



Pleuni Pennings <pspennings@gmail.com>

Newest MiSeq Run

Kline, Christopher J <cjk14@pitt.edu>

Mon, Mar 18, 2019 at 6:11 AM

To: "Ambrose, Zandrea" <zaa4@pitt.edu>

Cc: Pleuni Pennings <pspennings@gmail.com>, Kaho Tisthammer <ktisthammer@gmail.com>

Hi Pleuni and Kaho,

I just shared the latest R21 run from over the weekend to Pleuni. Attached is the sample sheet for this run. Again, the far left column is the sequencing sample number and this time I added what week necropsy was for each animal. I think that is pretty much all you need for analysis but if not, please let me know what other information I can get for you.

Thanks and good luck!

Chris

Christopher Kline

Lab Manager- Ambrose Lab

University of Pittsburgh

Department of Microbiology & Molecular Genetics

(412) 383-9881

From: Zandrea Ambrose <zaa4@pitt.edu>

Date: Wednesday, March 13, 2019 at 4:20 PM

To: "Kline, Christopher J" <cjk14@pitt.edu>

Cc: Pleuni Pennings <pspennings@gmail.com>, Kaho Tisthammer <ktisthammer@gmail.com>

Subject: Re: Newest MiSeq Run

Yes, we use the week they were euthanized in, even if it is a few days later.

Sent from my iPhone

On Mar 13, 2019, at 4:00 PM, Kline, Christopher J <cjk14@pitt.edu> wrote:

Hi Pleuni,

Here are the dates for all the animals in this run. Tara was nice enough to give us the actual dates of SIV infection and necropsy. She also got very specific on how many weeks and days for each animal. I think we usually just round down on the dates and give weeks post SIV but I can let Zandrea correct me on that one if she would like.

Coinfected Latents (Date of infection-Date of necropsy)

16314: 8wk 4d; 5/22/15-7/16/15

20615: 6wk 5d; 6/17/16-8/3/16

3516: 9wk; 11/23/16-1/25/17

30816: 8wk; 8/7/17-10/2/17

3216: 9wk 5d; 11/23/16-1/30/17

There were 4 animals that were SIV only and the next sequencing run (which I just started a few minutes ago so fingers crossed on that one) there are a lot of samples from the SIV only animals, including those 3 samples that I erroneously sent you in this runs' sample sheet.

When this run I just started is done, I'll share that data with you too and will make sure to send you the sample sheet and dates for those animals as well. Please let me know if there is anything else you need from me.

Thanks,

Chris

Christopher Kline

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From: Pleuni Pennings <pspennings@gmail.com>

Date: Wednesday, March 13, 2019 at 11:54 AM

To: "Kline, Christopher J" <cjk14@pitt.edu>

Cc: Kaho Tisthammer <ktisthammer@gmail.com>, Zandrea Ambrose <zaa4@pitt.edu>

Subject: Re: Newest MiSeq Run

Thanks! Could you tell us for each animal when the died?

Also, will there be a second SIV-only animal? I thought there were 4?

Thanks!

Pleuni

Pleuni Pennings

Assistant Professor

Department of Biology, San Francisco State University

Website: <http://pleunipennings.wordpress.com/>

Recent paper in Plos Genetics on [fitness costs of mutations in HIV](#).

On Mar 12, 2019, at 1:32 PM, Kline, Christopher J <cjk14@pitt.edu> wrote:

Yes. It's the numbers in the first column that are labeled 1-24. That corresponds with the 1-24 from the BaseSpace run.

Chris

Christopher Kline

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From: Kaho Tisthammer <ktisthammer@gmail.com>

Date: Tuesday, March 12, 2019 at 4:14 PM

To: Pleuni Pennings <pspennings@gmail.com>

Cc: "Kline, Christopher J" <cjk14@pitt.edu>, Zandrea Ambrose <zaa4@pitt.edu>

Subject: Re: Newest MiSeq Run

I believe it's the number in the first column since all samples are numbered 1-24 at BaseSpace, right Chris?

On Mar 12, 2019, at 1:11 PM, Pleuni Pennings <pspennings@gmail.com> wrote:

Thanks!

