Novogene

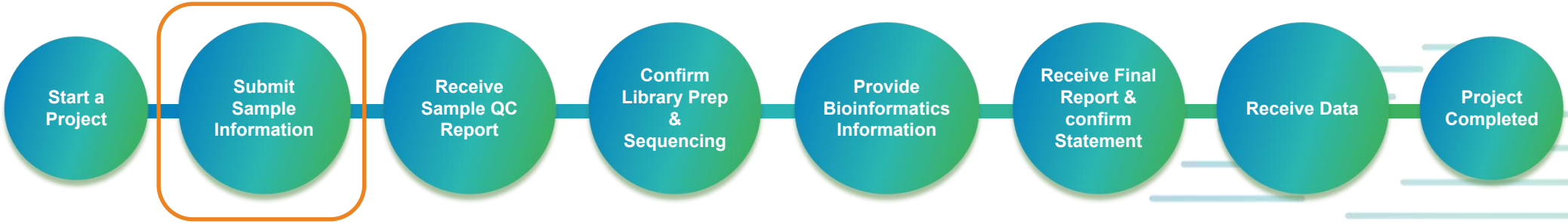
How to submit Sample Information Form (Premade Libraries)

Novogene Customer Service System (CSS) Instruction Guide

June 2024

CSS Overview

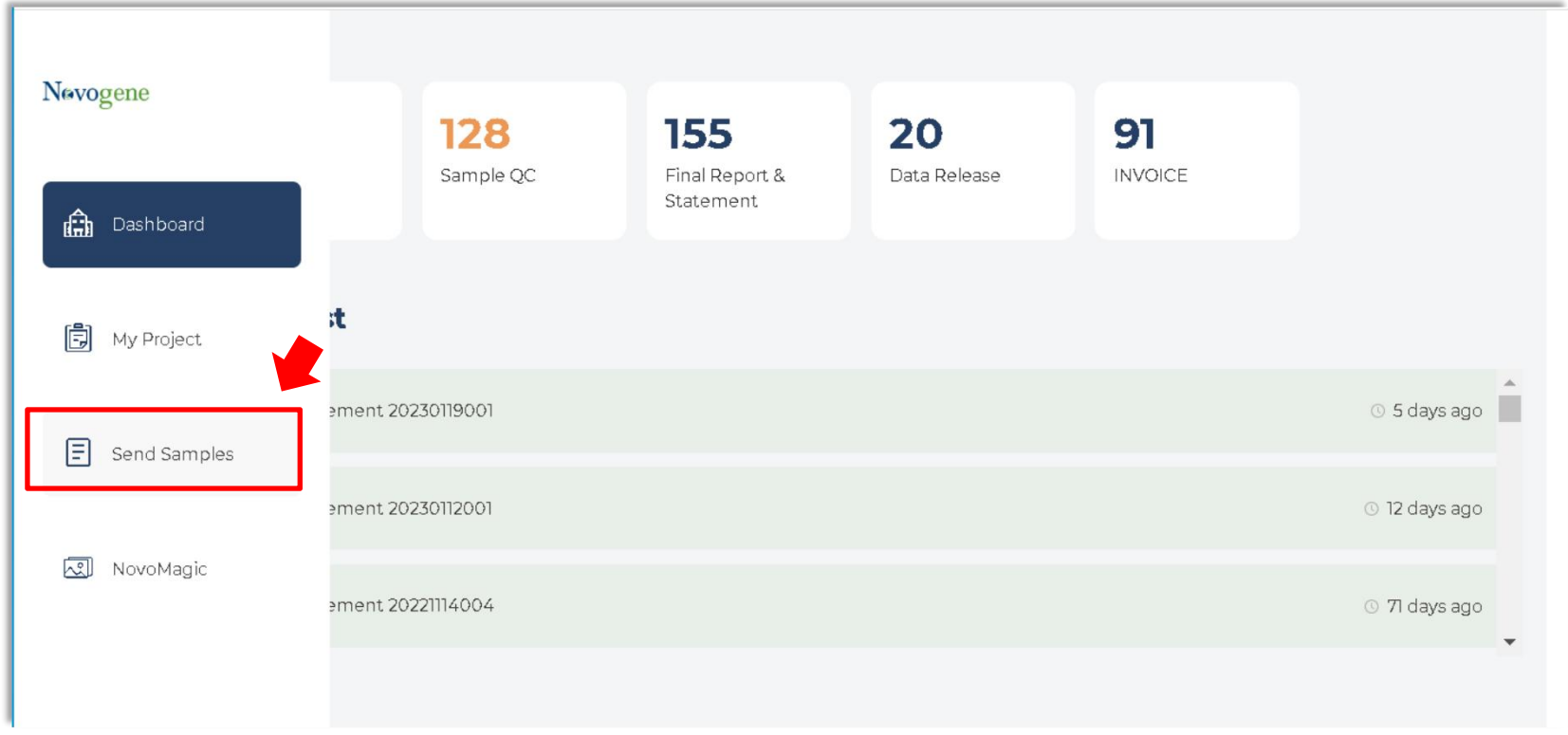
In Novogene, you can manage the sequencing project(s) on CSS through these simple steps.



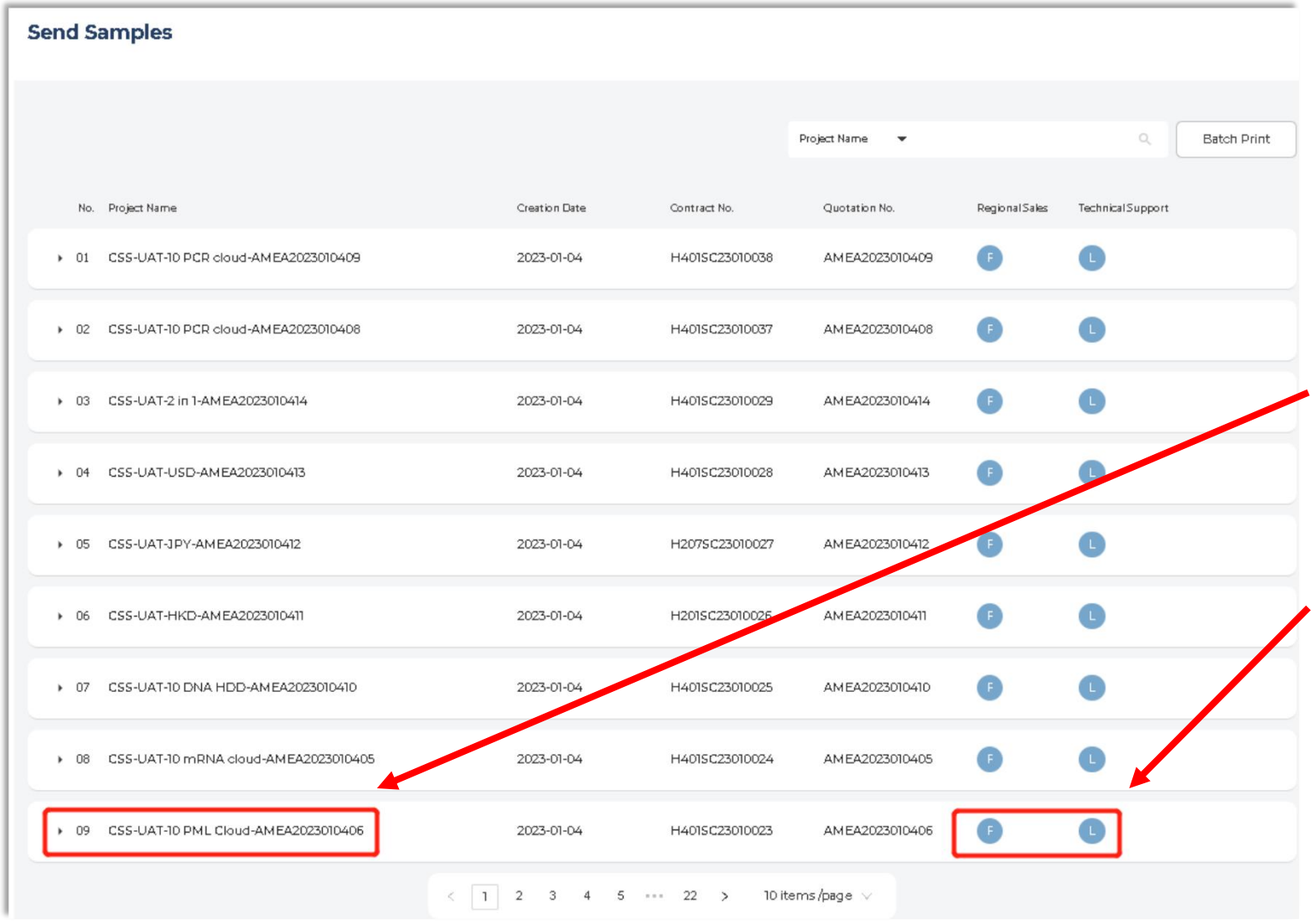
In this guide, we will show you how to submit Sample Information Form for your Premade Libraries using CSS.

Opening the Send Samples menu

To submit sample information, please locate the [Send Samples] menu on the sidebar your screen.



