



Welcome to the Novogene premade library sample submission guide!

ADVANCING GENOMICS
IMPROVING LIFE

In this guide, you will find a detailed walkthrough of the Novogene sample submission process for premade libraries. Please note that you can reach out to your dedicated technical support representative at any time for help.

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Step 1: Locate your project on CSS

Quick Access

- Total Project: 0
- My Team: 0
- Sample QC: 0
- Library QC: 0
- Final Re: 0

To Do List

Click the "Send Samples" button here to begin the sample submission process

Send Samples

Search for projects here

No.	Project Name	Creation Date	Contract No.	Quotation No.	Regional Sales	Technical Support
01	TEST-Davis-US-2-Premade Partiallane NovaSeq PE150-300G-WO...	2023-03-03	H2025C23030470	NVUS2023030253	F	E
02	TEST-US-Davis-2-Premade Lane NovaSeq PE150-1-WOBI-NVUS20...	2023-03-03	H2025C23030468	NVUS2023030252	E	E

- Here, you'll find all of your Novogene sequencing projects (past and present)
- Your newest project should be at the top of the list
- You can also search for any project using the quotation number in the 'Project Name' search field (you can find your quotation number on your Novogene quote)
- Your designated Technical Support representative contact information can be found here too (see image above)

Step 2: Begin a new submission

To begin the sample submission process, click on the project name and then click **"Add New Batch"**

Send Samples

Project Name

No.	Project Name	Creation Date	Contract No.	Quotation No.	Regional Sales	Technical Support
01	TEST-Davis-US-2-Premade Partiallane NovaSeq PE150-300G-...	2023-03-03	H2025C23030470	NVUS2023030253	E	E
	Product Name	2023-03-03				Add New Batch
	Pre-made libraries partial lane sequencing (PE150)					

Carefully review all information on the next page. Click **Confirm** to proceed to the next step.

Start a New Batch

Please read the instructions below before you start the new batch. To avoid any issues/delays, please ensure you follow all the points that are important. If you have any questions, please check out our [FAQ](#) section in the Help Center.

Aa

Sample Name

Library/Sub-library Name must begin with a letter of the alphabet and contain a maximum of 17 alphanumeric characters or underscores.

1.5 ml

Tube Size

Send samples in 1.5 ml or 2.0 ml microcentrifuge tubes. 96-well plates and other tubes will risk processing delays and handling fees.

☑

Sample Requirement

Please refer to your quotation for the sample requirements. Any sample failing to follow the sample requirements may risk processing delays.

☠

Biosafety Level

Novogene does not currently accept blood-borne pathogens or purified viral genomes, as well as other agents classified at Biosafety Level 2 or above ("Infectious Sample"). Please notify your Novogene Sales and obtain Novogene's written approval before submitting any such infectious sample(s). Novogene reserves the right to accept or reject the submission of any infectious sample at its sole discretion. Any infectious sample(s) submitted without prior written approval shall be immediately destroyed or returned.

📄

Tube Labelling

Sample names on the tube must match with the Sample Information Form. Please do not include other information on the tube to avoid any discrepancy.

📦

Sample Protection

Seal each tube with parafilm before packaging. We highly recommend placing the sample tubes in a container such as a 50ml tube or cryobox to prevent sample tubes from being crushed by dry ice or other packing materials. Cotton or absorbent papers can be used to prevent tubes from being jostled inside the container.

📦

Shipment and Delivery

Novogene highly recommends that you choose FedEx overnight or international express shipping with dry ice, and to avoid weekend delivery.

I confirm that I have read, understand and agree to the above policy and procedure.

