6/19/2020 1:24

Re:BioProject ID PRJNA607174

Incoming Received

AM From

xiaokpcc@163.com

To

bioprojecthelp@ncbi.nlm.nih.gov;

Attachment #

Dear Curator:

The SRA data in the bioproject PRJNA607174 had been released few days ago, but I want upload one more SRA data in this bioproject.

Can I update a new SRA data under this project? If allowed, please tell me how to do it.

I look forward to your reply as soon as possible.

Thank you very much!

Kangpeng Xiao

```
At 2020-04-22 17:01:32, bioprojecthelp@ncbi.nlm.nih.gov wrote:
>Dear Kangpeng Xiao,
>This is an automatic acknowledgment that your submission:
                  SUB6982752
>SubmissionID:
>BioProject ID: PRJNA607174
>Title:
>has been updated, eg by the linkage of one or more BioSamples. The
locus tag prefixes for
>each linked BioSample are included in the locustagprefix.txt file that can
accessed
>from this BioProject in the submission portal:
>https://submit.ncbi.nlm.nih.gov/subs/bioproject/SUB6982752/overview
>In addition, you can view the locustagprefix.txt files for all of your
BioProjects from the BioProject submission page,
>https://submit.ncbi.nlm.nih.gov/subs/bioproject/.
>Please use the BioProject ID PRJNA607174 with your correspondence and your
data submissions.
>Send questions to bioprojecthelp@ncbi.nlm.nih.gov, and include the
BioProject ID and organism name.
>Regards,
>NCBI BioProject Submissions Staff
>Bethesda, Maryland USA
>***************
>(301) 496-2475
>(301) 480-2918 (Fax)
>bioprojecthelp@ncbi.nlm.nih.gov (for BioProject questions/replies)
>info@ncbi.nlm.nih.gov (for general questions regarding NCBI)
>************
```

6/19/2020 3:16 Re: case #CAS-557246-T9N1F3: Re:BioProject ID PRJNA607174 TRACKING:000300000004709 Outgoing Sent

nlm-support@nlm.nih.gov

To xiaokpcc@163.com;

Attachment #

From

Dear Kangpeng Xiao,

Thank you for your email. You can submit additional Biosamples and/or sequence data for an existing BioProject at any time. Simply initiate a new submission in the appropriate submission portal wizard. You can enter the BioProject ID for your existing BioProject, and the new submission will be linked automatically.

If you have other comments or questions, please reply to bioprojecthelp@ncbi.nlm.nih.gov.

Best regards,

Carol DeWeese Scott, Ph.D. BioProject Curation Staff

* PLEASE DO NOT MODIFY THE SUBJECT LINE OF THIS EMAIL WHEN RESPONDING TO ENSURE CORRECT TRACKING *

Case Information:

Case #: CAS-557246-T9N1F3 Customer Name: 肖康鹏

Customer Email: xiaokpcc@163.com Case Created: 2020-06-19T05:24:04Z

Summary: Re:BioProject ID PRJNA607174

Details:

Dear Curator:

The SRA data in the bioproject PRJNA607174 had been released few days ago, but I want upload one more SRA data in this bioproject.

Can I update a new SRA data under this project? If allowed, please tell me how to do it.