Selecting a Project to Send Samples

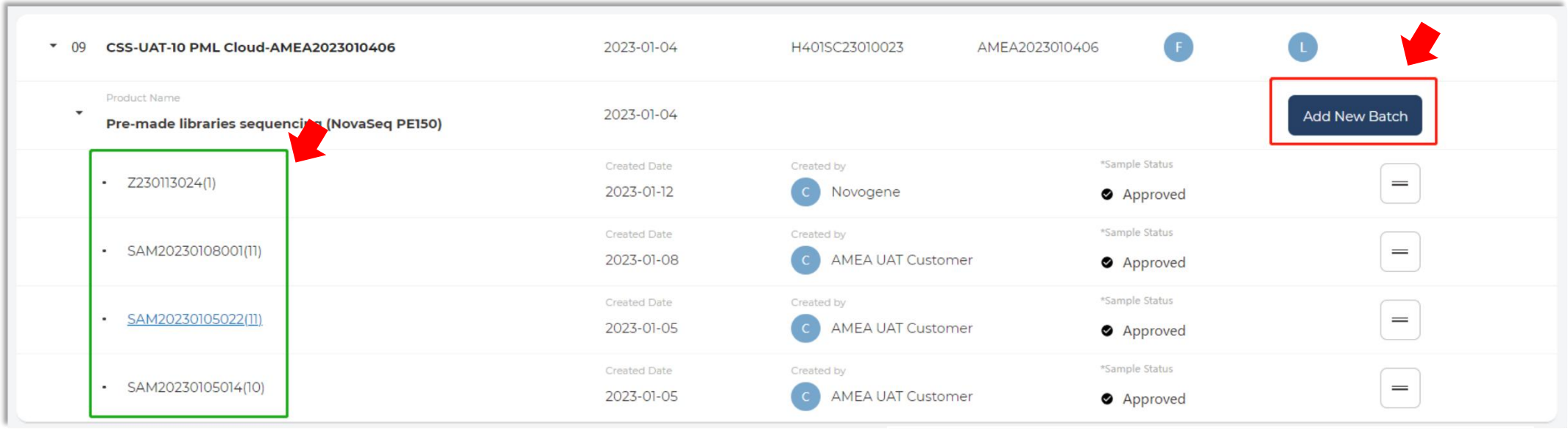


Click on the [Project Name] to expand the project and submit samples.

Hover your cursor over the [name icon] to view the email addresses of the Novogene Representatives for your project. You can contact them if you have any queries.

Creating a New Sample Information Form

Click [Add New Batch] to start a new batch.

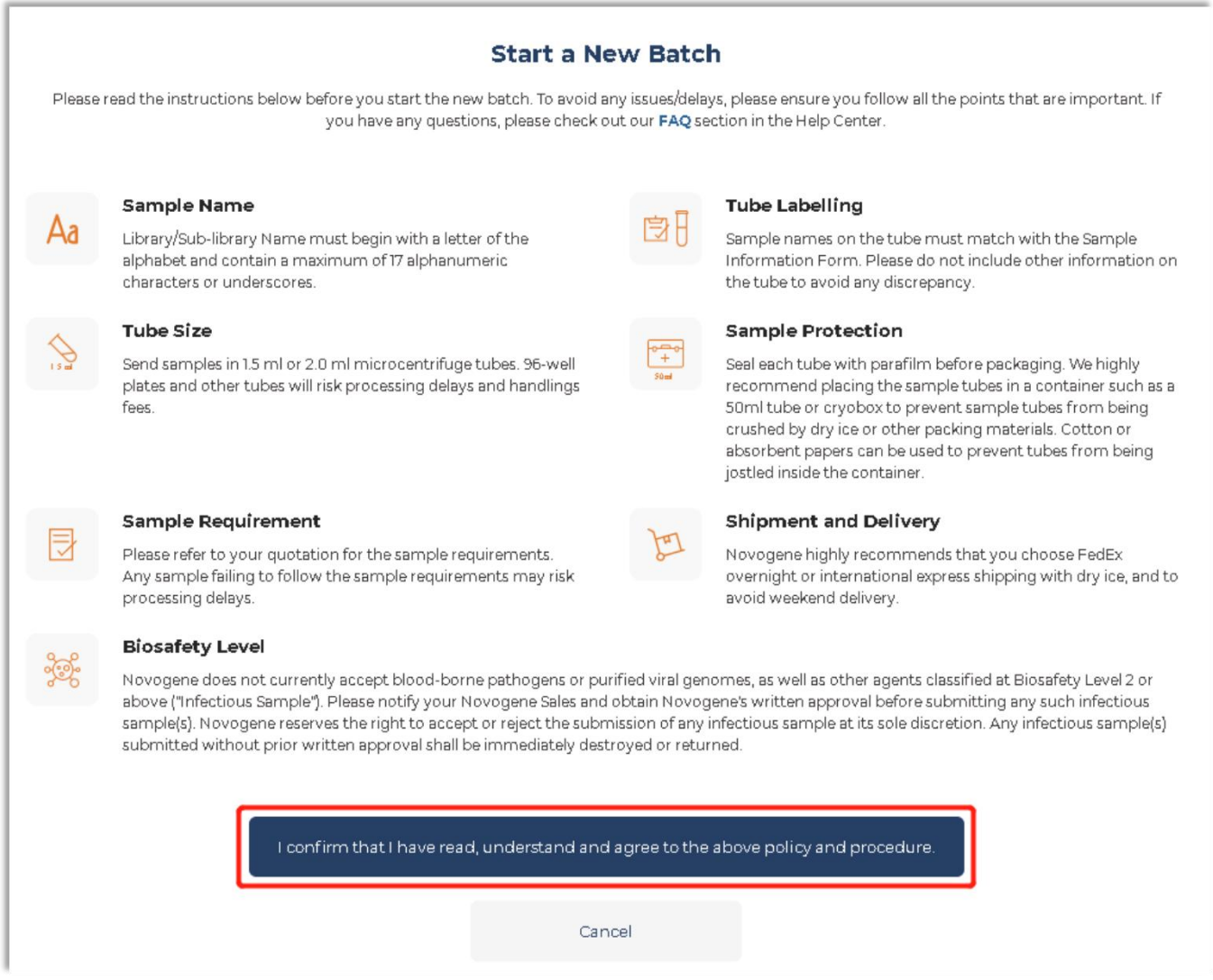


Here is a list of Sample Information Forms (SIF) that you have created previously.
The number in the bracket indicates the number of samples you have on the SIF.

Sample Status:

- [Editing] means that the SIF has not been submitted.
- [Submitted] means that the SIF has been submitted.
- [Approved] means that the SIF has been checked and accepted by the Novogene Representative.

Understanding the send samples Policy and Procedure



These are useful tips and instructions for sample preparation.

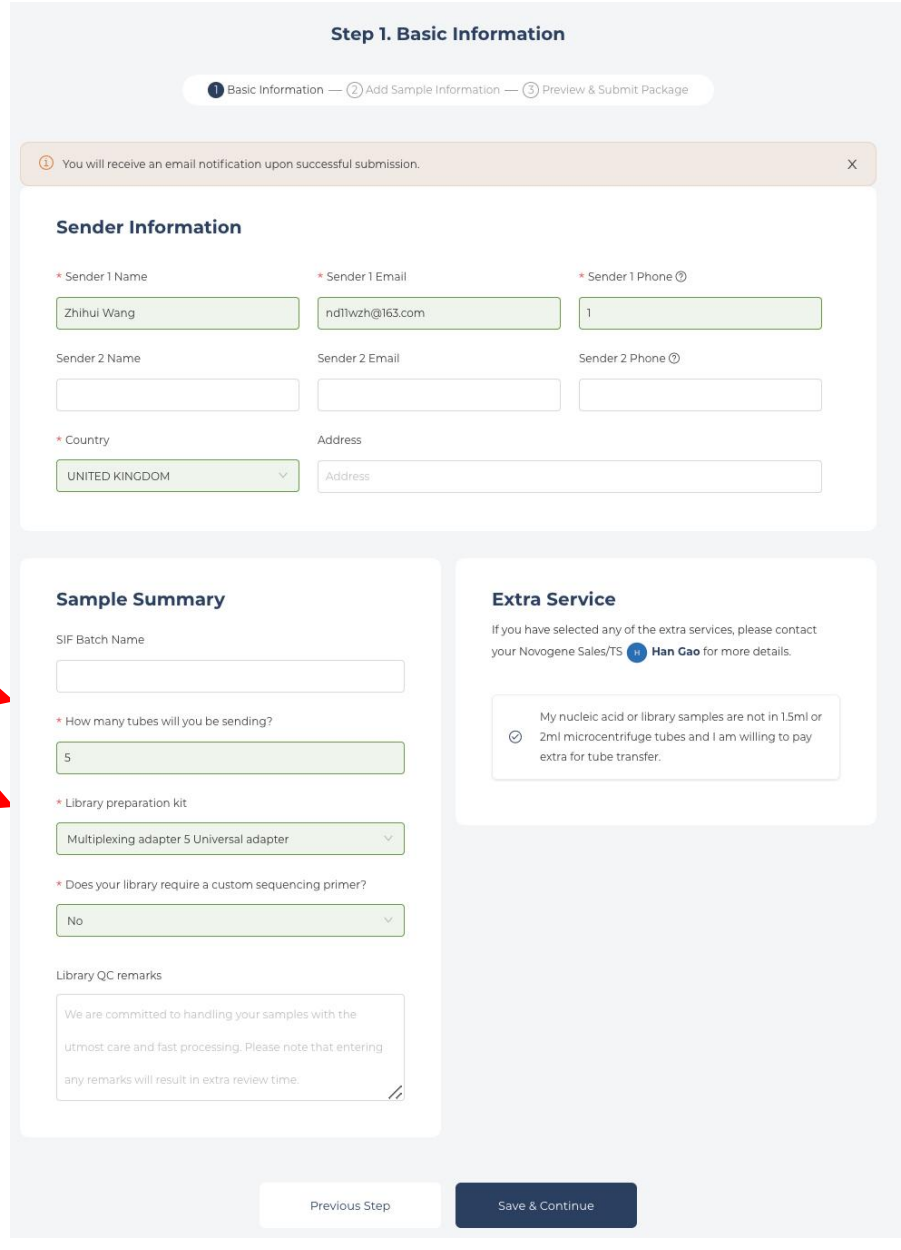
The Library Name has a maximum of **17 alphanumeric characters** and **MUST** begin with an alphabet.

Please **read and follow** the instructions carefully to ensure that there will be no discrepancies when your samples reach our lab.