- Following these instructions will ensure your samples are processed without delay
- Novogene sample requirements are listed on your quotation, or they can also be found [HERE](#)

Step 3: Complete basic information

Next, we'll collect some basic information related to your project

Novogene

Step 1. Basic Information

1 Basic Information
2 Add Sample Information
3 Preview & Submit Package

Sender Information

* Sender 1 Name

* Sender 1 Email

* Sender 1 Phone ☎

Sender 2 Name

Sender 2 Email

Sender 2 Phone ☎

* Continent

* Country

Address

- Sender name, email, and phone number should automatically populate (these can also be edited manually)
- If you'd like to add information for a **2nd sender**, you can do so here

NOTE: the 2nd sender will only receive email confirmation that the sample submission form has been submitted but they will NOT be able to access the project on CSS. To grant additional access to another user, please use the MY TEAM function

Sample Summary

SIF Batch Name


* How many tubes will you be sending?

* Library preparation kit

* Does your library require a custom sequencing primer?

* Select special instructions for library QC if any

Extra Service

If you have selected any of the extra services, please contact your Novogene Sales/TS  **Eric Iverson** for more details.

My nucleic acid or library samples are not in 1.5ml or 2ml microcentrifuge tubes and I am willing to pay extra for tube transfer.

Previous Step
Save & Continue

- Complete all required fields in the 'Sample Summary' Section (those with an asterisk). When finished, click '**Save & continue**'
- If your project requires a **custom sequencing primer**, please confirm that this was previously communicated to our team (*if you need help with this, or anything else, please contact Technical Support*)



Step 4: Complete the excel template

Next, you will add your sample information to CSS!

Import from File

Please upload the **Excel & CSV** format for validation. Please download and fill in the latest version of the Sample Information Form below. You can then upload the file in Excel & CSV format via the box below for validation.

After uploading the file, you may still amend it in the next step or re-upload an amended file.

You can always check out our video tutorials in our [Help Centre for more information](#).

Upload your file

Choose or Drag and Drop file (.xlsx, .csv). Please use the correct Novogene template.

Download Excel Template

Download Sample Info Guide

- Click **Download Excel Template** to download the sample information excel sheet
- Open the downloaded excel sheet and complete all required fields. See the sections below for more information

Library Type:

Library Type (Required)	Library Name (name on tube) (Required)
Premade-10X transcriptome library	
Premade-10X whole genome library	
Premade-Chip-seq library	
Premade-Reduced-Representation Genome	
Premade-Hi-C library	
Premade-Others (with fixed bases)	
Premade-Others (without fixed bases)	
Premade-10X VDJ Library	

- Please choose the correct library type for your sample. See Appendix A for more information.

Tip: For 10X libraries, choose the correct 10X library type to prevent demultiplexing errors. If you do not see your specific 10X library type listed, please check the table in **Appendix A** or contact your Technical Support Representative for help.

Library name and sub-library name:

A	B	C
Library Type (Required)	Library Name (name on tube) (Required)	Sub-library Name(for pooled library) (Required. If is not pooled library, just keep it the same as Library Name)
Premade-Eukaryotic cDNA library	A1	A1
Premade-Eukaryotic cDNA library	A2	SubLib1
Premade-Eukaryotic cDNA library	A2	SubLib2

- Library and sub-library names are limited to 17 characters and can only contain letters, numbers, or underscores (no spaces or any other special characters, e.g. #, +, -, etc.)
- Tip:** If you have already labeled your samples, and they violate our naming rules, please contact Technical Support for help

- Non-Pooled Libraries* (samples containing a single library) – See sample ‘A1’ above:

Library Name = Name on the sample tube (must match exactly, no exceptions)

Sub-library Name = Same as the ‘Library Name’

- Pooled Libraries* (Sample containing multiple libraries, aka sub-libraries, within the same tube) – See sample ‘A2’ above:

Library Name = Name on the sample tube (must match exactly, no exceptions). Each sub-library must have the same ‘Library Name’ (this links all sub-libraries to the same tube/sample)

Sub-library Name = Must be unique and cannot match any other sub-library name

Data Delivery Method:

B	C	D
Library Name (name on tube) (Required)	Sub-library Name(for pooled library) (Required. If is not pooled library, just keep it the same as Library Name)	Data Delivery Method (Required)
A1	A1	
A2	SubLib1	<ul style="list-style-type: none"> Lane sequencing-With Demultiplexing Lane sequencing-Without Demultiplexing Lane sequencing-BCL File Partial lane sequencing-With Demultiplexing Partial lane sequencing - Without Demultiplexing (Not available for Clients in North and South America)
A2	SubLib2	

- Choose the data delivery method that meets your project needs:

Lane sequencing (for clients purchasing an entire lane – Novaseq 6000, Novaseq X Plus, or Hiseq)

- With demultiplexing* → Novogene will demultiplex your data. Index information is required (next section)
- Without demultiplexing* → Novogene will not demultiplex your data, but we do require some index information. Please see the next section for help.
- BCL File* → Delivery of the run BCL file. Index information is not required (please reach out to your Technical Support representative **asap** if you have not done so already)

Partial Lane sequencing (for clients purchasing a partial Novaseq S4 lane):

- *With demultiplexing* → Novogene will demultiplex your data, requires index information
- *Without demultiplexing* → UNAVAILABLE (partial lane libraries **must** be demultiplexed)

i7 and i5 Index Information:

B	C	E	F
Library Name (name on tube) (Required)	Sub-library Name(for pooled library) (Required. If is not pooled library, just keep it the same as Library Name)	i7 Index Sequences (Required when data need be multiplexing)	i5 Index Sequences
A1	A1	ACTGAGGA	GGATCGAT
A2	SubLib1	CAGCAGTA	TATGCAGT
A2	SubLib2	TGCGAAGC	AGCATGCC

• Index orientation

- All index sequences should be provided in the **V1.0 orientation (workflow A/Forward)**
- See **Appendix B** for more information

- i7 index information is required for every library/sub-library*
- i5 index is optional (include if your library is dual indexed)

Insert Size and Library Status:

G	H
Insert Size(bp) (Required)	Library Status (Required)
300	Others
300	Others
300	Others

- *Insert Size* → Average insert size of your library (this can be estimated or measured prior to sending the samples. Novogene will measure the insert size prior during QC testing)
- *Library Status* → Select 'others' if your sample is dissolved in water or TE buffer. If library is lyophilized, select 'dry powder' (please note that lyophilized samples incur an additional rehydration fee)

Total Data Amount and Data Unit:

B	C	I	J
Library Name (name on tube) (Required)	Sub-library Name(for pooled library) (Required. If is not pooled library, just keep it the same as Library Name)	Total Data Amount (Required)	Data Unit (Required)
A1	A1	100	G raw data
A2	SubLib1	200	G raw data
A2	SubLib2	200	G raw data

- *Total Data Amount* → Amount of data requested per library

The total amount of data requested should match the amount of data on your Novogene quotation

Note about pooled libraries: The data amount listed for each sub-library in the pool should be the same and should reflect the amount of data requested **for the entire pooled sample**.

In the example above, the pooled library A2 will receive 200 Gb raw data total. Each sub-library will receive an amount of data that is dependent on the ratio of libraries within the pool (the pooling ratio is determined prior to sending the sample to Novogene and *cannot be adjusted by our lab*)

- *Data Unit* → Must be listed as 'G raw data'

If you need assistance converting from 'M raw reads' to 'G raw data', please see **Appendix C** or reach out to your technical support representative for assistance

