

Subject: Re: NCBI check: contamination still present

Date: June 19, 2017 at 5:45 PM

To: Terrance Shea tshea@broadinstitute.org



Great, thanks Terry. I'll get those submitted to NCBI and get those checked.

Best, Matt

On Jun 19, 2017, at 5:36 PM, Terrance Shea tshea@broadinstitute.org wrote:

Hi Matt, all-

I apologize for missed adapter. We will have to take another look at our screening updates.

I have removed the regions reported by NCBI for SM-AZXXN and SM-AZXXO.

In the FTP area there is a new folder titled "20170619" and within this are two .tar.gz files for SM-AZXXN and SM-AZXXO.

Let us know if anything further is found.

Terry

On Mon, Jun 19, 2017 at 11:56 AM, Lau, Matthew K.

<matthewklau@fas.harvard.edu> wrote:

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Also, Terry, just got this too:



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Matt

Postdoctoral Research Fellow Harvard Forest Harvard University 324 N Main St Petersham, MA 01366

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On Jun 19, 2017, at 8:29 AM, Sarah Young stowey@broadinstitute.org wrote:

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Cc: Sarah Young stowey@broadinstitute.org, Jim Bochicchio jboch@broadinstitute.org, Ellison, Aaron aellison@fas.harvard.edu, Caroline Cusick ccusick@broadinstitute.org

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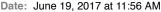
Director, Operations, Finance and Computation Broad Technology Labs The Broad Institute 75 Ames Street Cambridge, MA 02141

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E: stowey@broadinstitute.org

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Beter Ives 10, 0017 at 11,50 AM



To: Sarah Young stowey@broadinstitute.org



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E: stowey@broadinstitute.org

From: Ellison, Aaron aellison@fas.harvard.edu Subject: RE: NCBI check: contamination still present

Date: June 18, 2017 at 6:06 PM

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

I hope they do it quickly.

Best, Aaron

From: Lau. Matthew K. Sent: Sunday, June 18, 2017 18:02

To: Ellison, Aaron <aellison@fas.harvard.edu> Subject: Re: NCBI check: contamination still present

Hey Aaron, they may need to trim the Ns and the end of the sequences too, I didn't check this, but the end of the error report lists the adapters that were detected and where in the genomes.

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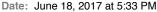
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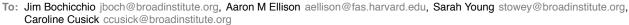
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Some of the sequences hit primers or adaptors used in Illumina or 454 or other sequencing strategies or platforms. Primers at the end of a sequence should be removed. However, if primers are present within sequences then you should strongly consider splitting the sequences at the primers because the primer sequence could have been the region of overlap, causing a misassembly.

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Trim: Sequence name, length, span(s), apparent source scaffold00094 712997 15373..15411 adaptor:NGB00843.1 scaffold00121 612406 387957..387996 adaptor:NGB00843.1 scaffold00264 303333 247297..247333 adaptor:NGB00843.1 scaffold00282 286384 154047..154082 adaptor:NGB00843.1 scaffold00424 169256 91684..91733 adaptor:NGB00843.1 scaffold00635 94765 70145..70194 adaptor:NGB00843.1 scaffold02309 19718 14150..14191 adaptor:NGB00843.1 scaffold03495 10772 8825..8858 adaptor:NGB00843.1

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Knowledge is knowing that a tomato is a fruit, wisdom is not putting it in a fruit salad.