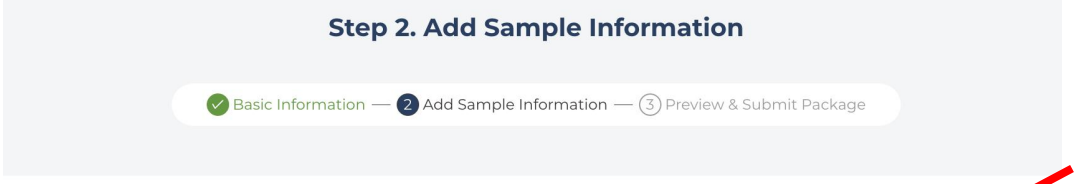
Click [I confirm] to continue.

Sender Information & Sample Summary

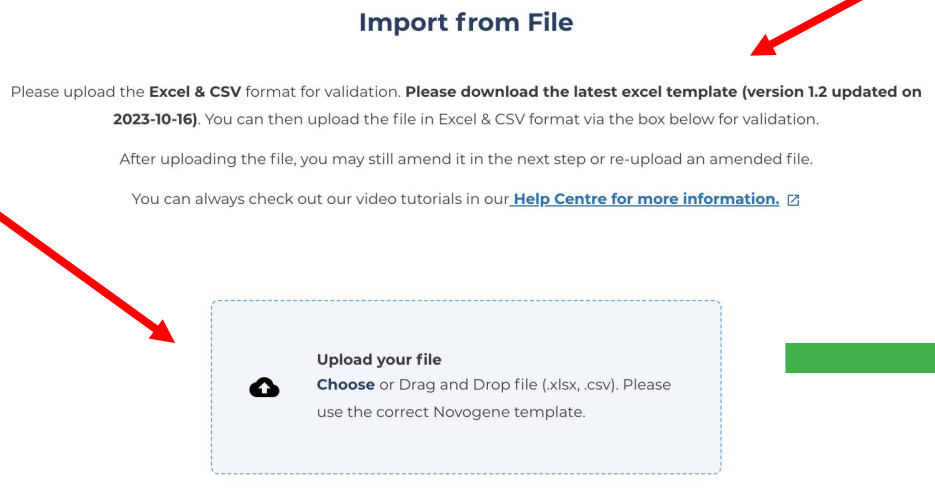
- **Sender Information** will be used by our Novogene Representative related to this SIF.
- You can **customize** the name your batch up (max: 8 characters).
- Please fill in the number of **physical** tubes you will be sending, including the back-up samples.
- Select the **library preparation kit** you've used from the dropdown list。If you choose Others, please specify it.
- Select "**Yes**" if you are using customised primers.Please specify your requirments for sequencing.
- You can write note for requirment for library QC stage .
- Click [Save & Continue] to proceed



Adding Sample Information

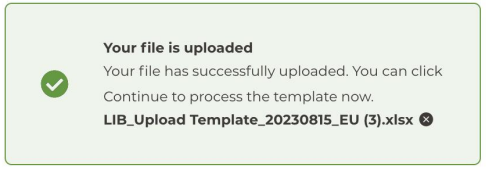


Please check the latest update date for upload template here.

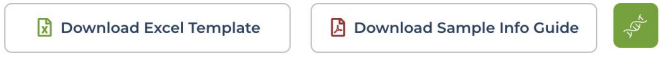


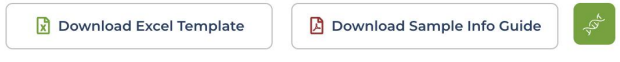
Step 2: Click [Upload your file] or drag and drop to upload your sample information form.

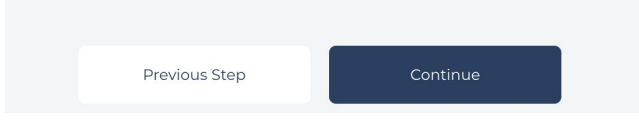
Step 3: When upload is completed, click [Continue] to proceed.



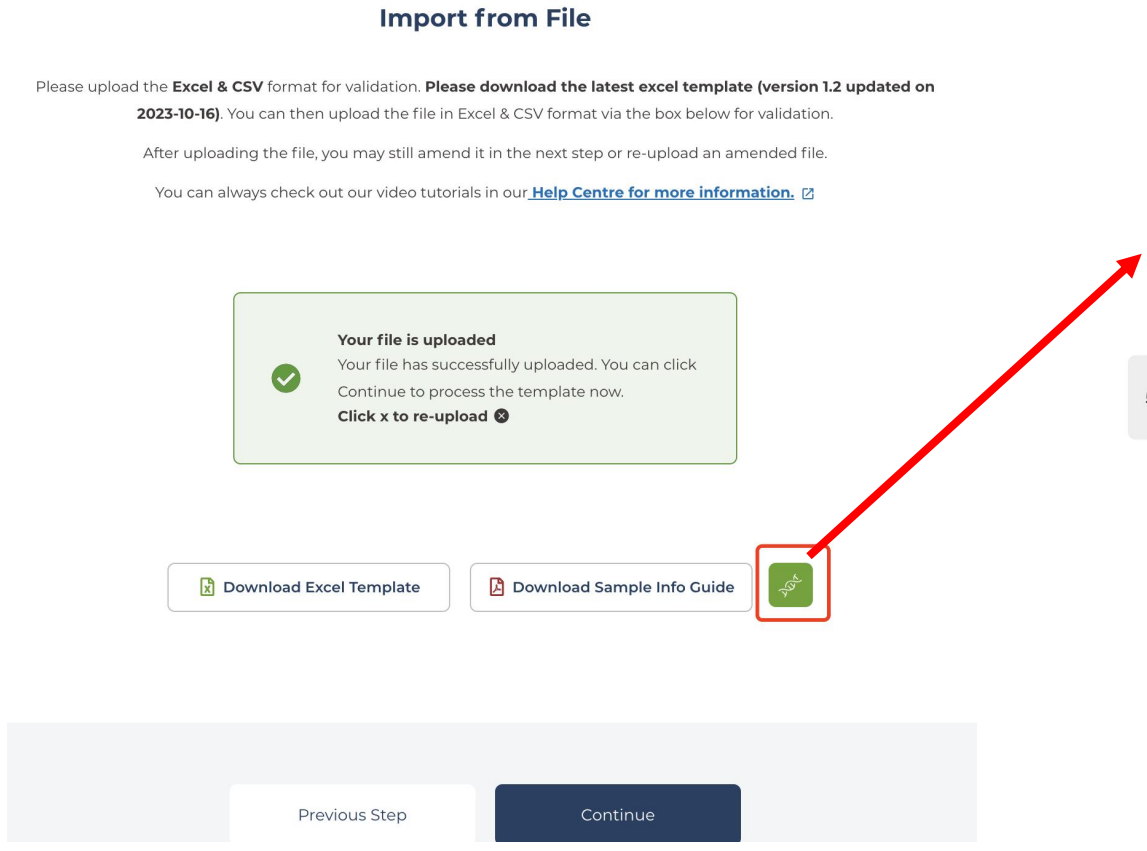
Step 1: Click [Download Excel Template] to download the sample information form.







Instruction for i5 and i7 Index



Click on the green icon [ ] to bring up the **premade library instruction** guide.

Filling up a Sample Information Template

	A	B	C	D	E	F	G	H	I	J	K	L
1	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)	Data Delivery Method (Required)	i7 Index Sequences (Required when data need be multiplexing)	i5 Index Sequences	Insert Size(bp) (Required)	Library Status (Required)	Total Data Amount (Required)	Data Unit (Required)	Concentration(ng/ul)	Volume(ul)
2	Premade-WES Library	PML-A	PML_Test_1	Partial lane sequencing-With Demultiplexing	TGCAATGTTC	GCTTGTCGAA	300	Others	12	G raw data		
3	Premade-WES Library	PML-A	PML_Test_2	Partial lane sequencing-With Demultiplexing	TTAATACGCG	CACCTCGGGT	300	Others	12	G raw data		
4	Premade-WES Library	PML-A	PML_Test_3	Partial lane sequencing-With Demultiplexing	CCTTCTAGAG	AATACAACGA	300	Others	12	G raw data		
5	Premade-WES Library	PML-A	PML_Test_4	Partial lane sequencing-With Demultiplexing	GCAGTATAGG	TTCCGTGCAC	300	Others	12	G raw data		
6	Premade-WES Library	PML-A	PML_Test_5	Partial lane sequencing-With Demultiplexing	TGCAATGTTC	GCTTGTCGAA	300	Others	12	G raw data		
7	Premade-WES Library	PML-B	PML_Test_6	Partial lane sequencing-With Demultiplexing	TTAATACGCG	CACCTCGGGT	300	Others	20	G raw data		
8	Premade-WES Library	PML-B	PML_Test_7	Partial lane sequencing-With Demultiplexing	TGCAATGTTC	GCTTGTCGAA	300	Others	20	G raw data		
9	Premade-WES Library	PML-B	PML_Test_8	Partial lane sequencing-With Demultiplexing	TTAATACGCG	CACCTCGGGT	300	Others	20	G raw data		
10	Premade-WES Library	PML-B	PML_Test_9	Partial lane sequencing-With Demultiplexing	CCTTCTAGAG	AATACAACGA	300	Others	20	G raw data		
11	Premade-WES Library	PML-B	PML_Test_10	Partial lane sequencing-With Demultiplexing	GCAGTATAGG	TTCCGTGCAC	300	Others	20	G raw data		
12	Premade-WES Library	PML-B	PML_Test_11	Partial lane sequencing-With Demultiplexing	AATTCCGGTT	AAAAAATTCC	300	Others	20	G raw data		
13												

A) Library Type: The type of library that you are sending

B) Library Name: This name should match what is written on the tube. Maximum of 17 characters begin with an alphabet. If you are sending pooled library, fill in the pooled library name and on the physical tube.

C) Sub-library Name: The name of the individual libraries in the pooled library. In this example, there are 2 pooled libraries, PML_A and PML_B.

D) Data Delivery Method: This will be the method of sequencing e.g., Lane sequencing with demultiplexing or Partial lane sequencing with demultiplexing.