Step 5: Upload the excel template

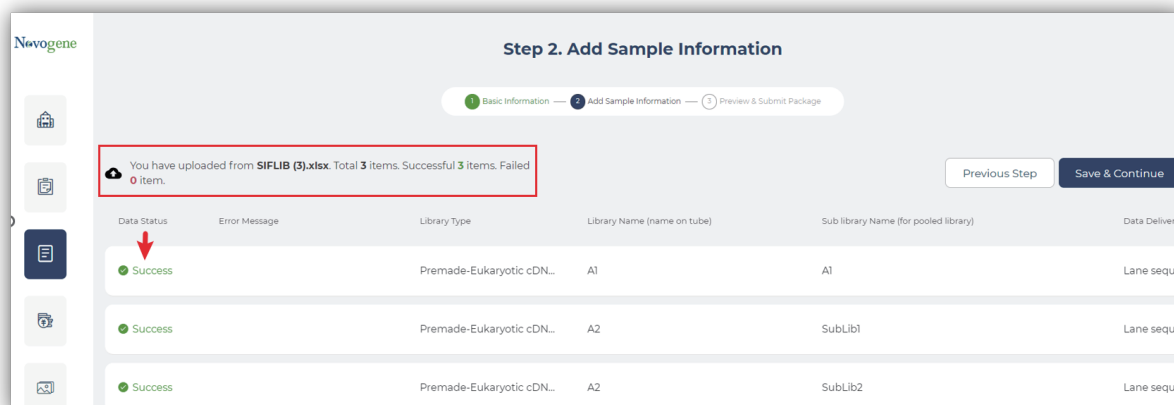
Drag and drop the file OR click the 'upload your file' button and upload the file from your computer

The screenshot displays two versions of the 'Import from File' interface. The left version shows a blue box with the text 'Upload your file' and 'Choose or Drag and Drop file (.xlsx, .csv). Please use the correct Novogene template.' Below this box is a red arrow pointing to the text 'Drop your excel template here'. At the bottom are two buttons: 'Download Excel Template' and 'Download Sample Info Guide'. The right version shows a green box with a checkmark and the text 'Your file is uploaded' and 'Your file has successfully uploaded. You can click Continue to process the template now.' Below this box is a 'Continue' button. At the bottom are the same two buttons as in the left version.

- Once the upload is complete, the upload box should turn from **blue** to **green**
- Click '**Continue**'

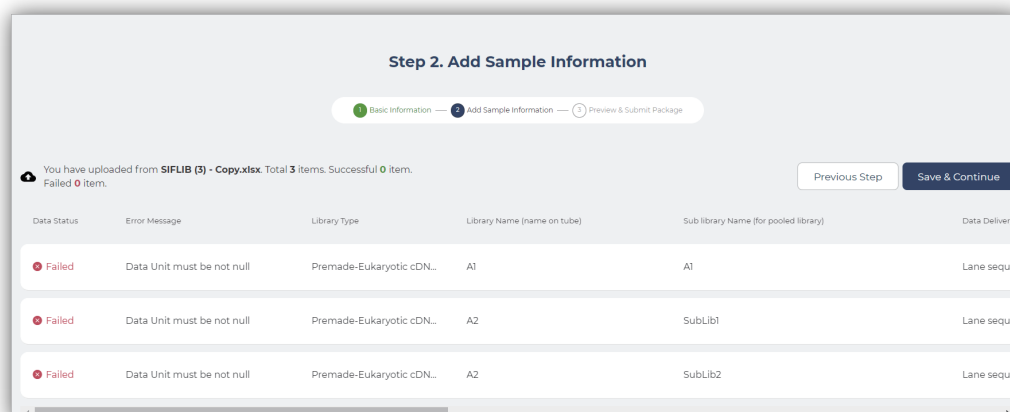
Step 6: Confirm all samples were uploaded successfully

After uploading the excel file, the system will review the information and will notify you of any issues



- At the top of the screen, you can view the number of **successful** and **failed** samples
In this example, all three libraries were uploaded successfully (no issues)
- Click **Save & Continue** if the file was uploaded correctly. If not, see the example below for further instructions.

