
Re: Dear Wenji, David and Davit - we will have a lab meeting tomorrow at 2:30-4 pm to go over the mes13 bioinformatics ms. Tony

1 message

David Cheng <davichen@scarletmail.rutgers.edu>

Mon, Jan 22, 2018 at 12:06 AM

To: Ah-ng Kong <kongt@pharmacy.rutgers.edu>

Cc: Davit Sargsyan <sargdavid@gmail.com>

Attached are 2 excels from Deseq2. Genes in yellow are genes where HG went in 1 direction, and MITC reversed it and would be ideal candidates for validation. Renyi and I chose a cutoff in basemean > 10 though as 2 over 1 not as significant as 20 over 10

Very difficult to find papers with RNA-seq n = 1, but those that do, don't use DESeq2, for whatever reason it's not correct so I discussed with Davit about comparing a few tools like edgeR, NOIseq, IsoDE, etc, using n = 1 instructions in those packages, to do analysis. I don't think it'll change the data much, but using DESeq2 could be a big no no for readers/reviewers who would see obvious flaws.



On Sun, Jan 21, 2018 at 8:59 AM, Ah-ng Kong <kongt@pharmacy.rutgers.edu> wrote:

Dear Wenji, David and Davit - we will have a lab meeting tomorrow at 2:30-4 pm to go over the mes13 bioinformatics ms.

Please send what you all have so far.

Tony

Sent from my iPhone

2 attachments **WJ2-WJ1 - Copy.xlsx**
2707K **WJ3-WJ2 - Copy.xlsx**
2692K