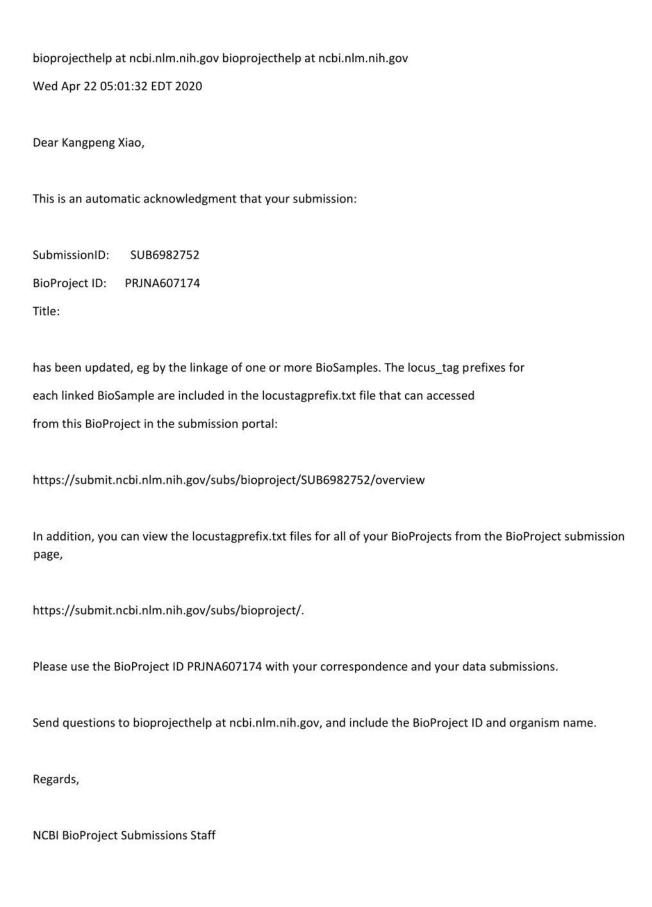
I look forward to your reply as soon as possible.

Thank you very much!

Kangpeng Xiao

```
At 2020-04-22 17:01:32, bioprojecthelp@ncbi.nlm.nih.gov wrote:
>Dear Kangpeng Xiao,
>
>This is an automatic acknowledgment that your submission:
>
>SubmissionID: SUB6982752
>BioProject ID: PRJNA607174
>Title:
>
>has been updated, eg by the linkage of one or more BioSamples. The locus_tag prefixes for
>each linked BioSample are included in the locustagprefix.txt file that can accessed
```

```
>from this BioProject in the submission portal:
>https://submit.ncbi.nlm.nih.gov/subs/bioproject/SUB6982752/overview
>In addition, you can view the locustagprefix.txt files for all of your
BioProjects from the BioProject submission page,
>https://submit.ncbi.nlm.nih.gov/subs/bioproject/.
>Please use the BioProject ID PRJNA607174 with your correspondence and your
data submissions.
>Send questions to bioprojecthelp@ncbi.nlm.nih.gov, and include the
BioProject ID and organism name.
>Regards,
>NCBI BioProject Submissions Staff
>Bethesda, Maryland USA
>********
> (301) 496-2475
>(301) 480-2918 (Fax)
>bioprojecthelp@ncbi.nlm.nih.gov (for BioProject questions/replies)
>info@ncbi.nlm.nih.gov (for general questions regarding NCBI)
>**************
```



Bethesda, Maryland USA

(301) 496-2475
(301) 480-2918 (Fax)
bioprojecthelp at ncbi.nlm.nih.gov (for BioProject questions/replies)
info at ncbi.nlm.nih.gov (for general questions regarding NCBI)

bioprojecthelp at ncbi.nlm.nih.gov bioprojecthelp at ncbi.nlm.nih.gov			
Tue Feb 18 04:46:21 EST 2020			
Dear Kangpeng Xiao,			
This is an automatic acknowledgment that your submission:			
SubmissionID: SUB6982752			
BioProject ID: PRJNA607174			
Title:			
has been successfully registered with the BioProject database. After review by the database staff, your project information will be accessible with the following link, usually within a few days of the			
release date that you set (or the release of linked data, whichever is first):			
http://www.ncbi.nlm.nih.gov/bioproject/607174			
Please use the BioProject ID PRJNA607174 with your correspondence and your data submissions.			
Send questions to bioprojecthelp at ncbi.nlm.nih.gov, and include the BioProject ID and organism name.			
Regards,			
NCBI BioProject Submissions Staff			
Bethesda, Maryland USA			

(301) 496-2475			
(301) 480-2918 (Fax)			

bioprojecthelp at ncbi.nlm.nih.gov (for BioProject questions/replies)	
info at ncbi.nlm.nih.gov (for general questions regarding NCBI)	

sra at ncbi.nlm.nih.gov sra at ncbi.nlm.nih.gov Wed Apr 22 01:41:16 EDT 2020

Dear Kangpeng Xiao,

This email confirms that NCBI has completed your request to release the data associated with the BioProject on 2020-04-22. Please allow four hours for the data to be indexed and searchable in Entrez.

