

**To:** Adam Rosendorff[arosendorff@theranos.com]; Daniel Young[dyoung@theranos.com]  
**Cc:** Sunny Balwani[sbalwani@theranos.com]; Elizabeth Holmes[eholmes@theranos.com]  
**From:** Mona Ramamurthy [/O=THERANOS ORGANIZATION/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=MONA RAMAMURTHYF7E]  
**Sent:** Sat 5/24/2014 8:32:05 PM (UTC)  
**Subject:** RE: RE:

Yes, congrats, Daniel. Fantastic news. I will send you an invite for us to discuss further.

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**From:** Adam Rosendorff  
**Sent:** 5/24/2014 12:26 PM  
**To:** Daniel Young  
**Cc:** Sunny Balwani; Elizabeth Holmes; Mona Ramamurthy  
**Subject:** Re: RE:

Daniel

Congratulations on cracking this.

Regards,

Adam

Sent from my iPhone

On May 24, 2014, at 12:08 PM, "Daniel Young" <[dyoung@theranos.com](mailto:dyoung@theranos.com)> wrote:

Sounds good. I'll get together with Mona and draft the strategy.

-Daniel

On May 24, 2014, at 12:03 PM, "Sunny Balwani" <[sbalwani@theranos.com](mailto:sbalwani@theranos.com)> wrote:

\*\*\*\* Attorney Client Privileged communication \*\*\*\*

Daniel.

This is truly great progress and a big competitive advantage for us.

We need to keep this project, the code, calibration and everything we learned here as Theranos trade secret. Everyone who was working on this needs to understand this. This also should not be communicated to anyone in CLIA who doesn't need to know how we do this calibration and how we got where we are on this project. Besides Adam no one in CLIA needs to know our secret sauce and if Adam thinks anyone else needs to know this then we need get them under same agreement around our trade secret. There as no on the industry capable of doing what we have accomplished here because of massive learnings and trial and erros. We need to protect this.

As such, lets meet with Mona early week to make sure whoever from biomath team working on this project protects the confidentiality of this effort. Moreover, the team in CLIA and R&D that ran the validation process also needs to sign our trade secret document.

I will leave it upto Mona and you to draft a strategy around this so EAH and I can sign off and implement.

Thanks.

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**From:** Daniel Young  
**Sent:** Friday, May 23, 2014 9:49 PM  
**To:** Elizabeth Holmes  
**Cc:** Sunny Balwani  
**Subject:** RE:

I wanted to update you on the ISE studies in preparation for switching back to the diluted ISE protocols on Tuesday:

- √ With our new approach, we have now shown that we can process and run ISE's with diluted venous samples with great accuracy and precision (shown now over 10 days and 48 subjects)
- √ This week we adapted this approach to samples from pCTN/capillary samples. Learnings this week were:
  - Our real-time calibrators need to be diluted on the Tecan along with the samples to capture all process-dependent factors that impact sample processing and assay results
  - With this refined approach, we have now shown that we can get on average very accurate results from pCTN samples for ISE's
  - Based on these results, we are ready to deploy this process on Tuesday (we are just finalizing software updates now and completing QA testing before we move it to production)
- √ Additional issues that I plan to have the team address next week while generating data to be added to our amended validation reports include:
  - We have seen that diluted venous samples have much better precision than diluted pCTN/capillary samples; I want to confirm why this is the case. My two hypotheses are:
    - ⌘ Tecan processing introduces variance
    - ⌘ Variance introduced by the capillary sample collection and/or variance from pCTN circuits
    - ⌘ These hypotheses will be tested next week, and could lead to further process improvements/refinements
  - We started this week measuring lithium in our pCTN/capillary samples to assess heparin concentrations. Initial data suggest a wide range of concentrations in our capillary samples, and possibly concentrations that are very high. We are exploring the impact of this in more detail next week in our studies. One side effect of high heparin may be clumping of cells and platelets, which could lead to these elements being caught in the gel/plasma. We are exploring how this may or may not impact ISE and other GC assay results. More to come on this topic.

Please let me know if you have any questions.

Thanks,  
Daniel