EMP500 Sample Organization

Thanks for helping organize samples for EMP500! You will be labeling and (in some cases) aliquoting samples for one study at a time. This is a two-step process: 1. Evaluate what needs to be done and what supplies are needed for your study. 2. Aliquot material and label the tubes, then put them into labeled boxes.

Evaluate samples and procure materials

After your study is assigned, open up the 'EMP500 reorganization' Google Docs spreadsheet. You'll be recording information here.

1. Enter your names and date on the `Studies` spreadsheet tab for this study

The `Studies` tab includes one row per study; find your study and record your names and the date.

2. Check that all samples are accounted for

Find the samples tab for your study, for example `2-Berry`, `33-Mayer`, etc. There is a separate row for each aliquot of each sample. Is each sample represented?

if not: *check with Luke or Jon.*

3. Check if the samples are already aliquoted into 2mL tubes

If so, you will be able to simply attach a new printed barcode to these tubes.

if not: *check with Luke or Jon. You will need to re-aliquot the material into new, empty 2mL tubes.*

4. Get 2 bead tubes for DNA extraction

These are from the MO BIO PowerSoil 50-prep kits, and will contain bead solution liquid and garnet lysis beads.

5. Get new cardboard sample boxes (and labels) to store aliquots

All 2 mL aliquots from this study will be stored together in these new boxes. We have printed out several labels per study to mark these boxes.

Print barcodes

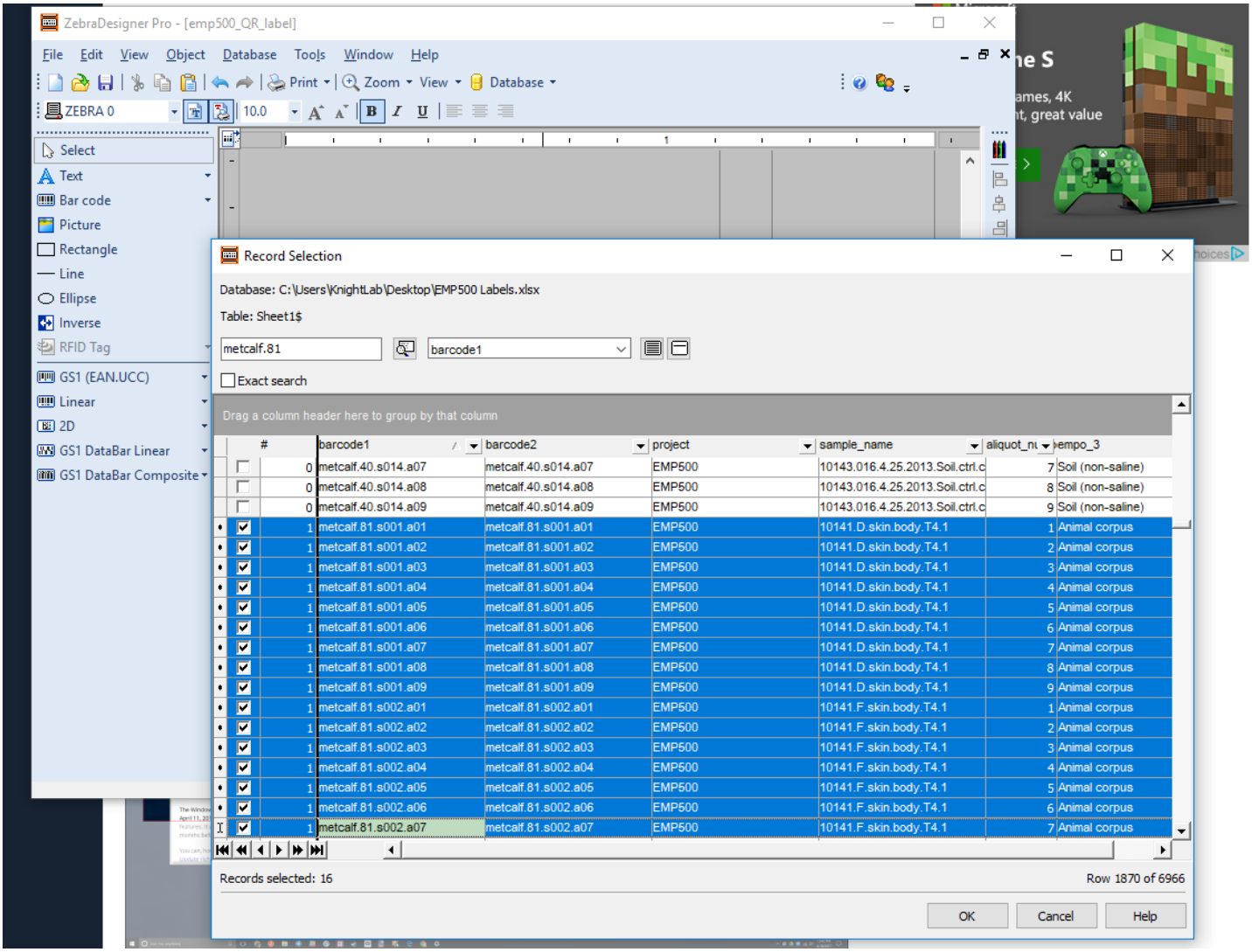
Each sample tube will have a barcode label for the side of the tube and a matching 'dot' barcode for the top. You will print these on-demand from the Zebra printer connected to the plate scanner computer.