Note that the following linked data has also been released to the public with the BioProject's release.

BioProject: PRJNA607174

Please contact sra at ncbi.nlm.nih.gov if you need to suppress this data from the public view, make other modifications, or if it has been 2 weeks and you do not see all your data public at https://www.ncbi.nlm.nih.gov/bioproject/PRJNA607174.

Thank you!

sra at ncbi.nlm.nih.gov sra at ncbi.nlm.nih.gov Wed Apr 22 01:40:46 EDT 2020

Dear Kangpeng Xiao,

We've received your request to update the release date for the BioProject below to 2020-04-22.

Note that the following linked data will also be released on the same date:

BioProject: PRJNA607174

BioSamples:

SAMN14126321

SAMN14126322

SAMN14126323

SAMN14126324

SAMN14126325

SAMN14126326

SAMN14126329

If you have requested that Sequence Read Archive (SRA) data's release be deferred, you will receive a reminder of your upcoming release 2 weeks prior to the release date.

A final email will be generated to confirm the successful release of your data. Please contact sra at ncbi.nlm.nih.gov with any urgent questions or concerns.

Thank you!

3/10/2020 5:47 AM Request to delete two SRA terms of from my submission Incoming Received

From xiaokpcc@163.com

To sra@ncbi.nlm.nih.gov;sra@ncbi.nlm.nih.gov;

Attachment #

Dear administrator:

I uploaded two unrelated files in my Bioproject, can you help me to delete them?

The BioProject ID is PRJNA607174. The submission ID is SUB6988522.

The BioSample accession of two objects need to deletet: SAMN14126327 and SAMN14126328. Please help me to delete these two BioSample (SAMN14126327 and SAMN14126328) and their related SRA files.

Thank you very much.

Yours

Kangpeng Xiao 20200310

Re: case #CAS-503400-N7S9S2: Request to delete two SRA terms of from my submi... TRACKING:000393000005514 Outgoing Sent

From nlm-support@nlm.nih.gov

To xiaokpcc@163.com;

Attachment #

I have withdrawn SAMN14126327 and SAMN14126328, along with the associated SRA data.

Cheers,

Rick Lapoint SRA Curator

* PLEASE DO NOT MODIFY THE SUBJECT LINE OF THIS EMAIL WHEN RESPONDING TO ENSURE CORRECT TRACKING *

Case Information:

Case #: CAS-503400-N7S9S2 Customer Name: 肖康鹏

Customer Email: xiaokpcc@163.com Case Created: 2020-03-10T09:47:39Z

Summary: Request to delete two SRA terms of from my submission

Details:

Dear administrator:

I uploaded two unrelated files in my Bioproject, can you help me to delete them?

The BioProject ID is PRJNA607174.

The submission ID is SUB6988522.

The BioSample accession of two objects need to deletet: SAMN14126327 and SAMN14126328.

Please help me to delete these two BioSample (SAMN14126327 and SAMN14126328) and their related SRA files.

Thank you very much.

Yours

Kangpeng Xiao

20200310

Re:Re: case #CAS-503400-N7S9S2: Request to delete two

3/14/2020 SRA terms of from my submi... Incoming Received

8:57 AM TRACKING:000393000005514

From xiaokpcc@163.com

To nlm-support@nlm.nih.gov;nlm-support@nlm.nih.gov;nlm-

support@nlm.nih.gov;

Attachment #
Dear Curator:

I can see the two withdrew data from the reviewer link of PRJNA607174.

Will these withdrew data be downloaded by others when the project is released?

Thank you.