E) i7 and i5 Index Sequences: Please select i5 indexes under v1.0 reagent kits, Sample sheet v2 regardless of sequencing platform. **It is recommended to use dual indexes (i5 and i7) as single index libraries will result in longer turnaround times.

G) Insert Size: The size of the insert sequence.

H) Library Status: Select Others unless your libraries are in dry powder form

I) Total Data Amount: The amount of data output required. If you are sending a pooled library, the amount of data for each line will be the total data amount in terms of “G raw data” e.g., the data output for PML-A is 12G raw data. For PE150, only unit G is allowed.

Please see more examples on the next few pages

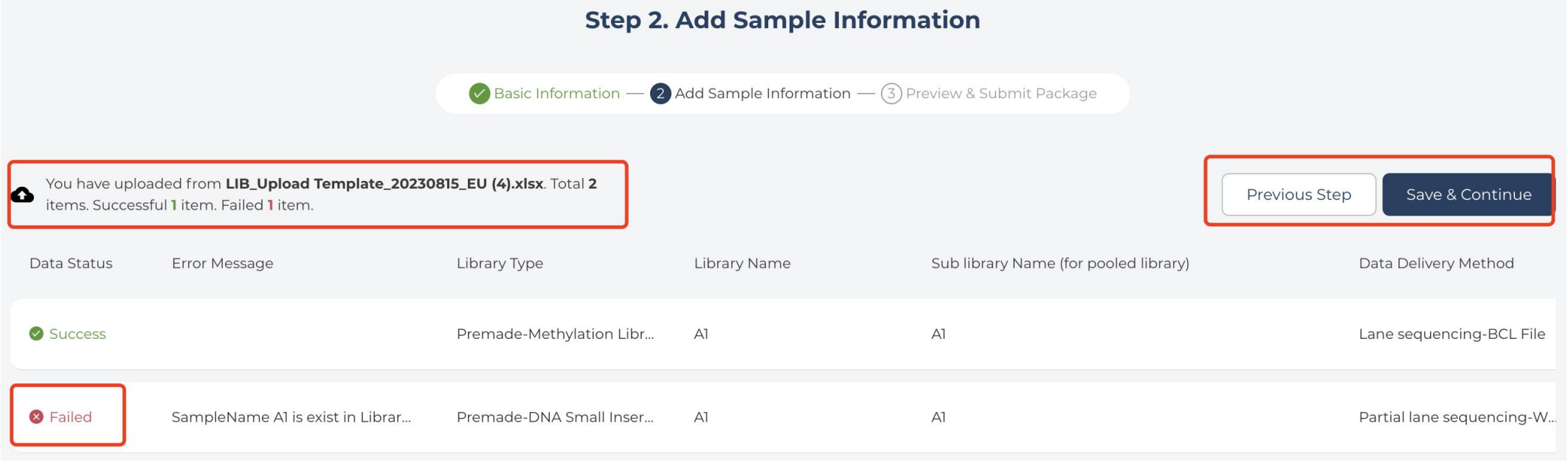
Reviewing Uploaded Information

Important! Please ensure all sample information are uploaded successfully.

For [Failed] items, please review the error message and reupload the SIF.

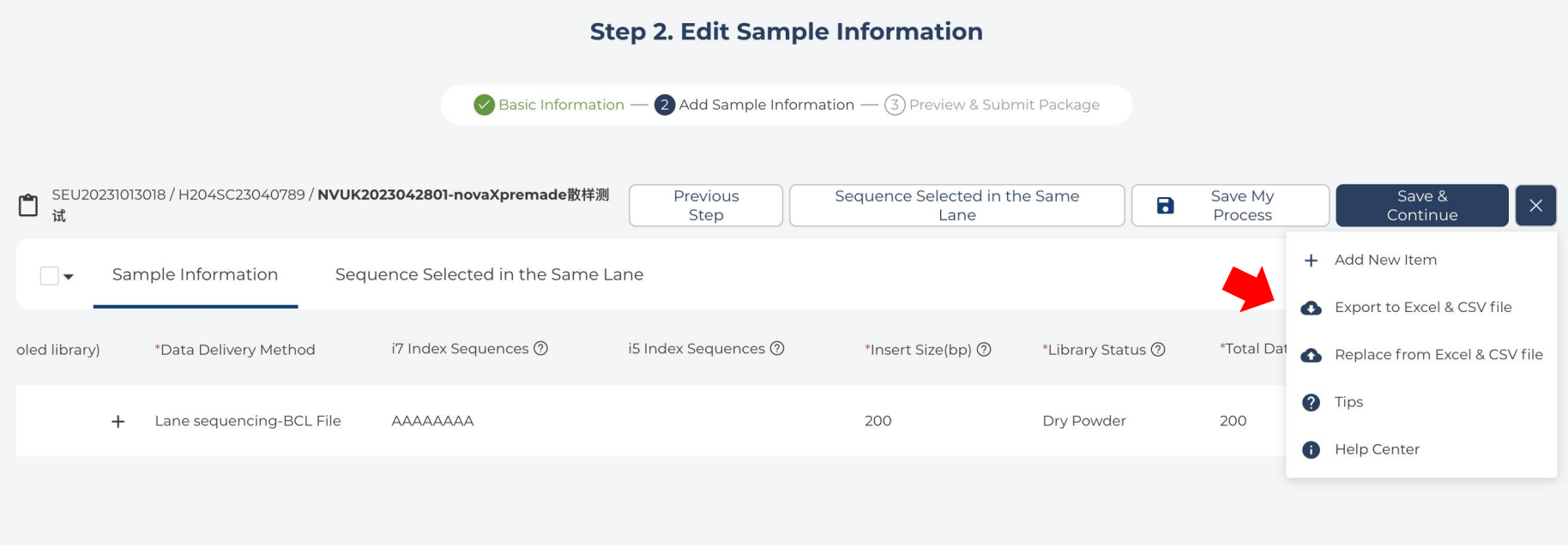
To reupload, click [Previous Step]

To proceed, click [Save & Continue]



Note: After you click [Save & Continue] ,we can only save the success items.

More information



You can find **more options** by clicking =

- **Add New Item**: add one more sample
- **Export to Excel & CSV File**: Exports current data to an excel file
- **Replace from Excel & CSV File**: brings you back to the template upload page
- **Tips&Help Center**: useful tips and FAQs

More Examples

Filling up Library Name and Total Data Amount

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Example 1: Partial Lane Sequencing Non-pooled Library

When you are sending individual libraries.

- Fill in the data amount needed for each individual library.
- Partial lane sequencing-With Demultiplexing: requires i5 and i7 index
- Partial lane sequencing-Without Demultiplexing: we don't provide this service anymore.

B	C	I
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)
S1	**S1**	**6**
S2	**S2**	**6**
S3	**S3**	**6**

Example 2: Partial Lane Sequencing Pooled Library

When you are sending 1 tube of pooled library (please make sure the pooled library is in the correct ratio).

- Fill in the total data amount for the pooled library. E.g., 18G for pooled library S.
- Partial lane sequencing-With Demultiplexing: requires i5 and i7 index.Do not mix libraries with the same index in the same library, otherwise they cannot be distinguished.

B	C	I
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)
S	**S1**	**18**
S	**S2**	**18**
S	**S3**	**18**

More Examples

Filling up Library Name and Total Data Amount

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Example 3: Whole Lane Sequencing Non-pooled Library(without phix)

When you are sending individual library for lane sequencing.

- Fill in the data amount per individual library. The sum of total data amount must not be more than the Total Lane Data Amount. e.g. 800G for one NovaSeq lane for PE150, or 375G for Novaseq Xplus-10B lane, or 1000G for Novaseq Xplus-25B.

B	C	I
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)
S1	S1	40
S2	S2	40
S3	S3	30

Example 4: Whole Lane Sequencing Non-pooled Library(with phix)

- Fill in the data amount per individual library with phix. The sum of total data amount must not be more than the Total Lane Data Amount.e.g. 800G for one NovaSeq lane for PE150, or 375G for Novaseq Xplus-10B lane, or 1000G for Novaseq Xplus-25B.
- e.g. If you need 10% phix for the lane, and you want 40G for the sample, then you need to fill in 44G as the total data amount for the sample.

B	C		I
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 amount needed	Total Data Amount (Required)
S1	S1	40	44
S2	S2	40	44
S3	S3	40	44

Filling up Library Name and Total Data Amount

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Example 5: Whole Lane Sequencing Pooled Library

When you are sending 1 tube of pooled library for lane sequencing.

- The Total data amount corresponds to the pooled library, not the sub-library.
- Hence, if the pooled Library S needs to be sequenced in 1 NovaSeq lane, S1, S2, S3 needs to indicate as 800G on every row.

B	C	I
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)
S	**S1**	**800**
S	**S2**	**800**
S	**S3**	**800**

Filling up Library Name and Total Data Amount

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Example 6: 10x Premade Library-(Single index-Non-pooled library)

- For certain 10x libraries, if there are **four i7 indexes per library**, fill in 4 lines of the same library and one i7 index for each library as shown below.

B	C	E	I
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)	Total Data Amount (Required)
S10X	**Sublibrary1**	**CGCTATGT**	**6**
S10X	**Sublibrary1**	**GCTGTCCA**	**6**
S10X	**Sublibrary1**	**TTGAGATC**	**6**
S10X	**Sublibrary1**	**CCTATCCT**	**6**

Filling up Library Name and Total Data Amount

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Example 7: 10x Premade Library-(Single index-Pooled library)

- When you are sending 1 tube of pooled 10X library for sequencing.The Total data amount corresponds to the pooled library, not the sub-library.*For example:Sublirary1 need 6G,Sublirary2 need 6G, so you need to fill in 12G for the Total Data Amount*.
- If there are four i7 index per sub-library, fill in 4 lines of the same sub-library and one i7 index for each sub-library as shown below.

