From: Lau, Matthew K. matthewklau@fas.harvard.edu

Subject: Re: ant sequencing Date: May 2, 2016 at 10:13 PM

To: Jim Bochicchio jboch@broadinstitute.org

Cc: Caroline Cusick ccusick@broadinstitute.org, Aaron M Ellison aellison@fas.harvard.edu



Hi Jim, thanks for the update. Please keep us posted if anything changes with the timeline for processing.

Good luck getting things optimized.

Best,

Matt

Postdoctoral Fellow Harvard Forest Harvard University 324 N Main St. Petersham, MA 01366 978-756-6165

On May 2, 2016, at 5:05 PM, Jim Bochicchio <<u>iboch@broadinstitute.org</u>> wrote:

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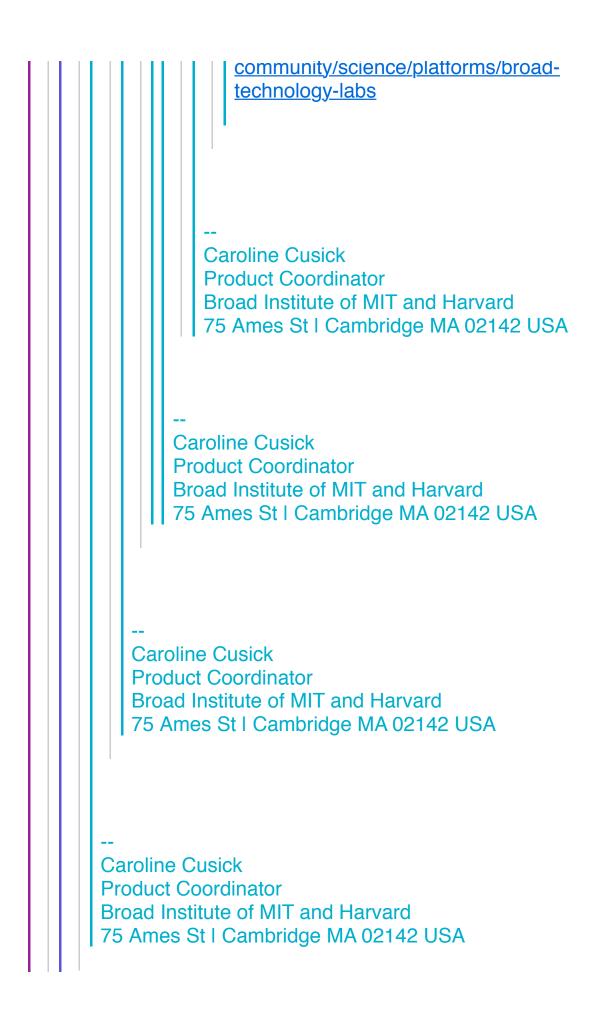
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Product Coordinator
Broad Institute of MIT and Harvard
75 Ames St I Cambridge MA 02142 USA
<PDO-8220 extraction quants.xls>

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Caroline Cusick Product Coordinator Broad Institute of MIT and Harvard 75 Ames St I Cambridge MA 02142 USA

Subject: Re: ant sequencing
Date: March 21, 2016 at 4:44 PM

To: Lau, Matthew K. matthewklau@fas.harvard.edu

Cc: James Bochicchio jboch@broadinstitute.org, Ellison, Aaron aellison@fas.harvard.edu



Hi Matt,

I'll put in the request to have caliper run on these samples, and send you the results once we have them.

thanks! Caroline

On Mon, Mar 21, 2016 at 3:38 PM, Lau, Matthew K.

<matthewklau@fas.harvard.edu> wrote:

Hi Caroline, wow, that's a lot of DNA! The original extraction last fall yielded only 1.5 ug. Looks like there's almost enough DNA for PacBio now. Are you running a caliper to check DNA quality before building the libraries?

Thanks, Matt

On Mar 21, 2016, at 2:42 PM, Caroline Cusick ccusick@broadinstitute.org wrote:

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PDO-8220 extract...nts.xls

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Caroline Cusick Product Coordinator Broad Institute of MIT and Harvard 75 Ames St I Cambridge MA 02142 USA

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Subject: Re: ant sequencing

Date: February 26, 2016 at 9:46 AM

To: Lau, Matthew K. matthewklau@fas.harvard.edu



Hi Matt,

Thanks for sending this along! I was just scanning it, and we need to have a "Collaborator Sample ID" for each sample (in addition to the "Collaborator Participant ID"). This is just a unique identifier for downstream processing and analysis, and is just how we can map our identifier to yours. Let me know if you have any questions!

thanks, Caroline

On Fri, Feb 26, 2016 at 7:04 AM, Lau, Matthew K. matthewklau@fas.harvard.edu wrote:

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Thanks, Matt

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