At 2020-03-10 22:49:54, "NLM Support" <nlm-support@nlm.nih.gov> wrote:

I have withdrawn SAMN14126327 and SAMN14126328, along with the associated SRA data. Cheers.

Rick Lapoint SRA Curator

* PLEASE DO NOT MODIFY THE SUBJECT LINE OF THIS EMAIL WHEN RESPONDING TO ENSURE CORRECT TRACKING *

Case Information:

Case #: CAS-503400-N7S9S2

Customer Name: 肖康鹏

Customer Email: xiaokpcc@163.com Case Created: 2020-03-10T09:47:39Z

Summary: Request to delete two SRA terms of from my submission

Details:

Dear administrator:

I uploaded two unrelated files in my Bioproject, can you help me to delete them?

The BioProject ID is PRJNA607174.

The submission ID is SUB6988522.

The BioSample accession of two objects need to deletet: SAMN14126327 and SAMN14126328.

Please help me to delete these two BioSample (SAMN14126327 and SAMN14126328) and their related SRA files.

Thank you very much.

Yours

Kangpeng Xiao

20200310

Re:Re: case #CAS-503400-N7S9S2: Request to delete two

3/16/2020 5:49 PM

SRA terms of from my submi... TRACKING:000393000005514 Outgoing Sent

From

nlm-support@nlm.nih.gov

To

xiaokpcc@163.com;

Attachment #

No, SAMN14126327 and SAMN14126328, and the associated SRA data will not be available for download when the rest of the submission is released.

Cheers,

Rick Lapoint **SRA Curator**

----- Original Message -----

From: 肖康鹏;

Received: Sat Mar 14 2020 08:55:55 GMT-0400 (Eastern Daylight Time) To: nlm-support@nlm.nih.gov; Inbound - NLM Support; Triage Team;

Subject: Re:Re: case #CAS-503400-N7S9S2: Request to delete two SRA terms of from my submi...

TRACKING:000393000005514

Dear Curator:

I can see the two withdrew data from the reviewer link of PRJNA607174. Will these withdrew data be downloaded by others when the project is released?

Thank you.

At 2020-03-10 22:49:54, "NLM Support" <nlm-support@nlm.nih.gov> wrote:

I have withdrawn SAMN14126327 and SAMN14126328, along with the associated SRA data. Cheers,

Rick Lapoint SRA Curator

* PLEASE DO NOT MODIFY THE SUBJECT LINE OF THIS EMAIL WHEN RESPONDING TO **ENSURE CORRECT TRACKING ***

Case Information:

Case #: CAS-503400-N7S9S2

Customer Name: 肖康鹏

Customer Email: xiaokpcc@163.com Case Created: 2020-03-10T09:47:39Z

Summary: Request to delete two SRA terms of from my submission

Details:

Dear administrator:

I uploaded two unrelated files in my Bioproject, can you help me to delete them?

The BioProject ID is PRJNA607174. The submission ID is SUB6988522.

The BioSample accession of two objects need to deletet: SAMN14126327 and SAMN14126328. Please help me to delete these two BioSample (SAMN14126327 and SAMN14126328) and their related SRA files.

Thank you very much.

Yours

Kangpeng Xiao

20200310

6/19/2020 7:39

Request to release data

Incoming Received

PM From

xiaokpcc@163.com

To

bioprojecthelp@ncbi.nlm.nih.gov;

Attachment #

Dear Curator:

I have uploaded a new sequence data under bioproject PRJNA607174, the new SRA accession ID is SRR12053850.

Please help me release this new sequence data (SRR12053850) as soon as possible.

Thank you very much.

Kangpeng Xiao

6/22/2020 12:15

Re: case #CAS-557677-B6K7R5: Request to release data

TRACKING:000414000006953

Outgoing Sent

PM From

nlm-support@nlm.nih.gov

To

xiaokpcc@163.com;

Attachment #

Dear Kangpeng,

I released this run. Please allow 24-48 hrs for propagation of the data to the public site.

