How to submit samples for Illumina/Short Read Sequencing (FGCZv10.2)

Creating an order in B-Fabric for HT Sequencing/Short Read Sequencing: RNA and DNA Samples

Important: Please precisely follow the instructions below when submitting **RNA or DNA samples for library preparation**.
If you are submitting **ready-made libraries** please follow the instructions **here** instead.

Update: There is the possibility to copy and paste sample names from an Excel-Spreadsheet now. Please refer to the section found **here**.

RNA samples

1. We need 300ng-2ug for standard library prep. Please check our application page for the requirements for the specific protocols https://fgcz-intranet.uzh.ch/FullServiceSequencing
   Dilute the samples to the same concentration. We prefer 100ng/ul, the lowest possible concentration is 2ng/ul for standard library prep. If this is not possible, please dilute to the highest concentration possible compared to your other samples.
   For low input RNA samples, please check with your coach as this will depend on the library prep kit.
2. Please dilute your samples in water or EB buffer.
3. Please use 1.5 ml tubes.

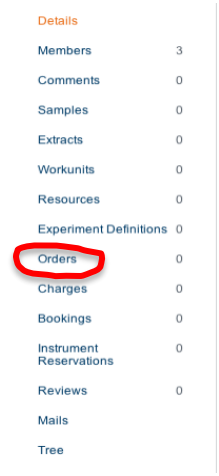
DNA samples

1. We need 100ng-500ng for standard library prep. Please check our application page for the requirements for the specific protocols https://fgcz-intranet.uzh.ch/FullServiceSequencing
   Dilute the samples to the same concentration. We prefer 100ng/ul, the lowest possible concentration is 2ng/ul for standard library prep. If this is not possible, please dilute to the highest concentration possible compared to your other samples.
   For low input DNA samples, please check with your coach as this will depend on the library prep kit.
2. Please dilute your samples in water or EB buffer.
3. Please use 1.5 ml tubes.
4. Please run your samples in a gel and attach the picture in the comments section of the order.

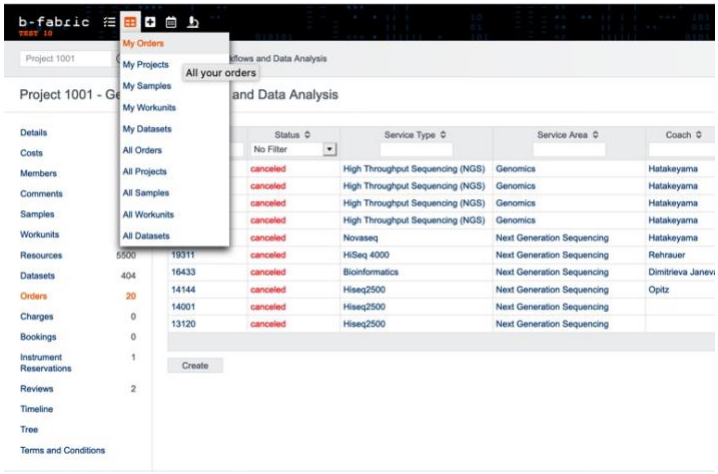
Order submission: step-by-step guide

1. Please login to your project main page B-Fabric. If you have more than one project at the FGCZ, please make sure you are in the correct project page.