Re sample id's : the numbers 1-24 in the first column? Or the numbers in the Sample ID column?

<Screenshot 2019-03-12 13.11.01.png>

Pleuni Pennings

Assistant Professor

Department of Biology, San Francisco State University

Website: <http://pleunipennings.wordpress.com/>

Recent paper in Plos Genetics on fitness costs of mutations in HIV.

On Mar 12, 2019, at 12:01 PM, Kline, Christopher J <cjk14@pitt.edu> wrote:

Oh yes. Nex mean necropsy and yes, the sample id corresponds with the sample number on the BaseSpace run.

I guess I neglected your other question... sorry about that!

Christopher Kline

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From: Zandrea Ambrose <zaa4@pitt.edu>
Date: Tuesday, March 12, 2019 at 2:56 PM
To: Pleuni Pennings <pspennings@gmail.com>, "Kline, Christopher J" <cjk14@pitt.edu>
Cc: Kaho Tisthammer <ktisthammer@gmail.com>
Subject: Re: Newest MiSeq Run

"Nex" means necropsy.

From: Pleuni Pennings <pspennings@gmail.com>
Date: Tuesday, March 12, 2019 at 2:16 PM
To: Christopher Kline <cjk14@pitt.edu>
Cc: Kaho Tisthammer <ktisthammer@gmail.com>, "Ambrose, Zandrea" <zaa4@pitt.edu>
Subject: Re: Newest MiSeq Run

Cool, thanks for responding so quickly!

These look like 27 samples, but I only see 24 in Basespace, is that correct?

What is nex?

Does the sample id correspond with the Basespace sample numbers?

Thanks!

Pleuni

Pleuni Pennings

Assistant Professor

Department of Biology, San Francisco State University

Website: <http://pleunipennings.wordpress.com/>

Recent paper in Plos Genetics on fitness costs of mutations in HIV.

On Mar 12, 2019, at 10:58 AM, Kline, Christopher J <cjk14@pitt.edu> wrote:

Hi Pleuni,

Sorry about that. Here is the sample sheet that includes the animal numbers, sample type and either collection date for plasma or collection site for tissues.

Chris

Christopher Kline

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(412) 383-9881

From: Pleuni Pennings <pspennings@gmail.com>

Date: Tuesday, March 12, 2019 at 1:55 PM

To: "Kline, Christopher J" <cjk14@pitt.edu>

Cc: Kaho Tisthammer <ktisthammer@gmail.com>, Zandrea

Ambrose <zaa4@pitt.edu>

Subject: Re: Newest MiSeq Run

Hi Chris,

Thanks for sharing this. Kaho and I were busy with our other project. Sorry for the delay!

How do we know which sample belongs to which animal / time point / collection site?

Thanks!

Pleuni

Pleuni Pennings

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Recent paper in Plos Genetics on fitness costs of mutations in HIV.

On Feb 25, 2019, at 9:17 AM, Kline, Christopher J
<cjk14@pitt.edu> wrote:

Hi Pleuni and Kaho,

Our latest sequencing run has finished up. Pleuni, I have shared the BaseSpace run with you so you should be able to access through your BaseSpace account. If you would like me to share the run with Kaho too, I'm more than happy to. Kaho, if you have a BaseSpace account through a different email, please let me know which one so I can send it to that.

There was an issue with the sample sheet when I did the run, so you might see there are two analyses of this run. Please make sure to use the analysis that was generated on 2019-02-25 because that one will be correct.

Also, because we didn't use primer ID for the library prep, I'm not able to process this run through Shuntai's pipeline. However, I believe you are able to organize the sequences yourself without it.

I'm guessing you'll at least need the primer sequences to organize the data. Here they are:

mac251 V1-F TACCAGCTTGGAGGAATGCGAC

mac251 V3-R AAGTCTGTGTCTCCATCATCCTTGTG

Please let me know if you need anything else!

Thanks,

Chris

Christopher Kline

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<Pleuni sample sheet for MiSeq #4.xlsx>



Pleuni Sample Sheet for MiSeq #5.xlsx

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