For making updates please refer to the Update

guide: https://www.ncbi.nlm.nih.gov/sra/docs/submitupdate/

Best regards,

Svetlana

If you have any questions or concerns regarding your **SRA** submission please don't hesitate to contact sra@ncbi.nlm.nih.gov (applies to new questions). We normally respond within 2 business days.

11/8/2020 4:29

AM Request update data

Incoming Received

From

xiaokpcc@163.com

To

sra@ncbi.nlm.nih.gov;sra@ncbi.nlm.nih.gov;

Attachment #

Dear Curator:

I submitted the amplicon sequencing data to SRA on October 30 (SRA accession no. SRR12950102) under the Bioproject PRJNA607174. Due to negligence, an amplicon sequence was missing from this data, the correct file should contain 33 sequences, but only 32 sequences were included in the submitted file. Can I resubmit a file to overwrite the original data? This is very important to us and we look forward to hearing from you. Thank you very much.

11/9/2020 9:32 Re: case #CAS-630560-S5D6W3: Request update data

AM TRACKING:000414000008360

Outgoing Sent

From

nlm-support@nlm.nih.gov

To

xiaokpcc@163.com;

Attachment #

Hello.

I had withdrawn this SRA records and you can submit a new one by making new SRA submission and using existing biproject's and sample's accessions for SRA metadata.

Please note, however, that judging by your description there are too few sequences in your file to qualify for SRA submission. SRA fastq files usually contain thousands or millions of sequences.

Please refer to the File Format guide: https://www.ncbi.nlm.nih.gov/sra/docs/submitformats/

Best regards,

Svetlana

If you have any questions or concerns regarding your **SRA** submission please don't hesitate to contact sra@ncbi.nlm.nih.gov (applies to new questions). We normally respond within 2 business days.

The NCDICD	database subsected as state
The NCBI SR	database submission staff

Dear Curator:

Svetlana Jazvovskaja

I submitted the amplicon sequencing data to SRA on October 30 (SRA accession no. SRR12950102) under the Bioproject PRJNA607174. Due to negligence, an amplicon sequence was missing from this data, the correct file should contain 33 sequences, but only 32 sequences were included in the submitted file. Can I resubmit a file to overwrite the original data? This is very

Thank you very much.

11/9/2020 9:51 Re:Re: case #CAS-630560-S5D6W3: Request update data

important to us and we look forward to hearing from you.

Incoming Received

AM TRACKING:000414000008360

From xiaokpcc@163.com

To nlm-support@nlm.nih.gov;nlm-support@nlm.nih.gov;nlm-support@nlm.nih.gov;

Attachment #

Dear Curator:

Please do not withdraw my original data for the time being (SRA accession no. SRR12950102). Our data is under editor review. We will update the data after the review results come out. I am very sorry about my previous request was not clearly stated, can you help me release the withdrawed original data as soon as possible? Thank you very much.

At 2020-11-09 22:32:18, "NLM Support" <nlm-support@nlm.nih.gov> wrote:

Hello,

I had withdrawn this SRA records and you can submit a new one by making new SRA submission and using existing biproject's and sample's accessions for SRA metadata.

Please note, however, that judging by your description there are too few sequences in your file to qualify for SRA submission. SRA fastq files usually contain thousands or millions of sequences.

Please refer to the File Format guide: https://www.ncbi.nlm.nih.gov/sra/docs/submitformats/

Best regards,

Svetlana

If you have any questions or concerns regarding your **SRA** submission please don't hesitate to contact sra@ncbi.nlm.nih.gov (applies to new questions). We normally respond within 2 business days.

Svetlana lazvovskaia The NCBI SRA database submission staff

Dear Curator:

I submitted the amplicon sequencing data to SRA on October 30 (SRA accession no. SRR12950102) under the Bioproject PRJNA607174. Due to negligence, an amplicon sequence was missing from this data, the correct file should contain 33 sequences, but only 32 sequences were included in the submitted file. Can I resubmit a file to overwrite the original data? This is very important to us and we look forward to hearing from you. Thank you very much.