2. Click on the "Orders" button listed on the left part of the screen:

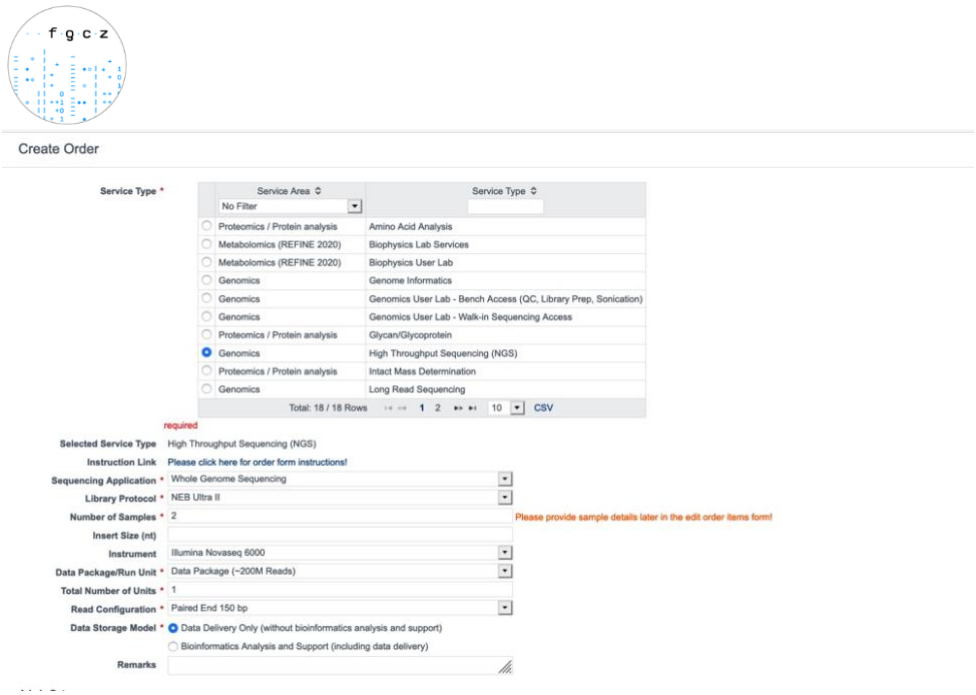


Or by clicking on the following icon on top of the screen:



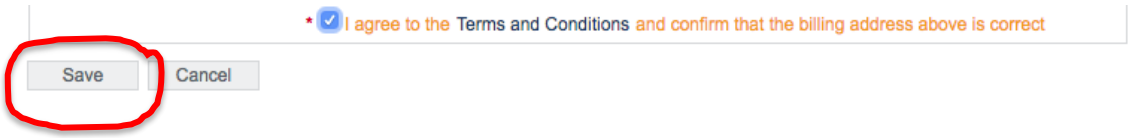
3. Click on the "Create Order" button.

4. Under "Service Area", click on "High Throughput Sequencing".
and fill up the form (select application, instrument, library protocol …) as best you can. If you indicate "I don't know", your coach will get in touch with you to clarify your order. See Example below.

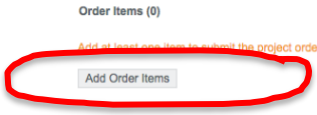


Note: Please indicate any special instruction in the "Remarks" field.

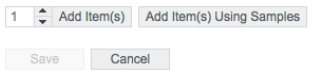
5. Check if the billing address is correct. Please note that ETH/UZH users will be required to enter their fund number for invoicing. If not sure about the fund number please ask your group leader. Click on Agree and Save.



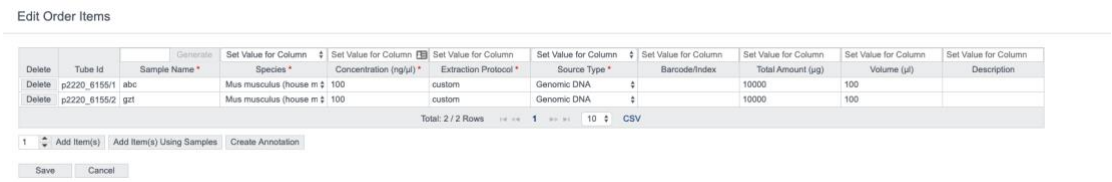
6. To add samples that you want to submit to your order, click on the "Add order items" button.



7. Please enter the number of samples you would like to submit.
Would you like to add new samples please click on "Add Item(s)"
Would you like to add already existing samples from previous orders within the same project, please click on "Add Item(s) Using Samples.