1. Open the Zebra printer software and find your study

Use the software to select only the samples from your study.

Click the 'print' icon, then click 'Select Records...' Type the pi name + study number into the search field; it will go to the point in the list where that study starts.

Select only the samples from the study by clicking the first record, holding shift, and scrolling down to click the last record from the study. They should then be highlighted in blue. Press the spacebar and wait a few seconds---the highlighted samples should now have a checkmark next to them.



2. Print the labels

Click 'OK' and then 'Print.'

if you only have a few aliquots: *some studies only have a handful of material per sample. To conserve labels, you can select just the rows that corresponde t the aliquots you can make. You can always print more if necessary.*

Aliquot samples and label tubes

Make sure that you have everything you need. Try to keep samples as cool as possible when out of the freezer. Make sure you have a clean work area set up and everything you need.

1. Gather materials

In addition to your rack of tubes, you will need sterile wooden applicators to transfer material to extraction tubes. For some sample types, you may need other implements---check with Luke or Jon if unsure.

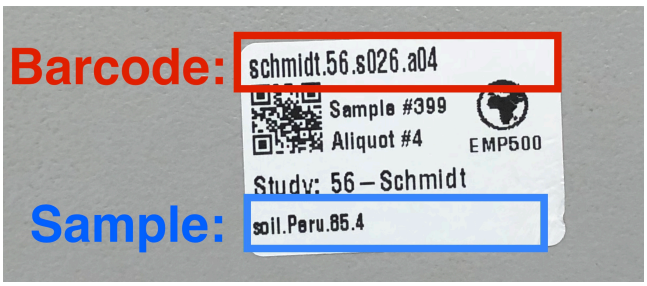
2. Pre-label empty tubes

You will add barcode labels to at least the two empty extraction bead tubes. If you are also transferring material to new dry 2 mL tubes, pre-label these as well.

3. Aliquot biological material to tubes for extraction

You may need to move less material than is present in the original tube. (Check with Jon or Luke.) If so, draw these from the one original tube rather than dipping into separate aliquots.

Make sure that the sample name on the original tube matches the sample name on the barcode label:



4. Attach new labels to additional 2 mL aliquots

For any remaining 2 mL tubes, quickly dry off the tube with a kimwipe and attach a new barcode label to the

side and top.

5. Scan barcodes into the Google Docs samples tab corresponding to your study

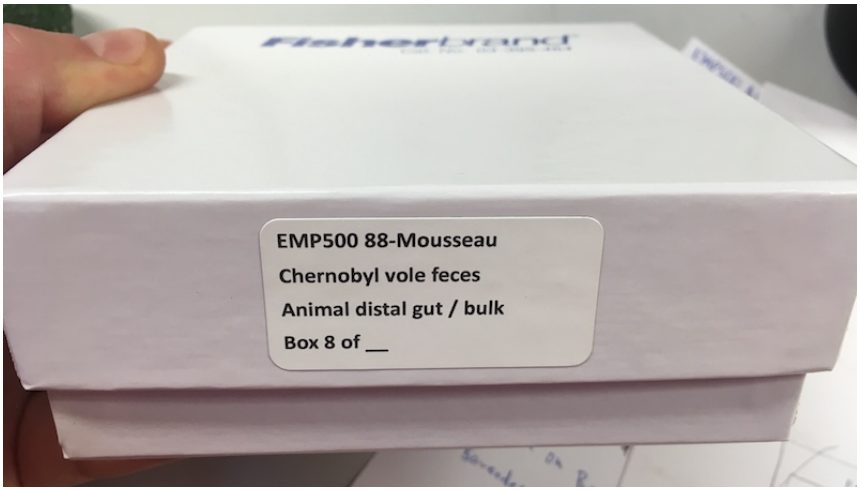
Make sure you've correctly matched the original tube label with the new barcode labels. The 'scanned_barcode' field of the Google Sheet will turn green if the label matches and red if it doesn't:

	A	B	C	D	E	F	G	H
		sample_name	sample_number	aliquot_number	empo_3	barcode	scanned_barcode	notes
0		sediment.Do5	1	1	Sediment (non-saline)	berry.2.s001.a01	berry.2.s001.a01	
1		sediment.Do5	1	2	Sediment (non-saline)	berry.2.s001.a02	berry.2.s001.a01	
2		sediment.Do5	1	3	Sediment (non-saline)	berry.2.s001.a03		
3		sediment.Do5	1	4	Sediment (non-saline)	berry.2.s001.a04		
4		sediment.Do5	1	5	Sediment (non-saline)	berry.2.s001.a05		

6. Place all aliquots into new labeled freezer box

The first two columns of the box should be occupied by the bead tubes for extraciton. Bulk aliquots go in columns 3-9.

Label the box like so:



7. Place new box into freezer rack and any remaining sample at the back of the freezer

You're done!