

**From:** Lau, Matthew K. [matthewklau@fas.harvard.edu](mailto:matthewklau@fas.harvard.edu)  
**Subject:** Fwd: Ant DNA caliper  
**Date:** September 6, 2016 at 3:39 PM  
**To:** Bowlen, Jeannette [bowlen@fas.harvard.edu](mailto:bowlen@fas.harvard.edu)

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Begin forwarded message:

**From:** Jim Bochicchio <[jboch@broadinstitute.org](mailto:jboch@broadinstitute.org)>  
**Date:** December 10, 2015 at 3:21:32 PM EST  
**To:** "Lau, Matthew K." <[matthewklau@fas.harvard.edu](mailto:matthewklau@fas.harvard.edu)>  
**Cc:** Sarah Young <[stowey@broadinstitute.org](mailto:stowey@broadinstitute.org)>, Caroline Cusick <[ccusick@broadinstitute.org](mailto:ccusick@broadinstitute.org)>  
**Subject:** Re: Ant DNA caliper

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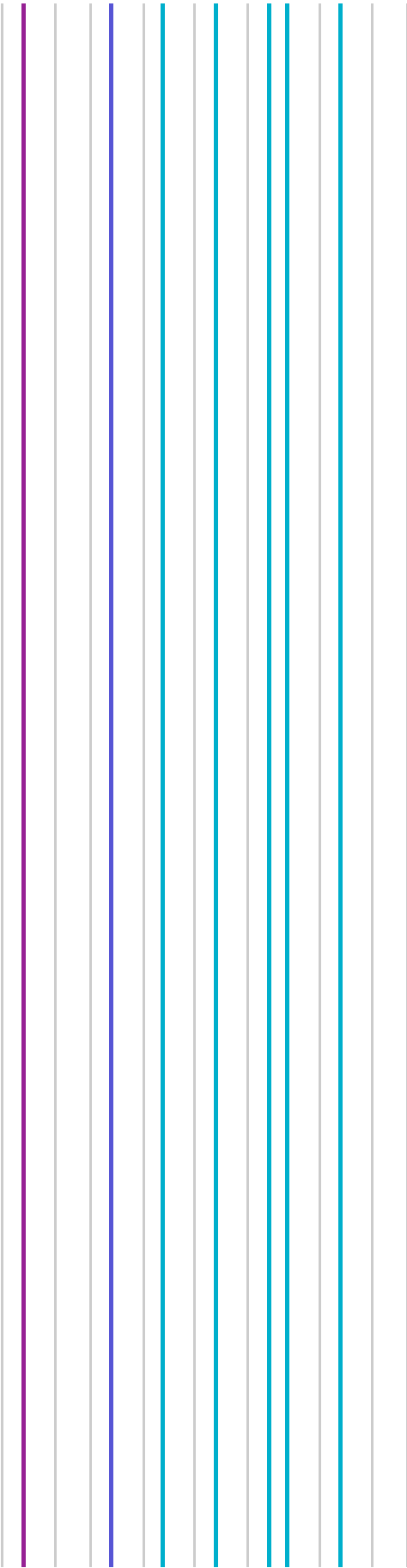
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**From:** Lau, Matthew K. matthewklau@fas.harvard.edu  
**Subject:** Re: Ant DNA caliper  
**Date:** December 10, 2015 at 3:01 PM  
**To:** Sarah Young stowey@broadinstitute.org  
**Cc:** Jim Bochicchio jboch@broadinstitute.org, Caroline Cusick ccusick@broadinstitute.org

---



Hi Sarah, thanks that makes sense and seems good to me as a baseline that we could then improve with the addition of jumping libraries.

Jim - this sounds good to me. Can you get a work request going? If so, just let me know what you need from me.

Cheers,

Matt

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

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**Date:** December 9, 2015 at 10:52 AM  
**To:** Jim Bochicchio jboch@broadinstitute.org  
**Cc:** Caroline Cusick ccusick@broadinstitute.org



Hi Jim, thanks for getting back with an estimate. One question, will the sequence quality from the assemblies (without additional Illumina Jump/PacBio data) be high enough to use as a reference genome for SNP calling?

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**Subject:** Re: Ant DNA caliper  
**Date:** December 3, 2015 at 1:44 PM  
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**Cc:** Caroline Cusick [ccusick@broadinstitute.org](mailto:ccusick@broadinstitute.org)

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Ok, we will discuss your project with your assembly group and get back to you soon with an estimate.

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**Subject:** Re: Ant DNA caliper  
**Date:** December 2, 2015 at 12:43 PM  
**To:** Jim Bochicchio jboch@broadinstitute.org  
**Cc:** Caroline Cusick ccusick@broadinstitute.org



Hi Jim, 250-284Mb is the range for the related genus Pogonomyrmex that has already been sequenced. Looking back at the source pub, the 3.8Mb might refer to the largest scaffold from [their](#) sequencing.

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DNAQ-21 KK  
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