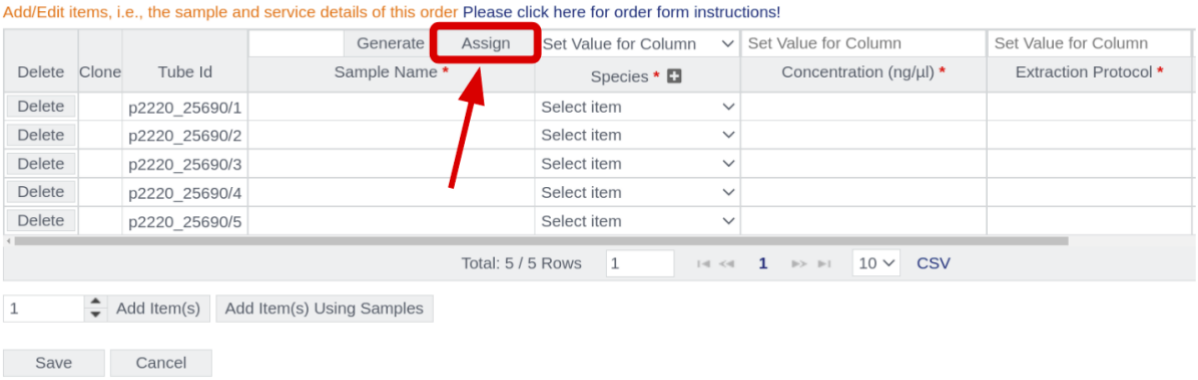
8. A table will open with fields for the number of samples you have chosen. If you have more samples, add any number of the fields by using the "Add Item(s)" option.



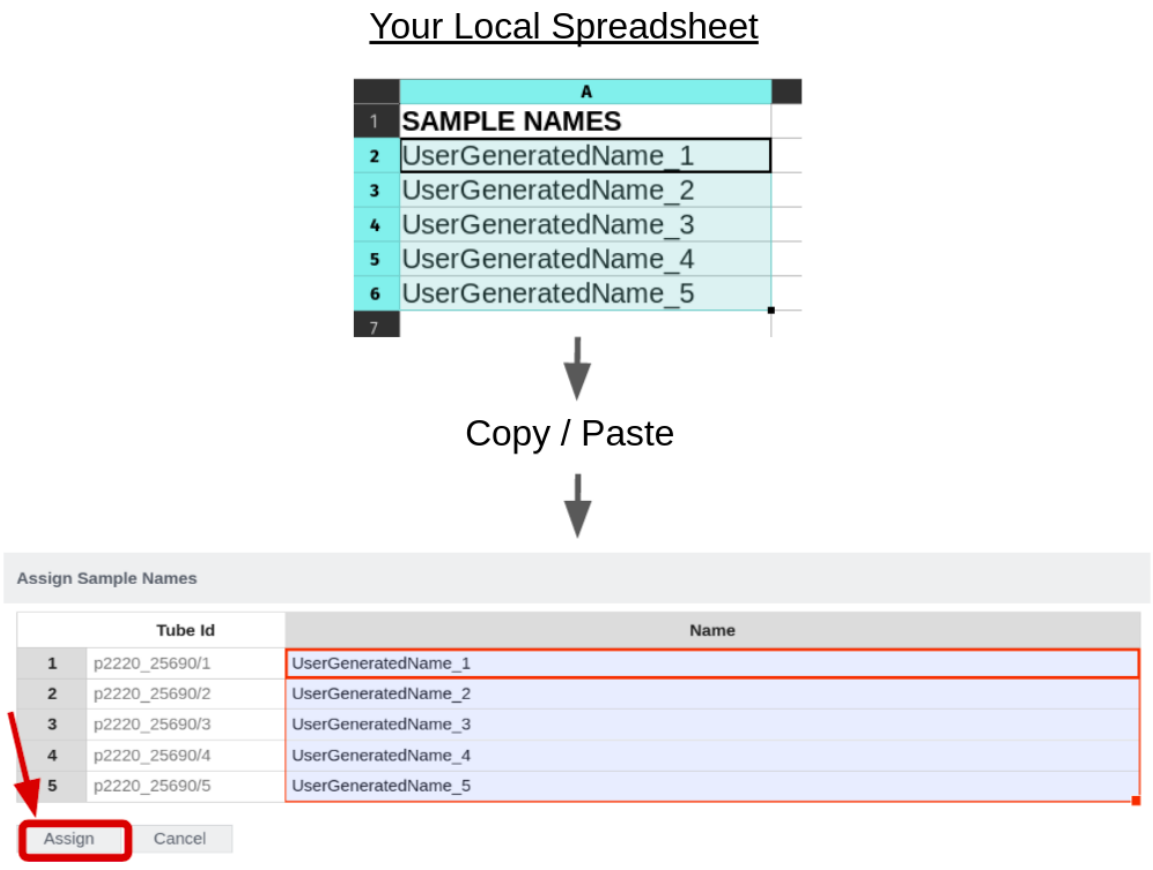
9. Enter the information about your samples like **Sample Name**, **Species**, **Concentration, Extraction Protocol ….**

