

Message

From: srquake@gmail.com [srquake@gmail.com]
on behalf of Stephen Quake [quake@stanford.edu]
Sent: 1/29/2008 11:14:57 PM
To: Joe DeRisi [joe@derisilab.ucsf.edu]
CC: Christina Fan [chfan@stanford.edu]
Subject: Re: 454 sequencing

thanks, we are just getting organized. for the first few runs do you want to arrange some kind of reagent barter? (ie i will float you here for 454 runs if you do the same; if it doesn't balance out in a half year or so we find a way to move cash back and forth).

steve

On 1/9/08, Joe DeRisi <joe@derisilab.ucsf.edu> wrote:

> 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
> >
> >

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Stephen Quake
Professor of Bioengineering
Stanford University

PLEASE REPLY TO: quake@stanford.edu

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SEQUENCING - STANFORD