From: **Lau, Matthew K.** matthewklau@fas.harvard.edu
Subject: Re: ant sequences
Date: September 13, 2016 at 5:52 PM
To: Jim Bochicchio jboch@broadinstitute.org
Cc: ccusick@broadinstitute.org, **Bowlen, Jeannette** bowlen@fas.harvard.edu

Hi Jim, alright, we're good to go with the accounting on our end. Go ahead and generate the quote when you get a chance.

Thanks,
Matt

On Sep 12, 2016, at 12:28 PM, Jim Bochicchio <jboch@broadinstitute.org> wrote:

> Hi Matt
>
> We can't make it below $5,000 since sequence is $2,500 per lane and you have to buy them in sets of 2 so $5,000 is the minimum we could quote you.
>
> Thanks
> Jim
>
> On Mon, Sep 12, 2016 at 10:53 AM, Lau, Matthew K. <matthewklau@fas.harvard.edu> wrote:
>> Hi Jim, sounds good. Go ahead and send us a quote for the additional sequencing. Jeanette has reminded me that it needs to be below the $5000 limit, so if you can please make it for $4999.99. If there's an issue with that let us know ASAP.
>>
>> Thanks,
>> Matt
>>
>> On Sep 11, 2016, at 7:53 PM, Jim Bochicchio <jboch@broadinstitute.org> wrote:
>>
>>> Hi Matt
>>>
>>> Yes, we are using all the data currently generated so it is a

mix of frags and jumps.

Thanks
Jim

On Fri, Sep 9, 2016 at 5:05 PM, Lau, Matthew K. <matthewklau@fas.harvard.edu> wrote:
> Hi Jim, can you generate jump assemblies with the current 20x coverage for all the samples?
>
> Thanks,
> Matt
>
> On Sep 8, 2016, at 9:19 AM, Jim Bochicchio <jboch@broadinstitute.org> wrote:
>
>> Hi Matt
>>
>> No this isn't holding up the assemblies. We told the analysts to proceed with the data they have on hand but if you decided to move ahead with additional sequencing let us know ASAP so the analyst can hold up on the assemblies until we get the new data otherwise it ends up being twice the amount of work for them.
>>
>> Thanks
>> Jim
>>
>> On Thu, Sep 8, 2016 at 9:08 AM, Lau, Matthew K. <matthewklau@fas.harvard.edu> wrote:
>>> Hi Jim, sorry for the slow reply on this. I'll get back to you shortly with an answer on the jump libraries. Meanwhile, I wanted to check though, this isn't holding up the frag sequencing, right?
>>>
>>> Thanks,

Matt

On Sep 6, 2016, at 5:08 PM, Jim Bochicchio <jboch@broadinstitute.org> wrote:

Hi Matt and Jeannette

Ok, if you want we can generate a quote for $5000 for 2 lanes of jump sequencing just so you will get some data before the grant runs out.

Thanks
Jim

On Tue, Sep 6, 2016 at 4:56 PM, Lau, Matthew K. <matthewklau@fas.harvard.edu> wrote:

Hi Jim, Jeanette and I discussed the quote and unfortunately the $15000 quote exceeds the grant's $5000 threshold for a required competitive bidding process. We'd therefore have to generate another round of inquiries into pricing from other vendors.

At this point, though, we're coming up to the grant spending deadline. I appreciate the offer to not charge us for the library construction, but we'll have to forego the additional sequencing for the jump libraries and just go with finishing up the frag libraries.

Let me know if you would like to chat about this.

Best,

Matt

On Sep 6, 2016, at 3:41 PM, Lau, Matthew K. <matthewklau@fas.harvard.edu> wrote:

Great, thanks Jim! I'm running downstairs to chat with

Great, thanks Jim. I'm running downstairs to chat with Jeanette.

Matt

On Sep 6, 2016, at 3:26 PM, Jim Bochicchio <jboch@broadinstitute.org> wrote:

Hi Matt

Ok, quote just came out via the quote server email. Let us know if you have any questions. We put in for 6 more lanes of sequencing which is $15,000. Once the quote is funded the sequencing will begin.

Thanks
Jim

On Tue, Sep 6, 2016 at 12:06 PM, Lau, Matthew K. <matthewklau@fas.harvard.edu> wrote:

Thanks Jim, that sounds great!

Best,
Matt

On Sep 6, 2016, at 10:23 AM, Jim Bochicchio <jboch@broadinstitute.org> wrote:

Hi Matt

Yes we should be able to sequence these in the next few weeks and will be able to fill it out at the end of Sept. We will send along the quote as soon as its available.

Thanks
Jim

On Wed, Aug 31, 2016 at 1:13 PM, Lau, Matthew K. <matthewklau@fas.harvard.edu> wrote:

Hi Jim, that sounds good. We're coming up on a spending deadline at the end of October though and will need to pay you for the sequences well before then.

Will you still be able to get sequences to us mid- to late-September? If so, go ahead and generate the quote and send to us (including our accountant Jeanette, CC'ed).

Thanks,

Matt

On Aug 31, 2016, at 11:39 AM, Jim Bochicchio <jboch@broadinstitute.org> wrote:

Hi Matt

Yes, you won't be charged for the library construction for the jumping libraries but we would need to generate a new quote if you want them sequenced.

Thanks
Jim

On Tue, Aug 30, 2016 at 1:40 PM, Lau, Matthew K. <matthewklau@fas.harvard.edu> wrote:

Hi Jim, thanks for the update and sorry to hear about the confusion, and thanks for offering not to charge us for the jump libraries. Just to be clear, do you need to draft a new contract to provide us with the

draft a new contract to provide us with the "free" jump coverage?

Thanks,

Matt

On Aug 30, 2016, at 8:42 AM, Jim Bochicchio <jboch@broadinstitute.org> wrote:

Hi Matt

The analysts are working on the assemblies but we noticed there was some confusion in the lab in which both fragment and jumping libraries were made for all 7 of your samples. Due to this, the sequencing was split between the frags and jumps so we currently only have about 30-40x frag coverage and 25x jump coverage. Do you want us to generate a new quote for some additional sequencing to bring both these numbers up to ~50x so we can then generate assemblies using both the frag and jump data? In addition, since this was a lab messaging issue on our end you obviously will not be charged for the jump library construction.

Thanks
Jim

On Mon, Aug 15, 2016 at 5:55 PM, Jim Bochicchio <jboch@broadinstitute.org> wrote:

wrote:

Hi Matt

Sorry for the delay, I've been out of the office. We just received the last of the sequencing data and are starting the assemblies. The assemblies should take about a month to complete but we will let you know if we have any issues.

Thanks
Jim

On Fri, Aug 12, 2016 at 9:25 AM, Lau, Matthew K. <matthewklau@fas.harvard.edu> wrote:

Hey Jim, what's the status on the test lane and jump libraries? Are things looking good to go?

Thanks,

Matt

On Jul 11, 2016, at 3:53 PM, Jim Bochicchio <jboch@broadinstitute.org> wrote:

Hi Matt

Was actually going to send you an update this afternoon. We've finished the PCR-Free libraries and are currently running a test lane on them before requesting the full coverage and the jumps are in library construction this

are in library construction this week. We should have them submitted for a test lane early next week. Once we get the results from the test runs we will be able to give a final ETA for everything.

Thanks
Jim

On Mon, Jul 11, 2016 at 10:56 AM, Lau, Matthew K. <matthewklau@fas.harvard.edu> wrote:

> Hi Jim and Caroline, just checking in again. What's the status on the ant sequences?
>
> Thanks!
>
> Matt

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