

From: Lau, Matthew K. matthewklau@fas.harvard.edu
Subject: Re: sequence transfer
Date: November 7, 2016 at 4:17 PM
To: Jim Bochicchio jboch@broadinstitute.org
Cc: Jennifer Wineski jwineski@broadinstitute.org, Sarah Young stowey@broadinstitute.org, Caroline Cusick ccusick@broadinstitute.org



Hi Jim, that works for me. I just saw & accepted the updated meeting invite too.

Best,
Matt

On Nov 7, 2016, at 2:18 PM, Jim Bochicchio <jboch@broadinstitute.org> wrote:

Hi Matt

Can we bump our meeting until the 18th? We had a weekly check in with our analyst today and he doesn't think all of the assemblies will be ready this week.

Thanks
Jim

On Wed, Nov 2, 2016 at 2:25 PM, Lau, Matthew K. <matthewklau@fas.harvard.edu> wrote:

Awesome, thanks!

Matt

On Nov 2, 2016, at 1:32 PM, Jennifer Wineski <jwineski@broadinstitute.org> wrote:

Thank you Matt! We will see you on Thursday the 10th!

On Wed, Nov 2, 2016 at 1:14 PM, Lau, Matthew K. <matthewklau@fas.harvard.edu> wrote:

Hi Jenn, Thu Nov 10 at 11am works for me!

Best,
Matt

On Nov 2, 2016, at 12:00 PM, Jennifer Wineski <jwineski@broadinstitute.org> wrote:

[<jwineski@broadinstitute.org>](mailto:jwineski@broadinstitute.org) wrote.

Hi Matt,

Would Thursday, November 10th at 11am work for you?

Thank you,

Jenn

On Wed, Nov 2, 2016 at 11:50 AM, Lau, Matthew K.

[<matthewklau@fas.harvard.edu>](mailto:matthewklau@fas.harvard.edu) wrote:

OK, great. For now, both of the dates that Jim mentioned work for me.

Cheers,

Matt

On Nov 2, 2016, at 8:39 AM, Sarah Young

[<stowey@broadinstitute.org>](mailto:stowey@broadinstitute.org) wrote:

Yes, we just need a bit more time to pull the final analysis together.

Jenn will be in touch with meeting details shortly!

On Wed, Nov 2, 2016 at 8:32 AM, Lau, Matthew K.

[<matthewklau@fas.harvard.edu>](mailto:matthewklau@fas.harvard.edu) wrote:

Hi all, glad the improvement program ran! Does that change the meeting date (per Jim's email)?

Thanks,

Matt

On Nov 1, 2016, at 4:45 PM, Sarah Young

[<stowey@broadinstitute.org>](mailto:stowey@broadinstitute.org) wrote:

The good news is that we were able to get our improvement programs to run, and they reduced the contigs by a little under 10%! We just need a bit of extra time to pull together

all the analysis now that the improved assemblies are complete.

On Tue, Nov 1, 2016 at 4:27 PM, Jim Bochicchio
<jboch@broadinstitute.org> wrote:

Hi All

Looks like the informatics work will take a bit longer than anticipated. Would we be able to bump this Friday's meeting to next Thursday or possibly the following Monday?

Thanks
Jim

On Fri, Oct 28, 2016 at 10:16 AM, Lau, Matthew K.
<matthewklau@fas.harvard.edu> wrote:

Hi Caroline, awesome, thanks! Will let you know if I run into a snag I can't address in the FAQ's.

Cheers,

Matt

On Oct 28, 2016, at 10:07 AM, Caroline Cusick
<ccusick@broadinstitute.org> wrote:

Hi Matt,

The Aspera is ready! I've included the login information below, and a key to match our sample ID to the collaborator ID's you submitted as well as what type of each data is on each flowcell (All 7 samples were run as a pool). If you download the data through the web client, you'll need to download [Aspera Connect](#). Let me know if you run into any issues with the site, or have any questions!

The data will be stored here for a month before being deleted, so please move it over at your earliest convenience. If you have any questions or concerns, please email btlhelp@broadinstitute.org

Aspera Username: SN0107253
Aspera Password:
B26QN2YENHKT29B
Aspera FilePasscode: 6miXig7JX19I91f

For detailed instructions, examples and
FAQs, see:

[http://www.broadinstitute.org/
aspera/doc/aspera_shares_transfers.txt](http://www.broadinstitute.org/aspera/doc/aspera_shares_transfers.txt)

These instructions may changed, please
make a note.

This site is good for 30 days.

High Level Instructions

Method 1

Web download instructions

- Go to the Broad Aspera Shares Server at
(<https://shares.broadinstitute.org/>)
- Login with your Aspera Shares Credentials
- See detailed instructions for more
information

Method 2

Linux command line instructions

(Recommended for sites with >100 files.)

- This method is described in technical detail
in the referenced instructions.

thanks!
Caroline

On Thu, Oct 27, 2016 at 4:01 PM, Lau, Matthew K.
<matthewklau@fas.harvard.edu> wrote:

Hi Caroline, great, thanks for the update and the
heads-up!

Cheers,

Matt

On Oct 27, 2016, at 10:36 AM, Caroline Cusick
<ccusick@broadinstitute.org> wrote:

Hi Matt,

The Aspera is still staging, but it should come down either today/tomorrow, and I'll send along the login information. As a heads up, the total size of the raw files is ~0.69 TB.

thanks!
Caroline

On Thu, Oct 27, 2016 at 10:23 AM, Lau, Matthew K. <matthewklau@fas.harvard.edu> wrote:

Hi Caroline and Sarah, just checking in the status of the sequences. Did your bioinformatician work his magic? And/or, have the files been zipped and hosted on your file transfer system?

Best,

Matt

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"Knowledge is knowing a tomato is a fruit.
Wisdom is not putting it in a
fruit salad." — Miles Kingston

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