B	C	E	I
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)	Total Data Amount (Required)
S10X	**Sublibrary1**	**CGCTATGT**	**12**
S10X	**Sublibrary1**	**GCTGTCCA**	**12**
S10X	**Sublibrary1**	**TTGAGATC**	**12**
S10X	**Sublibrary1**	**CCTATCCT**	**12**
S10X	**Sublibrary2**	**CCTTAAGG**	**12**
S10X	**Sublibrary2**	**GGGCTTAA**	**12**
S10X	**Sublibrary2**	**AAGGTTCC**	**12**
S10X	**Sublibrary2**	**CTTAACTG**	**12**

More Examples

Filling up Library Name and Total Data Amount

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Example 8: 10x Premade Library（Dual-index library-Non-pooled library）

- For certain 10x libraries, if there is **only one i7&i5 index**, fill in 1 line for the library will be fine.Usually for dual-index plate, there will be only one unique i7 and one unique i5 sample index per well.

B	C	E		I
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	Total Data Amount (Required)
S10X	**SS001**	**TAGGGTCAAA**	**CTTCTAATGT**	**6**

Example 9: 10x Premade Library（Dual-index library-pooled library）

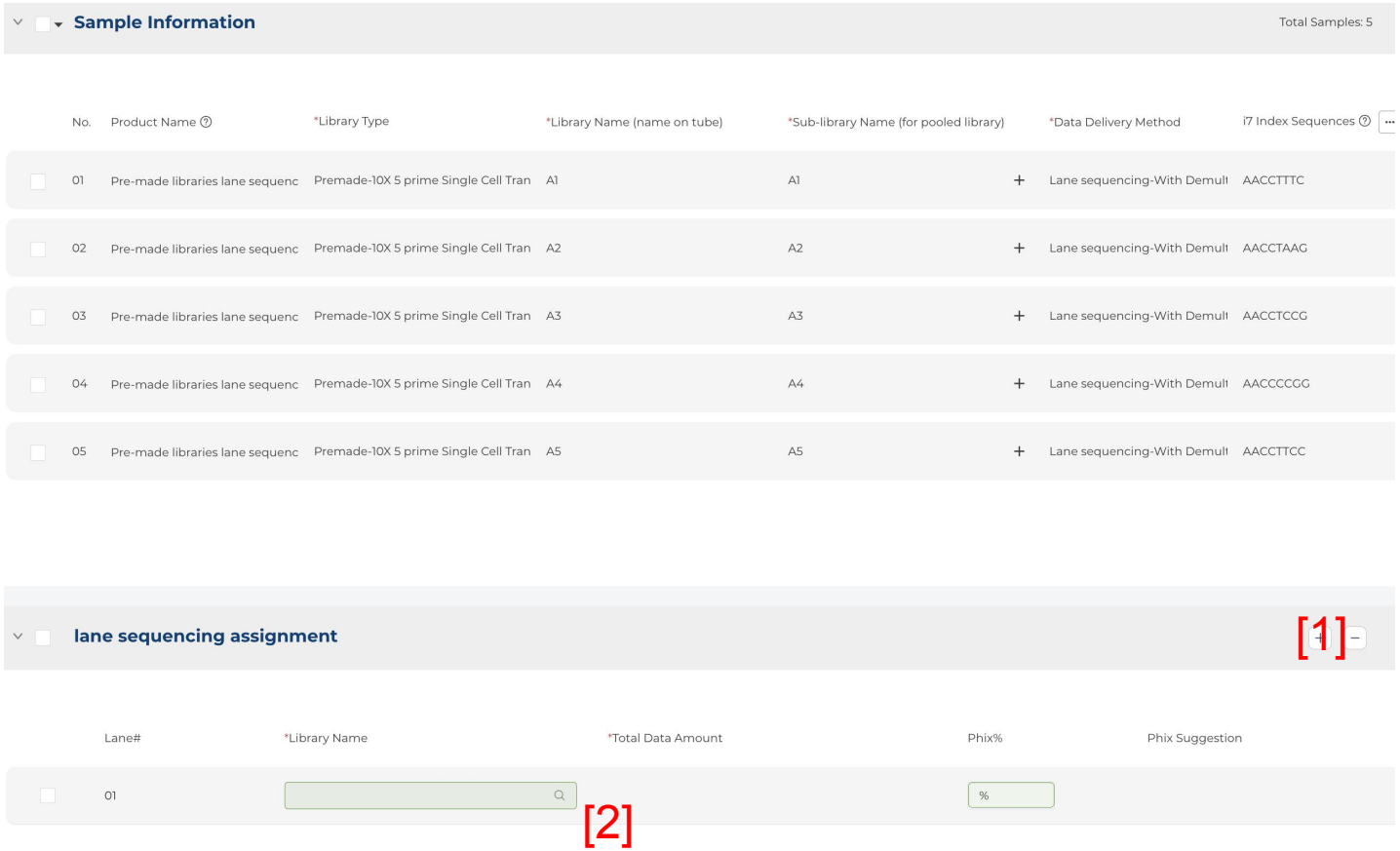
- When you are sending 1 tube of pooled 10X library for sequencing.The Total data amount corresponds to the pooled library, not the sub-library.

B	C	E		I
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	Total Data Amount (Required)
S10X	**SS001**	**TAGGGTCAAA**	**CTTCTAATGT**	**12**
S10X	**SS002**	**TAGGCAATAA**	**AGTGCGCACT**	**12**

Indicating Lane Sequencing

Step 1: click [1] +to add a lane. Only lane seqeuncing project will show this item.

Step 2: click [2] to select samples;



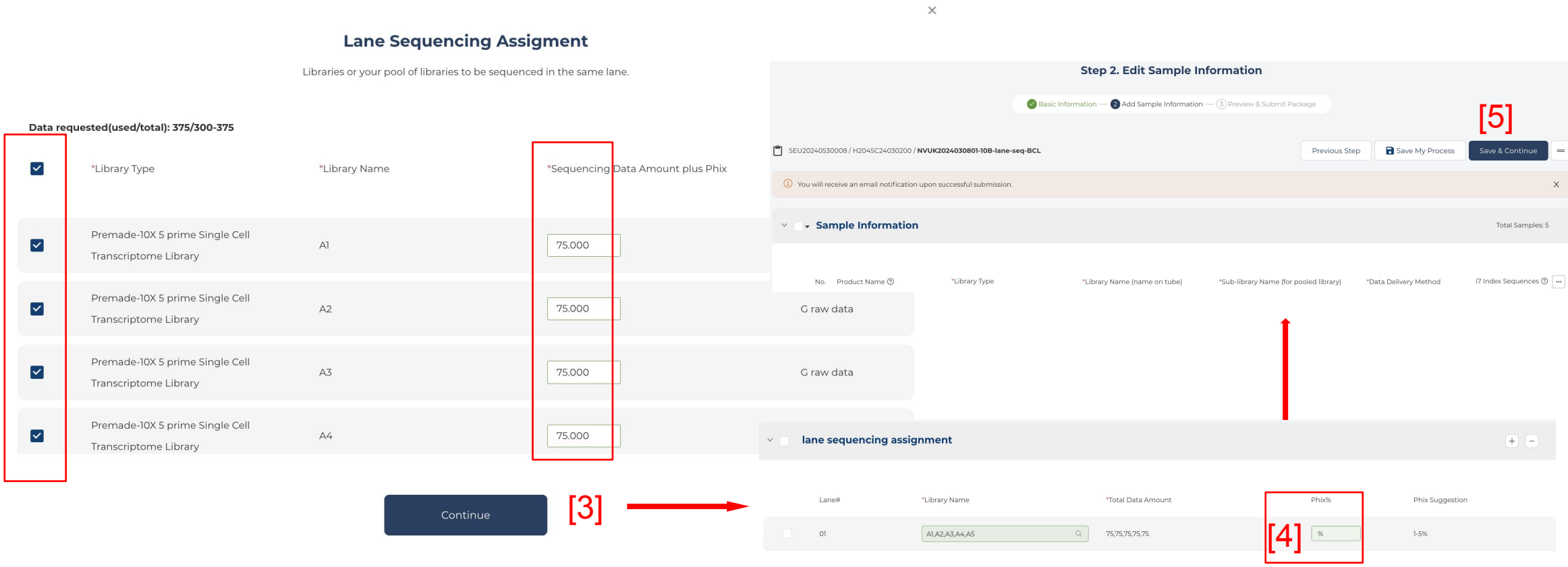
Next step please see next page

Indicating Lane Sequencing

Step 3: After choosing libraries and filling in data amount in the lane, click [3] 'Continue' to next step.

Step 4:Filling in [4]Phix%;if you don't need any, you can leave it or fill in 0.

Step 5: If everything is OK, Click [5] Save and continue to next step.