Example: One or more samples failed to upload



- Above is an example of a failed upload
- A description of the problem will appear under the 'Error Message' field (in this example, the data unit was not specified, and the upload failed)

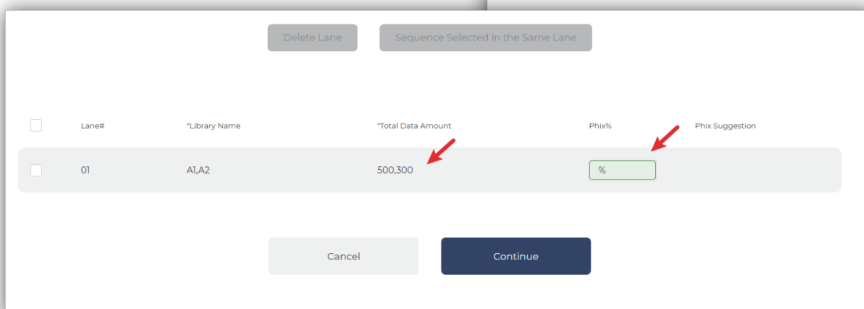
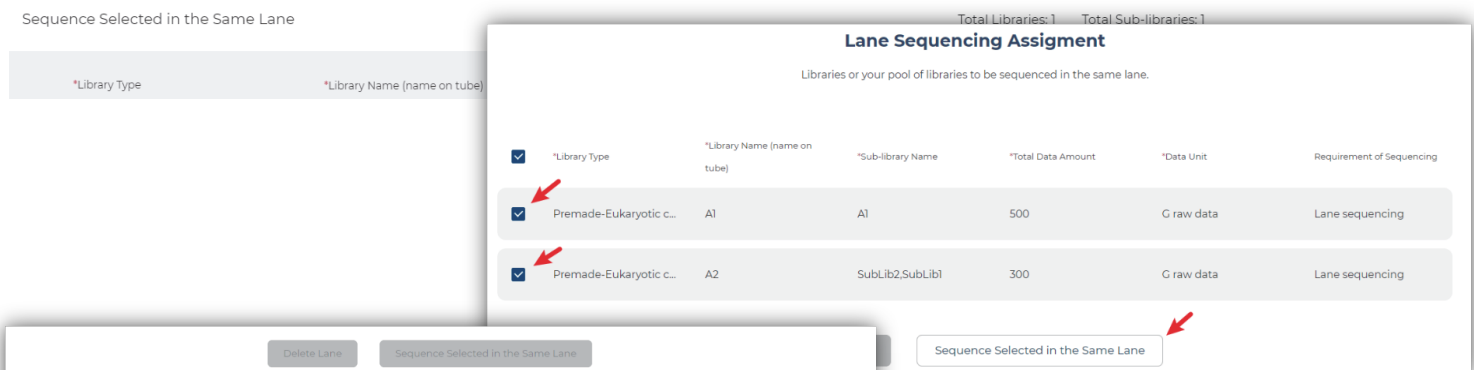
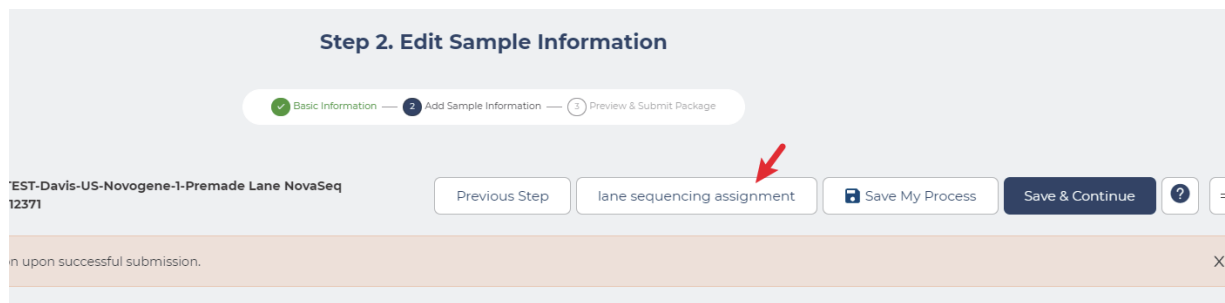
To revise:

1. Click **Previous Step**
2. Fix the mistake on the excel form
3. Re-upload the edited/fixed form and click **Continue**
4. Make sure all samples are listed as successful. If so, click **Save & Continue**

Step 7: Review and lane assignment*

*Lane assignment is only for full lane sequencing projects. **Partial lane customers please skip to the section below**

- 1 Click 'lane sequencing assignment'
- 2 On the next screen, select the libraries you'd like sequenced on the same lane (In this example, both libraries A1 and A2 are to be sequenced on the same lane). Then select 'Sequence in the Same Lane'
- 3 Confirm the total data amount is correct
 - Novaseq S4 lanes produce 800 G raw data
 - Hiseq lanes produce 110 G raw data
 - Novaseq X-Plus 10B lanes produce 375 G raw data
 - Novaseq X-Plus 25B lanes produce 1000 G raw data
- 4 Adjust the % of PhiX spike in per lane
 - If no PhiX is required, leave blank (do not add '0%')
 - If you are not sure about the PhiX spike in, please check your library prep kit or reach out to Technical Support for assistance
- 5 Click **Continue**, then **Save & Continue**



Partial lane customers:

- Review all information one more time, then click **'Save & Continue'** if everything is correct

Step 2. Edit Sample Information

1 Basic Information — 2 Add Sample Information — 3 Preview & Submit Package

SUS20230307027 / H2025C23030470 / TEST-Davis-US-2-Premade Partiallane
NovaSeq PE150-300G-WOBI-NVUS2023030253

Previous Step Save My Process Save & Continue

Sample Information Sequence Selected in the Same Lane Total Samples: 3

No.	Product Name	*Library Type	*Library Name (name on tube)	*Sub-library Name (for pooled library)	*Data Delivery Method
<input type="checkbox"/> 01	Pre-made libraries partial lane ...	Premade-Eukaryotic cDNA library	A1	A1	+ Partial lane sequencing-With...
<input type="checkbox"/> 02	Pre-made libraries partial lane ...	Premade-Eukaryotic cDNA library	A2	SubLib1	+ Partial lane sequencing-With...
<input type="checkbox"/> 03	Pre-made libraries partial lane ...	Premade-Eukaryotic cDNA library	A2	SubLib2	+ Partial lane sequencing-With...

Step 8: Index check

All index sequences are compared against a database to help ensure the sequences are in the correct orientation for demultiplexing. You may be prompted to review your index sequences if any potential issues are detected

Checking Reminder

Reverse Complementary Sequence Database Not Found

You may have provided the reverse complementary sequence(s) of 15 index(es) of the sample(s) below, please check and confirm:

SubLib1

Ignore and Continue Check Again

- Error code: *Reverse Complementary Sequence*

- Libraries with an index *potentially** submitted in the incorrect orientation will be listed here
- **Reminder:** all indexes should be submitted using the V1.0 orientation (workflow A/Forward)

- Error code: *Database Not Found*

- Libraries with an index that is not listed in the database. This could be due to a mistake in the sequence or because the index is part of a kit that is not included in the database*

* Please note that our database does not include ALL index sequences for every kit/manufacturer. If you are confident your index is in the correct orientation, you can ignore these warnings and proceed. **Keep in mind that additional fees/penalties may apply if the incorrect index results in complications during demultiplexing.**

To Continue → Click '**Ignore and Continue**'

To Revise → Click '**Check Again**' and complete the following steps:

- 1 Click '**Previous Step**'
- 2 Edit/revise the index sequences on your excel form and re-upload when finished
- 3 Proceed through all other steps, as indicated above, then click '**Save & Continue**' to proceed to the final steps

Step 9: Provide shipping information and review the pre-shipping checklist

Step 2. Edit Sample Information

1 Basic Information — 2 Add Sample Information — 3 Preview & Submit Package

Novogene Lab Address:

**ATTN: Sample Receiving Department,
Novogene Corporation Inc.**

2921 Stockton Blvd., Suite 1810, Sacramento CA
95817

Tel: 916-252-0068

* Transportation Condition

Select
▼

* Courier Provider

Select
▼


Tracking No.

