From: clement.s.chu@gmail.com on behalf of Clement Chu [clement.chu@ucsf.edu]
Sent: Thursday, April 17, 2008 2:50 PM
To: Christina Fan
Subject: Re: 454 sequencing
That sounds fine. Good luck with the library prep.

Clement

On Thu, Apr 17, 2008 at 1:57 PM, Christina Fan <chfan@stanford.edu> wrote:
Hi Clement,
I obtained a library prep kit from Alex and I will prepare the libraries next week (7 total). I will let you know when I have them ready, but let's plan to have a run on April 30. Is that ok?
Thanks for your help!
Christina

Clement Chu wrote:

> Hi Christina,
>
> Most days are ok as I am fairly flexible. What day would you like to perform the run? You can either perform cluster generation one day and begin sequencing the next, or you can do both on the same day (it makes for a long day).
>
> Clement
>
> -----Original Message-----
> From: Christina Fan [mailto:chfan@stanford.edu] Sent: Friday, April 11, 2008 5:41 PM
> To: Clement Chu
> Subject: Re: 454 sequencing
>
> Hi Clement,
> I emailed you a few days ago about setting up the dates for solexa sequencing.
> We would want to schedule for a run around May1, and another one the week following.
> Joe said he has reagents in stock for us.
> Just want to see what the dates are good for you.
> Thanks so much!
> Christina
>
> Clement Chu wrote:
>
> > Hi Steve and Christina,
> >
> > Sounds great. I can definitely get you guys on around that time frame.
>
> In
>
> > terms of reagent availability here, I would ask Joe. We don't have any stocked in the CAT but I know Joe and Jonathan have been buying multiple kits at once and are probably the best people to ask. The lead time on reagents direct from Illumina seems to be about 2 weeks or so.
> >
> > Best,
> > Clement

STANFORD EXHIBIT 2124

-----Original Message-----
From: srquake@gmail.com [mailto:srquake@gmail.com] On Behalf Of Stephen Quake
Sent: Friday, April 04, 2008 5:20 PM
To: Clement Chu
Cc: Christina H. Fan
Subject: Re: 454 sequencing

ok, we have our act together now and are interested in making a full run on may 1, plus or minus a few days. how is the sign up, reagenet availablility etc looking?

best,

steve

On Tue, Jan 29, 2008 at 1:38 PM, Clement Chu <Clement.Chu@ucsf.edu> wrote:

> Hi Steve,
>
> Good to hear from you. Joe certainly did mention your interest. We don't stock any reagents in the facility itself but if you need reagents on a quick timetable, Joe might be able to help you there. We are still restricting the user base so we could probably work you in within a week or so of when you have a library prepared. Let me know if you need any more
> info or if you have a timetable in mind.
>
> Best,
> Clement
>
> -----Original Message-----
> From: srquake@gmail.com [mailto:srquake@gmail.com] On Behalf Of Stephen
> Quake
> Sent: Tuesday, January 29, 2008 9:49 AM
> To: Clement.Chu@ucsf.edu
> Cc: Christina Fan
> Subject: Fwd: 454 sequencing
>
> Clement
>
> Joe Derisi might have told you we are interested in running a few samples on your Solexa. How long is the queue to get something on the machine and do you guys stock the sequencing reagents?
>
> best,

Steve

---------- Forwarded message ----------
From: Joe DeRisi <joe@derisilab.ucsf.edu>
Date: Jan 9, 2008 9:31 PM
Subject: Re: 454 sequencing
To: Stephen Quake <quake@stanford.edu>

Hi Steve,
Great. The Solexa guy here is Clement Chu. His email is Clement.Chu@ucsf.edu. I will let him know that you or someone from your lab will contact him.

Our machine is currently configured for 8 lanes/flowcell, with 330 tiles per lane. For a good library, you should get 20-30k clusters per tile, which, in an ideal world, would give you about 9 million reads per lane, each 36nt. In reality, folks are getting 2-4 million, and the 8th lane is usually reserved for a control. It is clear the read length can be extended, if you are willing to tolerate some additional errors.
Depending on your application, we can advise on library construction strategies.

thanks for dropping by the other day - it was a big help.

-joe

On Jan 9, 2008 3:06 PM, Stephen Quake <quake@stanford.edu> wrote:

> joe,
>
> the person in my lab to contact about a 454 run is rick white. each
> full run is 400,000 reads of ~ 250 bp each. the configuration is two
> large chambers, which are independently loaded (ie can be different
> samples). there are other configurations (up to 16 independent
> samples) and it is possible to do runs of shorter reads (100bp), which
> are slightly cheaper.
>
> best
>
> steve
>
> --
> ----------
> Stephen Quake
> Professor of Bioengineering
> Stanford University
>
> PLEASE REPLY TO: quake@stanford.edu

--

Stephen Quake
Professor of Bioengineering
Stanford University

PLEASE REPLY TO: quake@stanford.edu

No virus found in this incoming message.
Checked by AVG Free Edition.
Version: 7.5.516 / Virus Database: 269.19.15/1249 - Release Date:

1/29/2008

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Version: 7.5.516 / Virus Database: 269.19.15/1249 - Release Date:

1/29/2008

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