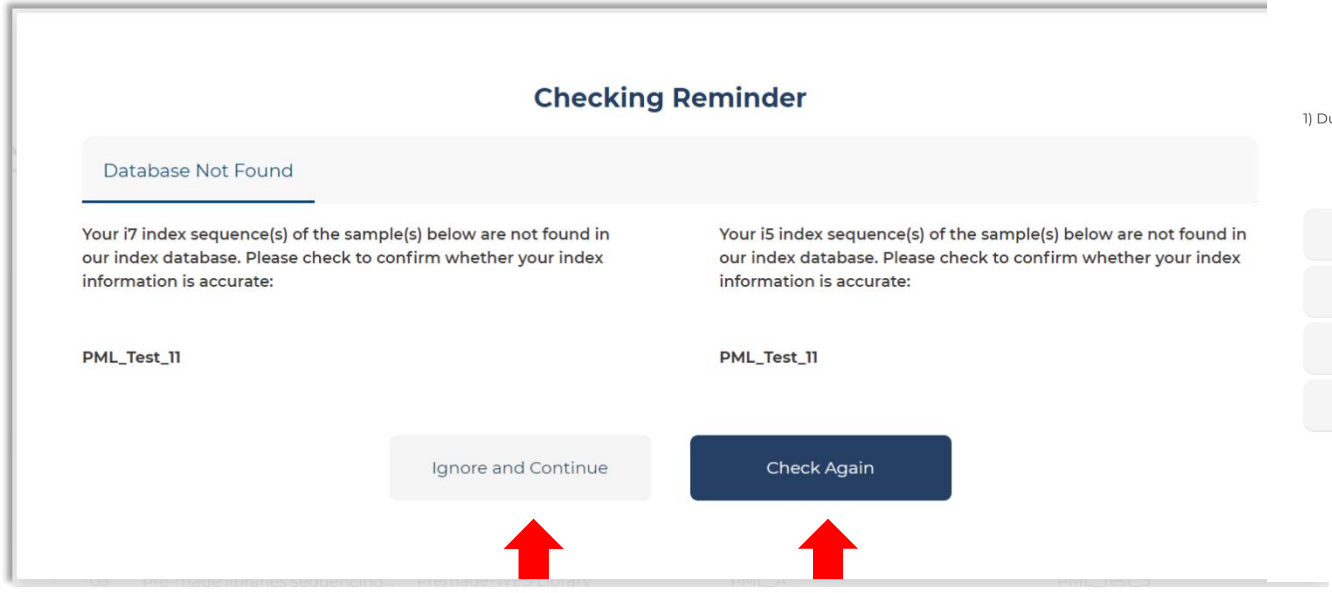
System check reminders

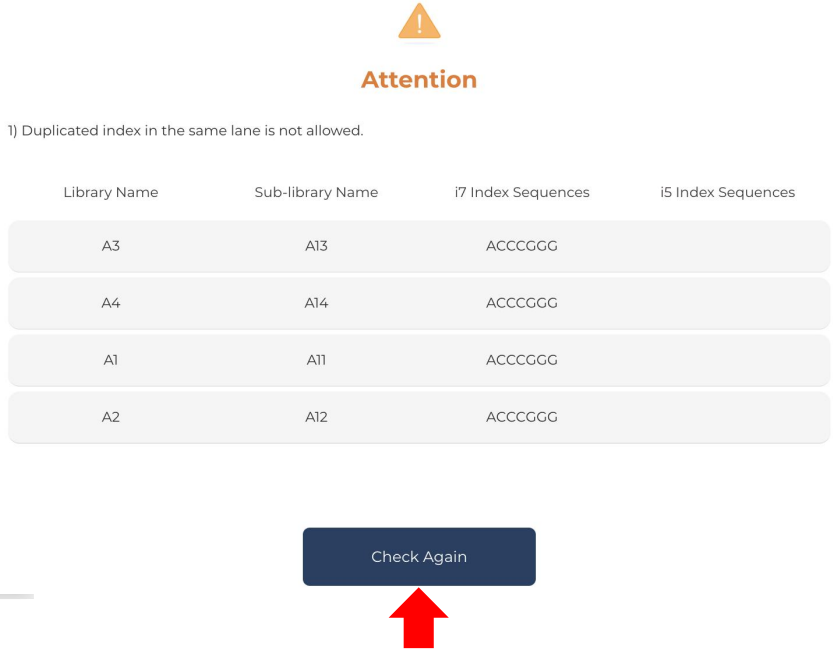
The system will check for indexes information, and you may see a prompt to double check the index information.

If you are sure that the index sequence information is correct, please click [Ignore and Continue]

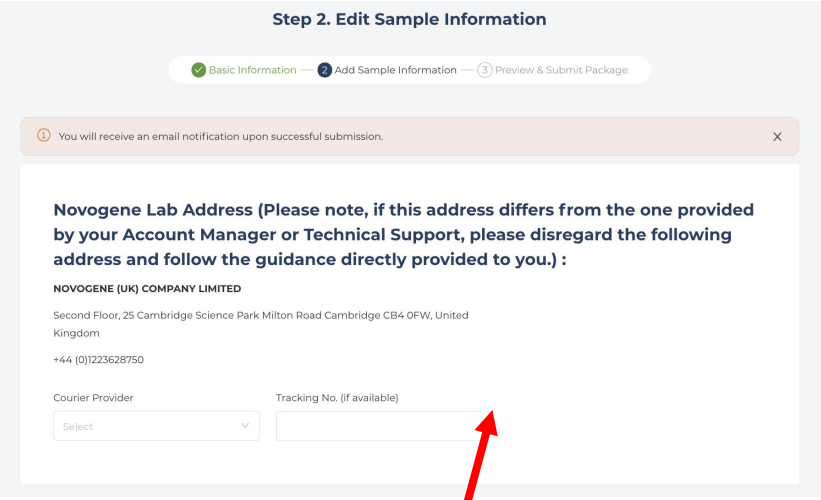
If you would like to re-check the information, click [Check Again] to go back to the previous page.

Duplicated index are not allowed in the same library or the same lane.You have to [Check Again] if it is in this situation.



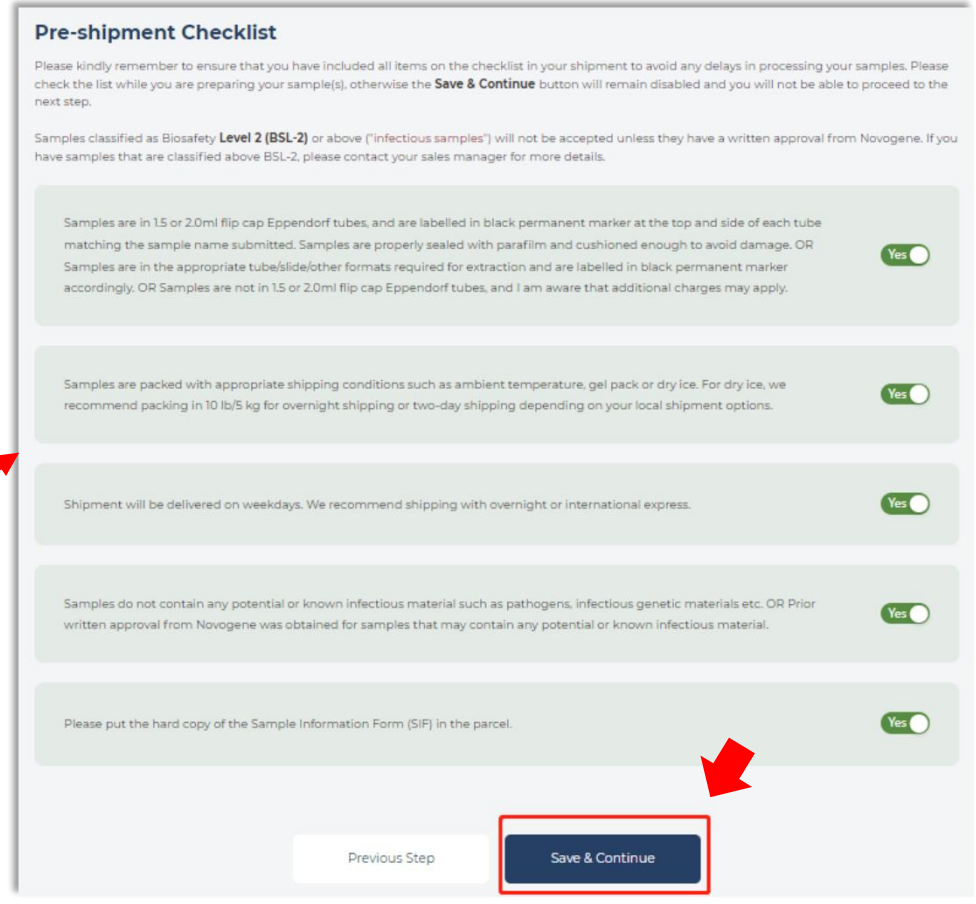


About the Samples Shipping Information

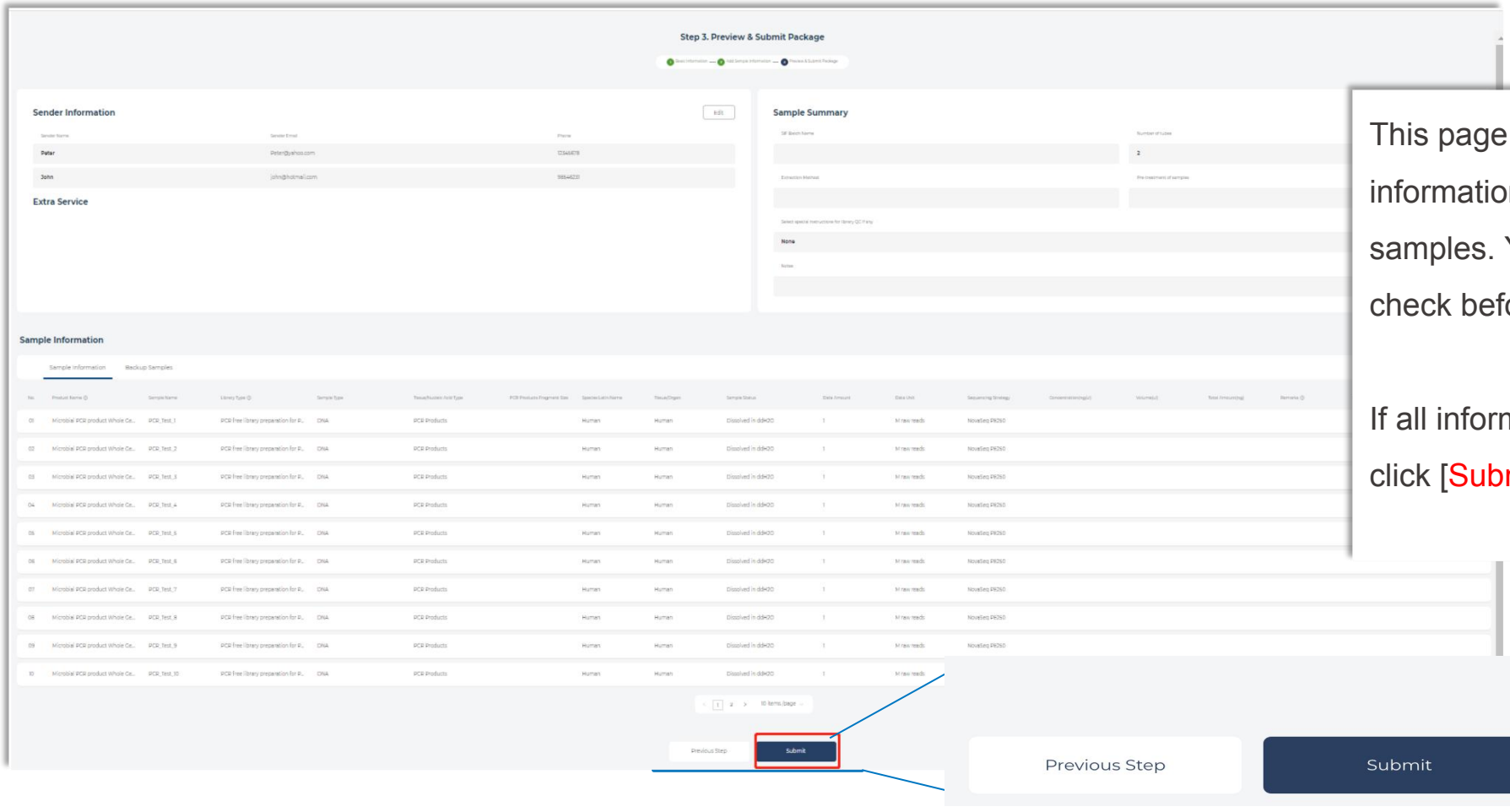


If you already have the tracking number, please help fill in this part. Which could help us login in your samples.