11/9/2020 9:54 Re:Re: case #CAS-630560-S5D6W3: Request update data
Outgoing Sent

AM TRACKING:000414000008360

From nlm-support@nlm.nih.gov

To xiaokpcc@163.com;

Attachment #

I reinstated this run.

Best regards,

Svetlana

If you have any questions or concerns regarding your **SRA** submission please don't hesitate to contact sra@ncbi.nlm.nih.gov (applies to new questions). We normally respond within 2 business days.

Svetlana lazvovskaia
The NCBI SRA database submission staff

----- Original Message -----

From: 肖康鹏;

Received: Mon Nov 09 2020 09:51:06 GMT-0500 (Eastern Standard Time) **To:** nlm-support@nlm.nih.gov; Inbound - NLM Support; Triage Team;

Subject: Re:Re: case #CAS-630560-S5D6W3: Request update data TRACKING:000414000008360

Dear Curator:

Please do not withdraw my original data for the time being (SRA accession no. SRR12950102). Our data is under editor review. We will update the data after the review results come out. I am very sorry about my previous request was not clearly stated, can you help me release the withdrawed original data as soon as possible? Thank you very much.

At 2020-11-09 22:32:18, "NLM Support" <nlm-support@nlm.nih.gov> wrote:

Hello,

I had withdrawn this SRA records and you can submit a new one by making new SRA submission and using existing biproject's and sample's accessions for SRA metadata.

Please note, however, that judging by your description there are too few sequences in your file to qualify for SRA submission. SRA fastq files usually contain thousands or millions of sequences.

Please refer to the File Format guide: https://www.ncbi.nlm.nih.gov/sra/docs/submitformats/

Best regards,

Svetlana

If you have any questions or concerns regarding your **SRA** submission please don't hesitate to contact sra@ncbi.nlm.nih.gov (applies to new questions). We normally respond within 2 business days.

Svetlana lazvovskaia
The NCBI SRA database submission staff

Dear Curator:

I submitted the amplicon sequencing data to SRA on October 30 (SRA accession no. SRR12950102) under the Bioproject PRJNA607174. Due to negligence, an amplicon sequence was missing from this data, the correct file should contain 33 sequences, but only 32 sequences were included in the submitted file. Can I resubmit a file to overwrite the original data? This is very important to us and we look forward to hearing from you. Thank you very much.

11/13/2020 9:53

Re:Error in SRA submission SUB8543863

Incoming Received

AM

From xiaokpcc@163.com

To sra@ncbi.nlm.nih.gov;sra@ncbi.nlm.nih.gov;

Attachment #

Dear Curator:

I uploaded two files (SUB8543863) to replace the previously withdrawn SRA datal (SRA accession no. SRR12950102). One file is fastq formt (converted from sanger sequencing data), and the other one is a tar ball file include all the raw amplicon chromatograms data.

I previously received enthusiastic NCBI staff reply that 'I recommend to upload fastq file with Sanger sequences and additionally tar ball with ab1 files. We'll load it provisionally for now and when ab1 loader will be available we will load them in a standard way.'

Please help us reload SRR12950102 with this two files.

Thank you very much!

Best wishes.

```
At 2020-11-13 22:10:04, sra@ncbi.nlm.nih.gov wrote:

>Dear Kangpeng Xiao,

>Your submission SUB8543863 could not be processed due to an error(s).

>To review your submissions and see the cause of the error, please log in to the NCBI Submission Portal at https://submit.ncbi.nlm.nih.gov/subs/

>Please contact SRA at sra@ncbi.nlm.nih.gov for guidance in fixing your submission. You will not receive an accession number until the submission is complete.

> Regards,

> NCBI SRA Submissions Staff
>Bethesda, Maryland USA

11/17/2020 8:58
AM

Incoming Received
```

From xiaokpcc@163.com

To sra@ncbi.nlm.nih.gov;sra@ncbi.nlm.nih.gov;

Attachment

Dear Curator:

Since the journal editor wanted to release raw Sanger sequences, we submitted the fastq file of the amplified sequence and the original ab1 file. We very much hope that these data will be released as soon as possible. Could you please tell us what we need to do further? Do I need to resubmit the sequence?