- Select the correct transportation condition from the dropdown list

- We highly recommend that you include dry ice in all shipments.
- How much dry ice should I include? At least 10 lb per day of shipping (e.g. overnight shipments should include ~10 lb of dry ice)
- Can I ship samples on any day of the week? No, please only ship samples Mon – Wed to help minimize shipping-related issues/delays

- Select the shipping courier from the dropdown list
- Provide a Tracking #, if available (if not, no worries! Please share the tracking # with your Technical Support representative when you have it)
- **Novogene Shipping Address:**

ATTN: Sample Receiving Department
Novogene Corporation Inc.
2921 Stockton Blvd.
Suite 1810
Sacramento, CA 95817
Tel: 916-252-0068



Please take a moment to review all shipping instructions (*this can prevent any unnecessary delays and will ensure your samples are processed efficiently*):

Samples classified as Biosafety **Level 2 (BSL-2)** or above ("infectious samples") will not be accepted unless they have a written approval from Novogene. If you have samples that are classified above BSL-2, please contact your sales manager for more details.

Samples are in 1.5 or 2.0ml flip cap Eppendorf tubes, and are labelled in black permanent marker at the top and side of each tube matching the sample name submitted. Samples are properly sealed with parafilm and cushioned enough to avoid damage. OR Samples are in the appropriate tube/slide/other formats required for extraction and are labelled in black permanent marker accordingly. OR Samples are not in 1.5 or 2.0ml flip cap Eppendorf tubes, and I am aware that additional charges may apply. No

Samples are packed with appropriate shipping conditions such as ambient temperature, gel pack or dry ice. For dry ice, we recommend packing in 10 lb/5 kg for overnight shipping or two-day shipping depending on your local shipment options. No

Shipment will be delivered on weekdays. We recommend shipping with overnight or international express. No

Samples do not contain any potential or known infectious material such as pathogens, infectious genetic materials etc. OR Prior written approval from Novogene was obtained for samples that may contain any potential or known infectious material. No

Please put the hard copy of the Sample Information Form (SIF) in the parcel. No

- After reviewing each item, click the toggle to **YES**
- Please remember that **we cannot accept** any samples that are classified as **BSL2 or above**. If you are sending samples BSL2 or higher (or you are not sure), *please contact your Technical Support representative before shipping*

Step 10: Final review and submission

- In this final step, please take one final opportunity to review your sample information
- If everything looks correct, click **Submit**
- **Congratulations**, you're finished!

Step 11: Technical support review and approval

What happens after you submit the Sample Information Form?

- 1 Your designated Technical Support representative will review your submission within 1-2 hr
- 2 After reviewing, your Technical Support representative will either approve the form (if everything looks good), or reject the form (if there is a problem)

If **Approved** → You'll receive an email notification confirming that you can ship your samples.

If **Rejected** → You'll receive an email notifying you that the form was rejected. Your Technical Support representative will reach out with more information to help you correct the form. After making those corrections, you'll need to re-submit the form (following the steps above).

Thank you for taking the time to review our sample submission guide. Please don't hesitate to contact us if you have ANY questions. Happy sequencing!