On the **Pre-shipment Checklist**, these items correspond to the send samples policy and instructions. All 5 items **must be followed and selected "Yes"** to proceed to the next step.



Preview and Submit Package

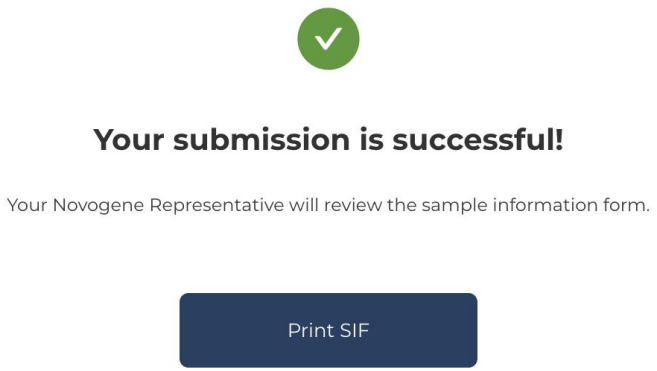


This page **summarizes** the information for this batch of samples. You can do one final check before proceeding.

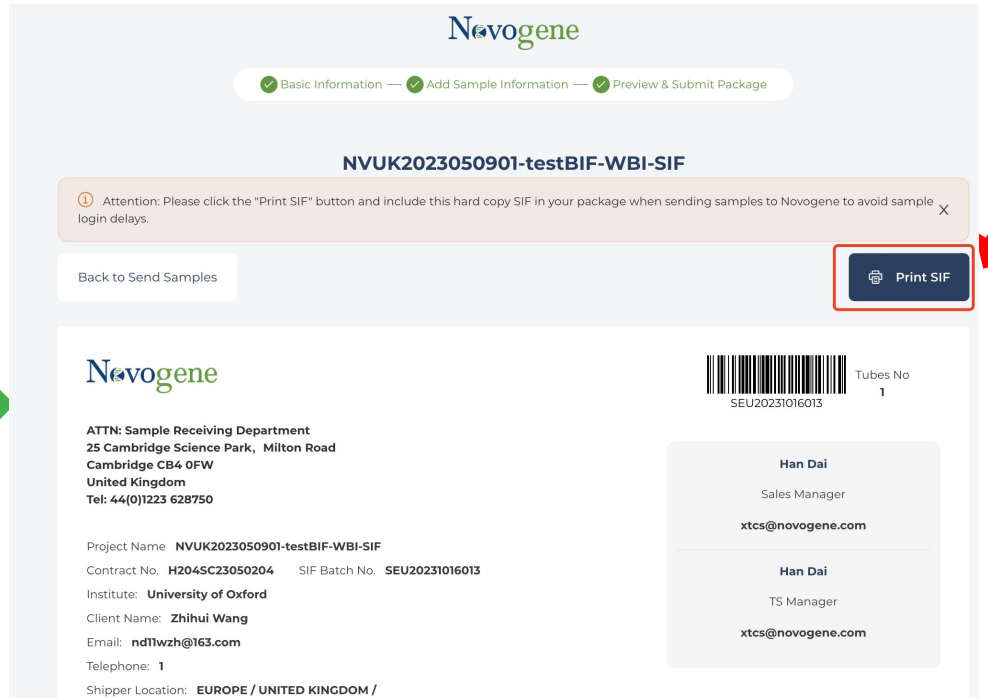
If all information are correct, click [Submit] to proceed.

Print Sample Information Form

With this, your sample information form is complete! Click [Print SIF] to proceed.

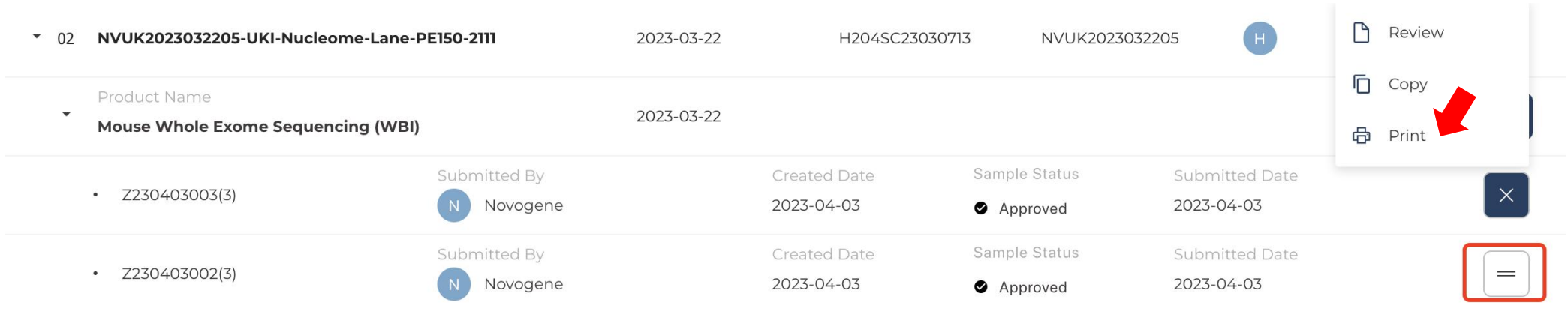


Please **place a hardcopy** of this form with your samples and before sending out your package. Click [Print SIF].



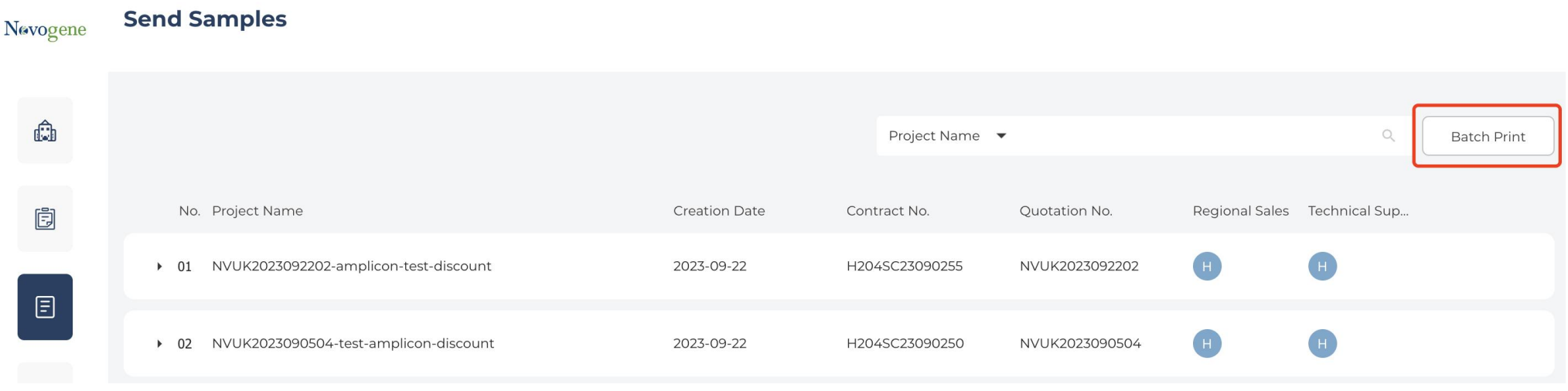
Print Sample Information Form

You can also Print SIF accoding to ic [Print] on [Send Sample]page.

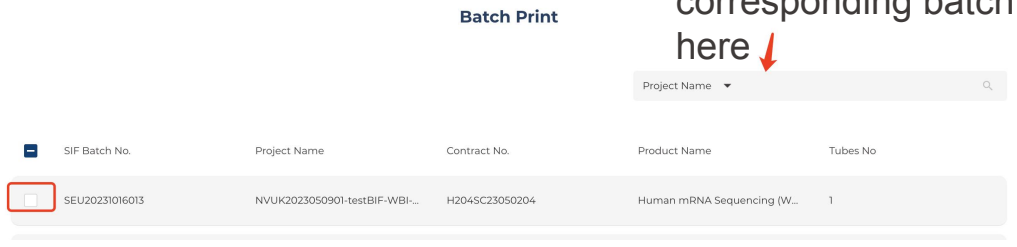


Print Sample Information Form

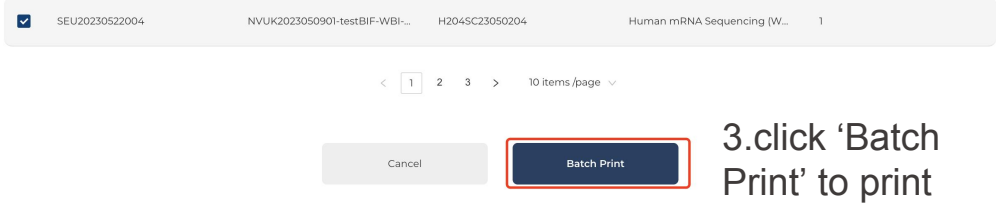
You can also Print SIF accoding to [Batch Print]button on [Send Sample]page.