Thank you very much, looking forward to your reply! Kangpeng Xiao

At 2020-11-13 22:51:18, "Kangpeng Xiao" <xiaokpcc@163.com> wrote:

Dear Curator:

I uploaded two files (SUB8543863) to replace the previously withdrawn SRA datal (SRA accession no. SRR12950102). One file is fastq formt (converted from sanger sequencing data), and the other one is a tar ball file include all the raw amplicon chromatograms data.

I previously received enthusiastic NCBI staff reply that 'I recommend to upload fastq file with Sanger sequences and additionally tar ball with ab1 files. We'll load it provisionally for now and when ab1 loader will be available we will load them in a standard way.'

Please help us reload SRR12950102 with this two files.

Thank you very much!

Best wishes.

```
At 2020-11-13 22:10:04, sra@ncbi.nlm.nih.gov wrote:
>Dear Kangpeng Xiao,
>
>Your submission SUB8543863 could not be processed due to an error(s).
```

>To review your submissions and see the cause of the error, please log in to the NCBI Submission Portal at https://submit.ncbi.nlm.nih.gov/subs/
>Please contact SRA at sra@ncbi.nlm.nih.gov for guidance in fixing your submission. You will not receive an accession number until the submission is complete.

>

>Regards,

>

>NCBI SRA Submissions Staff >Bethesda, Maryland USA

11/17/2020 2:47 case #CAS-633322-C2V3B7: RE: Error in SRA submission

PM SUB8543863 TRACKING:000422000003768

Outgoing Sent

From

nlm-support@nlm.nih.gov

To

xiaokpcc@163.com;

Attachment #

Dear Kangpeng Xiao,

Files have been processed and released, they should be available for download soon.

Please use BioProject accession PRJNA607174 to reference whole set in your publication and update it with publication details when you'll have them:

https://dataview.ncbi.nlm.nih.gov/object/PRJNA607174

Best, Inna

==

Inna Belaia SRA curator

----- Original Message -----

From: 肖康鹏:

Received: Tue Nov 17 2020 08:55:31 GMT-0500 (Eastern Standard Time)

To: NLM/NCBI List sra; SRA Support;

Subject: Error in SRA submission SUB8543863

Dear Curator:

Since the journal editor wanted to release raw Sanger sequences, we submitted the fastq file of the amplified sequence and the original ab1 file. We very much hope that these data will be released as soon as possible. Could you please tell us what we need to do further? Do I need to resubmit the sequence?

Thank you very much, looking forward to your reply! Kangpeng Xiao At 2020-11-13 22:51:18, "Kangpeng Xiao" <xiaokpcc@163.com> wrote:

Dear Curator:

I uploaded two files (SUB8543863) to replace the previously withdrawn SRA datal (SRA accession no. SRR12950102). One file is fastq formt (converted from sanger sequencing data), and the other one is a tar ball file include all the raw amplicon chromatograms data.

I previously received enthusiastic NCBI staff reply that 'I recommend to upload fastq file with Sanger sequences and additionally tar ball with ab1 files. We'll load it provisionally for now and when ab1 loader will be available we will load them in a standard way.'

Please help us reload SRR12950102 with this two files. Thank you very much!

Best wishes.

```
At 2020-11-13 22:10:04, sra@ncbi.nlm.nih.gov wrote:
>Dear Kangpeng Xiao,
>
>Your submission SUB8543863 could not be processed due to an error(s).
>To review your submissions and see the cause of the error, please log in to the NCBI Submission Portal at https://submit.ncbi.nlm.nih.gov/subs/
>Please contact SRA at sra@ncbi.nlm.nih.gov for guidance in fixing your submission. You will not receive an accession number until the submission is complete.
>
>Regards,
>
>NCBI SRA Submissions Staff
>Bethesda, Maryland USA
```