

**From:** Kline, Christopher J cjk14@pitt.edu   
**Subject:** Last R21 MiSeq Run  
**Date:** July 22, 2019 at 6:30 AM  
**To:** Pleuni Pennings pspennings@gmail.com  
**Cc:** Ambrose, Zandrea zaa4@pitt.edu

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CK

Hi Pleuni,

I was able to finish up the last MiSeq run for the mac251 (R21) samples over the weekend. Hopefully it all worked out ok... I only say that because one of the samples seemed to have an extraordinary percentage of the identified reads so it might have skewed the other reads down. I don't think I've seen this happen before so maybe you can let us know if this messed up the results at all.

I already shared the run with you on BaseSpace but I know you were planning on hiring a post-doc to analyze this data as well. So, if there is someone else you want me to share the run with, just let me know what email address I should send the invitation to.

Also, I'm attaching here the sample sheet so you know which samples are which. Sample 1 is our control sample. For that one, I PCR'ed a region of Env that includes our MiSeq region and cloned it into TOPO vector pCR2.1. Then I used that plasmid, along with the other samples that had already been made into cDNA, for the PCR steps so hopefully that will give us an idea of any PCR error rates for analysis.

Let me know if you need anything else and good luck!

Chris

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Christopher Kline  
Lab Manager- Ambrose Lab  
University of Pittsburgh  
Department of Microbiology & Molecular Genetics  
(412) 383-9881



samples for  
miseq...19.xlsx