Update: Assign sample names by copy and paste from a local spreadsheet

If you would like to assign sample names in bulk, you may copy/paste your own sample names from a local spreadsheet (seen below):

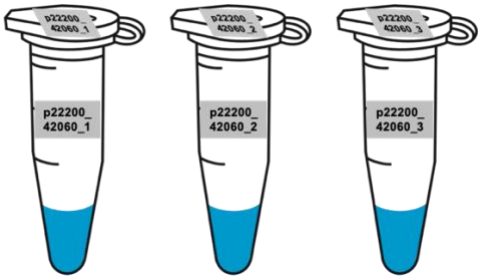


After clicking assign, a pop-up window will open where you may paste your own sample names. You must then copy the sample names from your local spreadsheet, navigate to the pop-up window, and press Ctrl + V to assign your sample names directly to the samples (seen below):



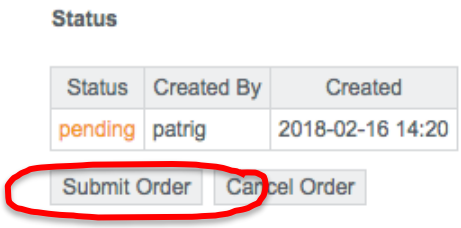
You must then click “Assign” and fill out the rest of the required fields (indicated with a red *).

10. Please leave the **Tube Id** unchanged and use these numbers (project ID + Order ID) when labeling your tubes. Please label your tubes on **TOP and on the side** with the Tube ID.



11. Click on “Save”

12. Click on “Submit Order” button on the bottom of the page.



13. Your project coach will check the order, accept the order and will add an offer based on your order. Please check the offer and if everything is in order, please bring the samples together with the signed offer and confirmation form. **Do not bring the samples if your order has not been accepted by your coach!**

    IMPORTANT: Once you bring or sent the samples, we will process the samples according to the order details accepted by your coach in Bfabric. We will only refer to the order form on the offer and NOT look at any off-Bfabric communication you had with any staff member.

14. The signed confirmation form means that you agree to our terms and conditions.

15. You will receive status updates every time a milestone is reached in the processing of your order. The current state can always be checked on the order page.

Sequencing Output [Disclaimer]: Please note that we cannot guarantee the exact read numbers per sample but do our best to provide the requested amount of data.

Creating an order in B-Fabric for HT Sequencing/Short Read Sequencing: Ready-made Libraries

Important: Please precisely follow these instructions when submitting **ready-made libraries**. If you are submitting **RNA or DNA samples for library preparation** please follow the instructions **here** instead.

1. Minimum order is 1 physically separated lane. *(1 lane of the Novaseq for SP, S1, S2 and half an S4 flowcell or 1 lane of HS2500).*
2. Pool samples together that will be sequenced on the same lane.
3. Dilute your samples to 10nM or an agreed upon concentration. We still need to QC and dilute your pooled libraries properly. We have to start with 10nM for the best results.

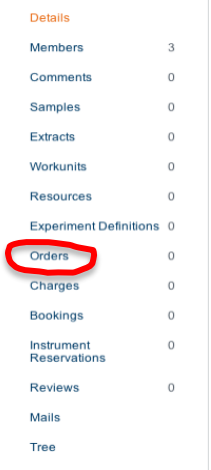
   At the end we will need 3 nM of your pooled libraries and use the following volumes:

