

From: Lau, Matthew K. matthewklau@fas.harvard.edu  
Subject: Re: ant genomes  
Date: February 14, 2017 at 5:15 PM  
To: Caroline Cusick ccusick@broadinstitute.org  
Cc: James Bochicchio jboch@broadinstitute.org



Great, I also just saw that Sarah emailed me with some suggestions as well.

Thanks!

Matt

On Feb 14, 2017, at 10:27 AM, Caroline Cusick  
<[ccusick@broadinstitute.org](mailto:ccusick@broadinstitute.org)> wrote:

Hi Matt,

I heard back from our analysts and they said the following,

"You're on the right track with the GATK website. Also try the forums (<http://gatkforums.broadinstitute.org/gatk/>), there are people that maintain them and they can be very helpful. It will be a process to figure out how to run GATK for your particular organism. I would suggest that you call SNPs genome-wide first, and then look to see where they fall to dive into individual genes. Also, it's important that you pick your best reference genome, and align data to that for analysis purposes. By best, I typically recommend the genome that looks most complete (maybe the largest?). Also, I should point out, GATK is mostly supported for human, so whenever one wants to utilize it for an alternative genome it's always a process to figure out the exact optimal parameters. The GATK people should be able to help out. Alternatively, I know you mentioned this but I forget the answer, if your data is haploid, then you could try using Pilon to call SNPs: <https://github.com/broadinstitute/pilon/wiki>."

let me know if you have any other questions!

thanks,  
Caroline

On Tue, Feb 14, 2017 at 9:10 AM Caroline Cusick

<[ccusick@broadinstitute.org](mailto:ccusick@broadinstitute.org)> wrote:

Hi Matt,

Happy belated new year to you too!

I'm going to pass your question on to our analyst (Terry) and will let you know his response as soon as I get it.

thanks!

Caroline

On Wed, Feb 8, 2017 at 10:23 AM Lau, Matthew K.

<[matthewklau@fas.harvard.edu](mailto:matthewklau@fas.harvard.edu)> wrote:

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2) I've been going over the sequence quality stats, and I'm starting to get into doing some comparative analysis of the sequences. I started looking at the GATK pages and the Genome analysis sections were listed as under-development. Can you point me in the right direction of info for using GATK to search for target genes and for comparing my genomes (e.g. genetic distances)?

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To: Jim Bochicchio jboch@broadinstitute.org  
Cc: stowey stowey@broadinstitute.org, Caroline Cusick ccusick@broadinstitute.org

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Hi Jim, thanks for checking in. Yes almost there. See you a bit.

Cheers,  
Matt

On Oct 21, 2016, at 2:50 PM, Jim Bochicchio  
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Hi Jim, thanks for the update. As a whole, what's left in the process? Can we schedule a meeting to go over the data sometime next week? My general schedule right now is to be in Cambridge on Fridays, but I'm happy to do another day with the exception of Tuesdays.

Cheers,

Matt

On Oct 3, 2016, at 1:12 PM, Jim Bochicchio  
[<jboch@broadinstitute.org>](mailto:jboch@broadinstitute.org) wrote:

Hi Matt

We just received the data from the additional two lanes of sequencing late last week and handed the data off to our analyst. We are awaiting an update ETA for this project and will let you know soon.

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Jim

On Fri, Sep 30, 2016 at 9:50 AM, Lau, Matthew K.

<[matthewklau@fas.harvard.edu](mailto:matthewklau@fas.harvard.edu)> wrote:

Hi Jim and Caroline, would you be able to give me a quick status update on the ant genome sequencing?

Thanks!

Matt

*Postdoctoral Fellow*  
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"Knowledge is knowing a tomato is a fruit.

Wisdom is not putting it in a fruit salad." — Miles Kingston

--

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Website: <http://www.broadinstitute.org/scientific-community/science/platforms/broad-technology-labs>

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**From:** Lau, Matthew K. matthewklau@fas.harvard.edu  
**Subject:** Re: ant genomes  
**Date:** October 3, 2016 at 4:51 PM  
**To:** Jim Bochicchio jboch@broadinstitute.org  
**Cc:** Caroline Cusick ccusick@broadinstitute.org  
**Bcc:** Aaron Ellison aellison@fas.harvard.edu



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