From: Stephen Quake [quake@stanford.edu]
Sent: Tuesday, April 08, 2008 10:15 AM
To: Joe DeRisi
Cc: Christina Fan
Subject: Re: solex run

we will bring the drive! the calibration thing is indeed challenging - roche also wants you to blow a run on titration. a number of people are simply using real time pcr, but i think digital is more precise - we are doing a bunch of side by side tests to verify. it's commercially available from fluidigm if you want to ask hhmi to pop for an instrument for you.

christina fan is the contact person for the solexa run.

best,

steve

On Sat, Apr 5, 2008 at 9:06 PM, Joe DeRisi <joe@derisilab.ucsf.edu> wrote:
> Hi Steve,
> Yes, we have reagents in stock for your Solexa run. Sharon, Charles,
> and Alex (the folks in my lab that have been working with Richard to
> get the 454 run on) will be the ones to get your run on here. Is
> Richard the guy that will be interacting with us for the Solexa?
> Planning ahead, the person in your lab that comes up to do the Solexa
> run should bring up a 1Tb portable hard drive. Anything smaller will
> not be able to fit the data. We can store the data during the run on
> the local machine, but it must be removed to make room for the next.
> I have been following this 454 run from the sidelines, and I thought
> only the Solexa was plagued with problems! Fortunately, the computer
> has never crashed on us during a Solexa run, as this would be a total
> disaster. Plenty of other strange things have happened, but not a
> crash.
> The idea of using digital PCR to pre-check the Solexa library is
> great. As you may know, the worst thing about the Solexa is the fact
> that it is nearly impossible to tell by simple methods how many
> clusters per unit mass a given library will yield before actually
> doing the cluster generation step. Illumina's answer is to blow a flow
> cell and do a serial dilution in separate lanes to determine the
> optimal concentration. Not a great solution, in my opinion. dPCR, on
> the other hand, might be the ticket.
> Thanks for tolerating the folks from my lab - they are an
> enthusiastic bunch and want to learn as much as the can about the
> process. As you can imagine, there is also a lot of nuance to pulling
> off a successful Solexa run.
>
>
> -j
>
>
>
> On Fri, Apr 4, 2008 at 5:36 PM, Stephen Quake <quake@stanford.edu> wrote:
> > joe
> >
> > we are gearing up for a full solexa run around may 1. do you have
> > reagents in stock that we could use?
> >
> > your 454 sample is running right now. unfortunately the computer
> > crashed just as the run began (this has been a lingering problem
> > with the system) and it looks like it will be challenging to get
> > sequence data out. there is a small chance we will get something
> > useful, so we are letting the run proceed tonight. but chances are

> > we will have to run it again next week. so it goes...
> >
> > steve
> >
> > --
> > ----------------------
> > Stephen Quake
> > Professor of Bioengineering
> > Stanford University
> >
> > PLEASE REPLY TO: quake@stanford.edu
> >
>

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Stephen Quake
Professor of Bioengineering
Stanford University

PLEASE REPLY TO: quake@stanford.edu
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