

**From:** Marc Salit -- Coronavirus Standards WG msalit@stanford.edu  
**Subject:** CSWG Meeting Summary 9 July 2021 - Study Update & Roadmap Manuscript  
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# Coronavirus Standards Working Group Meeting Summary

Dear Colleagues –

As always, it was great to work together this morning! The [slides are linked here](#), and [the recording and transcript is linked here](#).

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## Roadmap Manuscript

In reverse order of our meeting agenda, I first call attention to the draft manuscript that Tim Mercer and I have been working on:

**“A roadmap to better COVID-19 testing from  
the Coronavirus Standards Working Group”**

We made a presubmission inquiry, and have received affirmation that Nature Biotechnology will consider this paper.

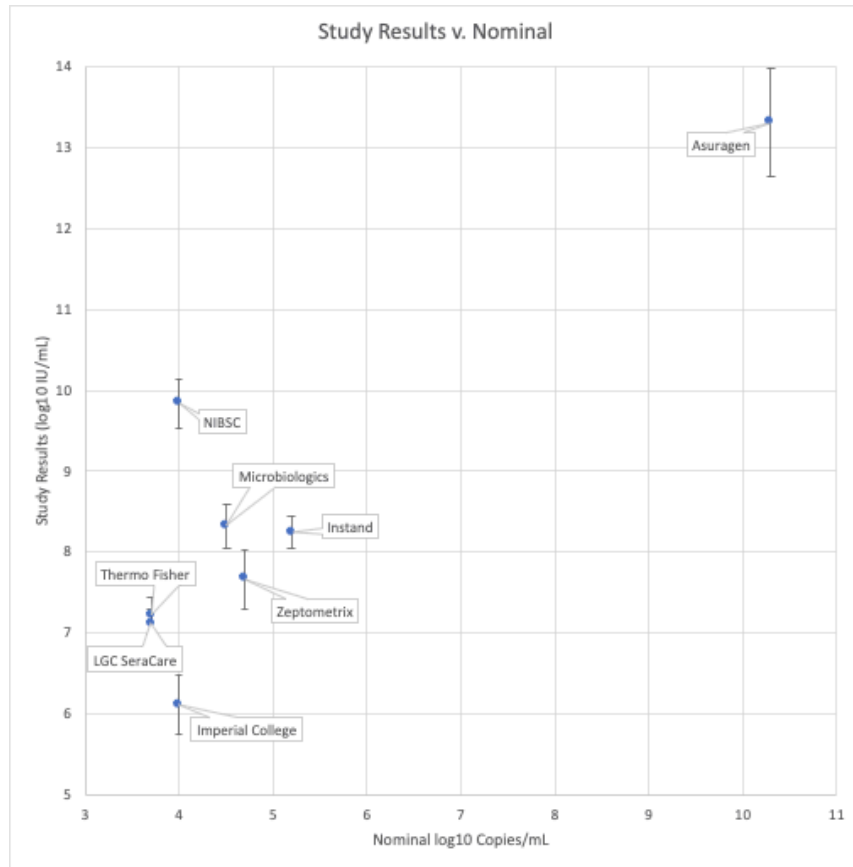
This manuscript is outlined on Slide 11 in the linked deck, and **is available for your contributions** in [this linked Google Doc](#), or in [this downloadable Word document](#). As Tim noted eloquently this morning, this working group is an assembly of terrific expertise with broad perspective, and we want to capture that in this paper. Please read, comment, edit, add sections, delete where we're wrong, and help us to have this roadmap capture the consensus of our group.

I am particularly enthusiastic for us to make strong recommendations; we are uniquely poised to do so, and I have experience with Nature Biotechnology's appetite to publish works that do so.

***Please have your first round of additions, edits, and comments prepared by 26 July.***

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## RNA Study Data and Results Analysis



We got into more details of the RNA study analysis and began a more serious consideration of the results. I was grateful to work together in real-time to evaluate anomalies and work through the details of the analysis (thanks Alina for your perfect question!). I have again updated the dashboard to fix the broken raw data tables.

The [analysis dashboard is linked here](#) at a stable web link. There have been some new analyses incorporated, including value assignments with 95% confidence intervals (Material Summary table), a comparison plot of our calibrated study results v. nominal genome copy abundance (Results v. Nominal plot), and fixes to some overlooked dilutions. Thanks to John Sninsky and Sebastien Fuchs for working together with me to prepare this session!

All the data tables (Raw, Lab:Target Material Results, and Material Summary) can be copied/pasted into Excel or your favorite tools for your local analysis, and I'm very happy and interested to extend, refine, or fix broken bits in the dashboard I've developed. Please reach out with any questions.

We've received and analyzed all the data, and we've resolved Unitage.

We discussed Next Steps:

- review anomalies
- evaluate trends in results
- develop key conclusions and takeaways
- disseminate values
- develop and publish a manuscript describing the work

I invite your thoughts, and will solicit input on the plan again at next week's meeting. I will make inquiry regarding parallel dissemination through a pre-print and submission to a journal.

Cheers and stay safe!

Marc

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