SP/S1	150ul
S2	200ul
S4	400ul

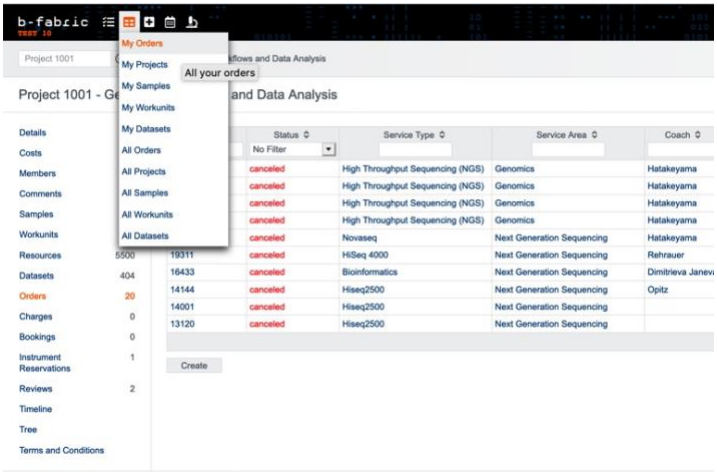
Order submission: step-by-step guide

1. Please login to your project main page B-Fabric. If you have more than one project at the FGCZ, please make sure you are in the correct project page.

2. Click on the "Orders" button listed on the left part of the screen:



   Or by clicking on the following icon on top of the screen:

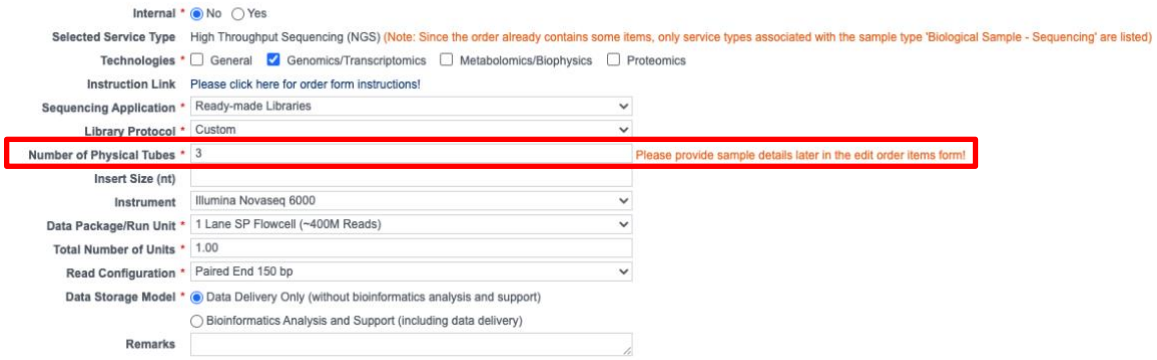


3. Click on the "Create Order" button.

4. Under "Service Area", click on "High Throughput Sequencing".
Select "**Ready-made Libraries**" under "Sequencing Application" and fill up the remaining form (Library Protocol, Instrument, Data Package/Run Unit, Read Configuration …) as best you can. If you indicate "I don't know", your coach will get in touch with you to clarify your order.

Important: When creating an order please select the **number of physical tubes** that you will deliver. This corresponds to the **number of pools** you have. If you have one pool select 1, if you have two pools select 2 etc. (see figure below).

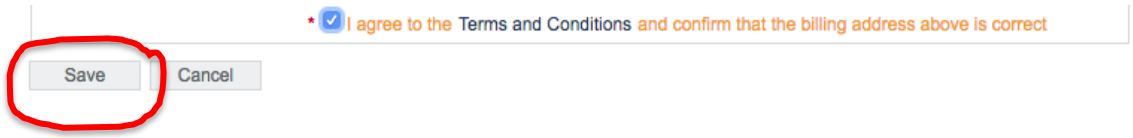
Each pool will get a **separate Tube ID** that you will have to use for the labelling later on.



Note: Please indicate any special instruction in the "Remarks" field.