1.click the button



2.search corresponding batch here



3.click ‘Batch Print’ to print

Print Sample Information Form

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SEU20210909004

Tubes No
2

NOVOGENE (UK) COMPANY LIMITED

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Project Name **HU_SOB_PE150_laneseq_WOBI**
Contract No. **H204SC21091223** SIF Batch No. **SEU20210909004**
Institute: **SeqOmics Biotechnológia Ltd**
Client Name: **István Nagy**
Email: **nagyi@seqomics.hu失效失效**
Telephone: **36304276152**
Shipper Location: **EUROPE / HUNGARY /**
Tracking No. (if available): **774707311011**
Transportation Condition: **Ice Pack**

Sample Information

No.	Library Name (name on tube)	Library Type	Library Status	Remark
01	MEOESZ1	Premade-DNA Small Insert Size Library (Animal or Plant)	Others	
02	MEOESZ2	Premade-DNA Small Insert Size Library (Animal or Plant)	Others	

—— END ——

This is the SIF style we printed out and needs to be shipped to us along with the package.

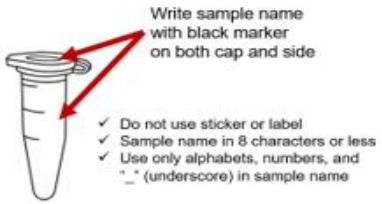
On this SIF, we can see the batch NO., Tube NO. and sample detail information. All of the information are important for us to claim your samples. So please make sure to print this file instead of excel upload template.

Sample Preparation Instruction

A. Sample Preparation

☐ **1. Sample Name**

Sample name must begin with alphabet and in maximum of 8 characters. Naming in alphanumeric and underscore are acceptable. Non-standard names will be amended following this naming requirements.



☐ **2. Sample Marking**

Write sample names at the top and the side of each tube with black permanent marker. Sample names on the tube must match with sample information form. Please do not include other information on the tube to avoid discrepancy.

☐ **3. Sample Tube**

Send samples in 1.5 ml or 2.0 ml microcentrifuge tubes. 96-well plates and PCR tube-strips cannot be accepted at this time. Incorrect tubes may risk processing delays and handlings fees.

☐ **4. Sample Protection**

Seal each tube with parafilm before packaging. To avoid crushing, we highly recommend placing the sample tubes in a container such as a 50ml tube or cryobox. Cotton or absorbent papers can be used to prevent tubes from moving inside the container.

☐ **5. Sample Requirements**

Please refer to your quotation for the sample requirements. Insufficient sample amount may risk processing delay.

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☐ **6. Samples Restriction**

In principal, we do not accept blood-borne pathogens, purified viral genomes, and infectious samples classified at biosafety level 2 or above. Please contact us before shipping infectious samples. If you are sending samples derived from animals and plants other than human specimens and experimental animals, you will need to include a confirmation sheet in advance. Details will be provided separately.

B. Packing and Shipping Samples

☐ **1. Check**

Pack the samples according to the Sample Information Form. If you are sending multiple projects, please pack them separately.

☐ **2. Print**

Attach a hard copy of Sample Information Form in the sample bag.

☐ **3. Notify**

Please email Sample Information Form and the courier tracking number to our Technical Support Representative in-charge prior to shipping samples. Samples shipped without Sample Information will be delayed in processing.

☐ **4. Ship**

Ship samples in appropriate shipping condition such as ambient, gel pack or dry ice. For dry ice, we recommend to pack in 10kg for two-day shipping depends on your shipping location. Please avoid weekend shipment or delivery.

Special note

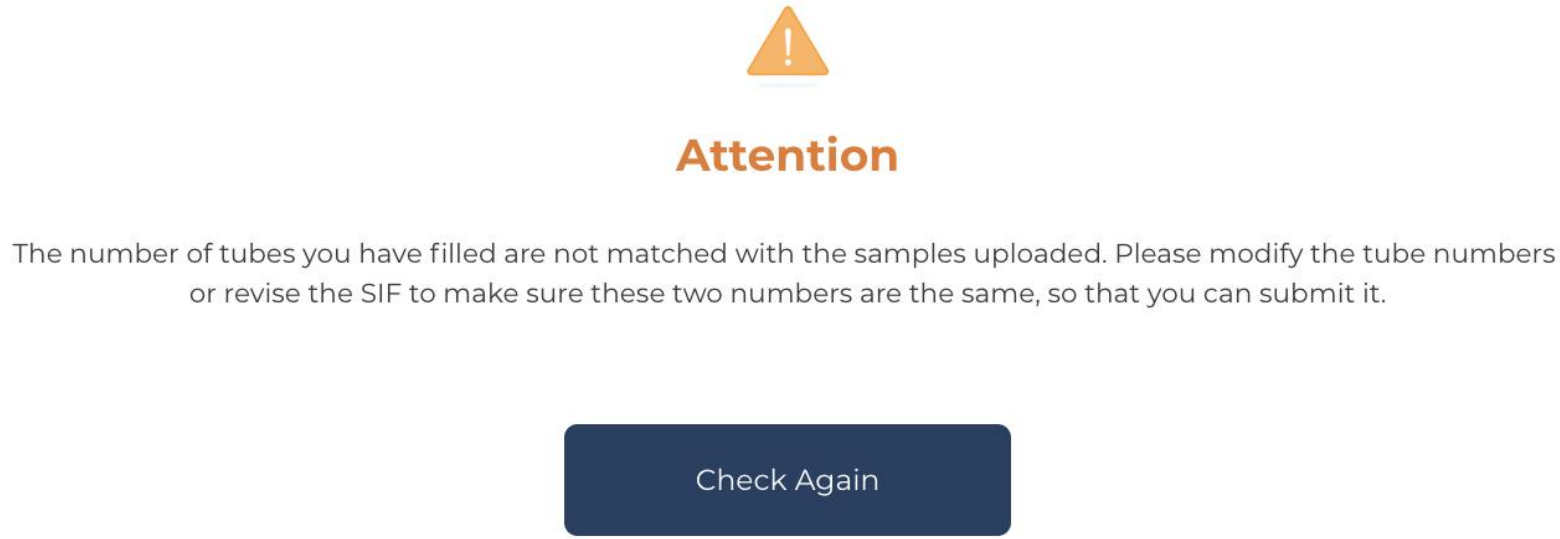
1.Due to inaccuracies or omissions in the provided index sequences, any re-sequencing costs incurred as a result will be the responsibility of the customer. We kindly request that you verify the correctness of all index information for your sublibraries, ensuring that the correct index sequences are used. In the event of contamination or suboptimal output caused by index-related issues, additional re-sequencing fees may apply.

2.For partial lane sequencing, we will pool different libraries in one lane, so usually there is no need to add phix.

FAQ

1.If I get a error to reminder me the number of tubes I have filled are not matched with the samples uploaded, how to treat?

Check if you have uploaded all the samples successfully, if yes, then you can check if you have filled in the wrong tube numbers on previous step.



FAQ

2.If I get a error to reminder me the intersize is unique in the library,what should I do?

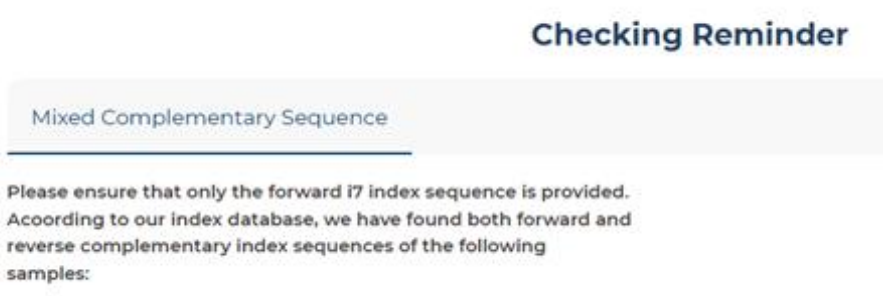
Please make sure to fill in the same number on SIF for all the sub-libraries of the same library.

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)	Data Delivery Method (Required)	i7 Index Sequences (Required when data need be multiplexing)	i5 Index Sequences	Insert Size(bp) (Required)
Premade-10X 5 prime Singl	A	A1	Lane sequencing-With Dem	AACCTTTC		300
Premade-10X 5 prime Singl	A	A2	Lane sequencing-With Dem	AACCTAAG		300
Premade-10X 5 prime Singl	A	A3	Lane sequencing-With Dem	AACCTCCG		300
Premade-10X 5 prime Singl	A	A4	Lane sequencing-With Dem	AACCCCGG		300
Premade-10X 5 prime Singl	A	A5	Lane sequencing-With Dem	AACCTTCC		300

FAQ

3.If I get an error to reminder me the index have issues, what should I do?

This is just a warning to double check the indexes. If these are correctly written, you can ignore this message.



FAQ

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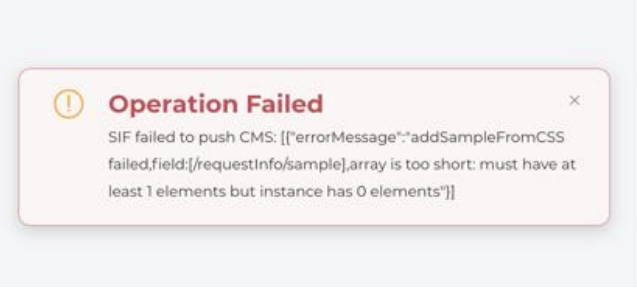
4.If I get an error to reminder that the SIF can’t push to CMS or Failed to upload, waht should I do?

You may used the wrong excel file. Please download the updated excel template in the step 2.



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Thanks!