NNNNNNNN**-** 3’NNNNNNNN
5. No more than 100 characters can be used in “special needs” field
6. Use one name in the Data return contact” field

\*Additional names can be listed in “special needs”

\*This will change in the future

1. Never allow your spell check to “check” your manifest

\* disable your spell check

\* a spell checked manifest will have significant issues when you try to submit it

1. There is full instructions for each field on the second tab of the manifest and as a .pdf on the TracSeq site
2. SUBMITTING FOR PLATES: if you are submitting a plate. Please,
	1. Plate loading order is in columns , NOT ROWS
		1. First sample is in A1
		2. Second sample in B1 ,
		3. Third is in C1 , 4th = D1 and so
		4. Last sample in a plate is H12
	2. Fill in the rows on the manifest in the order on the plate
		1. First sample in A1 = row 3 on manifest
		2. Second sample in B1 , = row4 on manifest
		3. Third is in C1 = row 5
		4. Last sample in a plate is H12 = row 98 on the manifest