Appendix A: Choosing the correct library type on the Sample Information Form

Please use the table below to help select the correct library type for 10X Genomics libraries and other related libraries. If you do not see your specific library type here, please reach out to Technical Support for help

Common 10X Genomics libraries (and related libraries)	Which library to choose on Sample Information Form
<ul style="list-style-type: none"> ▪ 10X scRNA 3' libraries (single and dual index) ▪ 10X scRNA Gene Expression library from 10X Chromium sc Multiome ATAC + Gene Expression Reagent Kits ▪ 10x Visium Spatial Gene Expression* 	Premade-10X Single Cell Transcriptome Library
<ul style="list-style-type: none"> ▪ 10X VDJ libraries (single and dual index) ▪ 10X scRNA 5' libraries (single and dual index) 	Premade-10X VDJ Library
<ul style="list-style-type: none"> ▪ 10X scATAC 	Premade-10X ATAC Library
<ul style="list-style-type: none"> ▪ 10X scATAC library from 10X Chromium Multiome ATAC + Gene Expression Reagent Kits (NOTE: this is for multiome ATAC libraries, not the multiome Gene Expression libraries) 	Premade-10X ATAC (Multiome) Library
<ul style="list-style-type: none"> ▪ 10X Cell Surface Protein (CSP), Feature Barcoding for Cell Surface Protein, CRISPR Screen, Cell Multiplexing. CITE-seq, ADT, Cell Hashing, Hashtag, ASAP-seq using 10x library kits. 	Premade-10X Feature Barcode Library

Appendix B: Choosing the correct index orientation

Our demultiplexing software requires the index sequence in V1.0 orientation (workflow A/forward).

For the i7 index, please refer to "i7 bases for sample sheet" in your library preparation guide.

For the i5 index, please select "i5 Bases for Sample Sheet NovaSeq 6000 with v1.0 reagent kits".

Here is an example from Illumina:

Index Name	i7 Bases in Adapter	i7 Bases for Sample Sheet	i5 Bases in Adapter	i5 Bases for Sample Sheet NovaSeq 6000 with v1.0 reagent kits, NovaSeq X Series, MiniSeq with Rapid reagents, MiSeq, HiSeq 2000/2500, NextSeq 1000/2000 (Sample Sheet v2)	i5 Bases for Sample Sheet iSeq, NovaSeq 6000 with v1.5 reagent kits, MiniSeq, NextSeq 500/550, HiSeq 3000/4000/X, NextSeq 1000/2000 (Sample Sheet v1)
UDI0001	CCGCGGTT	CCGCGGTT	AGCGCTAG	AGCGCTAG	CTAGCGCT
UDI0002	TTATAACC	TTATAACC	GATATCGA	GATATCGA	TCGATATC
UDI0003	GGACTTGG	GGACTTGG	CGCAGACG	CGCAGACG	CGTCTGCG

Here is an example from 10X Genomics Dual Index Kit TT, Set A:

	A	B	C	D	E
1	# Workflow A = Illumina Forward Strand Sequencing Workflow				
2	# Workflow B = Illumina Reverse Complement Sequencing Workflow				
4	index_nar	index(i7)	index2_workflow_a(i5)	index2_workflow_b(i5)	
5	SI-TT-A1	GTAACAT	AGTGTTACCT	AGGTAACACT	
6	SI-TT-A2	GTGGATC	GCCAACCCTG	CAGGGTTGGC	
7	SI-TT-A3	CACTACG	TTAGACTGAT	ATCAGTCTAA	

Appendix C: Converting from M raw read pairs to G of raw data

Please use the formula below to quickly convert from M raw reads to G. Note that this formula is only applicable for PE150 sequencing projects.

$$G \text{ of raw data} = (\# \text{ of } M \text{ raw read pairs}) \times (0.3)$$

Example:

20 M read pairs = ??? G of raw data

G of raw data = (M read pairs) x (0.3) = (20) x (0.3) = 6 G of raw data

Why is 0.3 used in the equation? This corresponds to 300 bp, which is the combined read length of read 1 and read 2 in PE150 sequencing. We would obtain the same answer if we multiplied 300 bp by 20 million (try it!)



Novogene Corporation Inc.

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