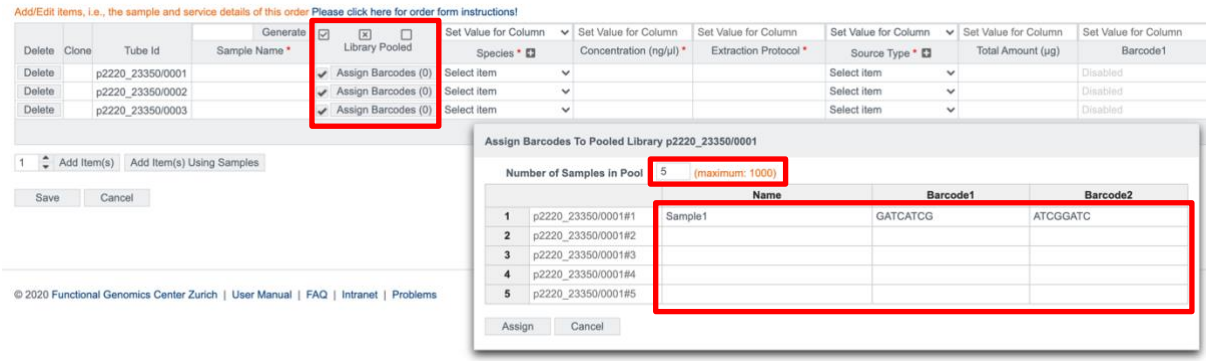
Important: Please fill up the form as best as possible by following the instructions in the section above. **We will rely on the information you provide in sequencing your libraries.** Please don't assume that we know how to sequence your libraries. We really prefer for you to be as specific as possible.

5. Check if the billing address is correct. Please note that ETH/UZH users will be required to enter their fund number for invoicing. If not sure about the fund number please ask your group leader. Click on Agree and Save.



6. A table will open with fields for the **number of physical tubes / pools** you have chosen previously.

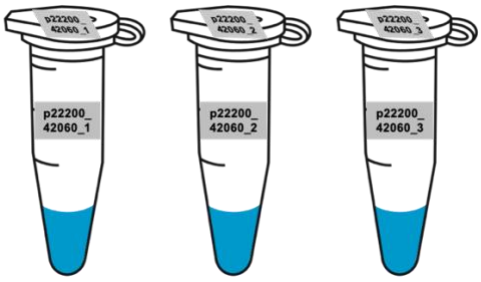
7. By default, the "**Library Pooled**" option will be selected on the "Edit order items" page. Click on "**Assign Barcodes**" and define the number of samples in each pool (see figure below).



8. **Important: For each sample in the pool the barcode sequences have to be assigned** (Barcode1 = i7. Barcode2 = i5). Please be aware that only unique barcodes / barcode combinations are accepted in a given pool. You can also define the sample names in the column on the left. It is possible to copy and paste the barcodes and sample names directly from a table.

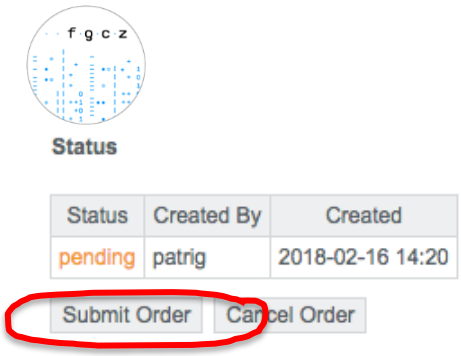
9. Enter the information about your pools like **Sample Name**, **Species**, **Concentration, Extraction Protocol ….**

10. Please leave the **Tube Id** unchanged and use these numbers (project ID + Order ID) when labeling your tubes. Please label your tubes on **TOP and on the side** with the Tube ID.



11. Click on "Save"

12. Click on "Submit Order" button on the bottom of the page.



13. Your project coach will check the order, accept the order and will add an offer based on your order. Please check the offer and if everything is in order, please bring the samples together with the signed offer and confirmation form. **Do not bring the samples if your order has not been accepted by your coach!**

    IMPORTANT: Once you bring or sent the samples, we will process the samples according to the order details accepted by your coach in Bfabric. We will only refer to the order form on the offer and NOT look at any off-Bfabric communication you had with any staff member.

14. The signed confirmation form means that you agree to our terms and conditions.

15. You will receive status updates every time a milestone is reached in the processing of your order. The current state can always be checked on the order page.

Sequencing Output [Disclaimer]: Please note that we cannot guarantee the exact read numbers per sample but do our best to provide the requested amount of data.