Homework: Workshop W5a

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Focusing on the RNA-seq methodology of either of the two articles listed below (whichever you prefer and you need not read them completely), answer the following questions:

1. What tissue was the RNA extracted from?
2. What RNA fractions were selected for sequencing (i.e. did the authors use polyA-tail capture to isolate mRNAs, or did they use rRNA depletion)?
3. How was the sequencing performed?
4. What software was used to align reads and to what reference genome?
5. What software was used to quantify gene expression from read alignments?
6. Briefly, what research questions do the authors answer using RNA-seq?

Please send your answers to abtbhatt@g.ucla.edu by December 15, 2021.

Articles:

- Kim, J.-W., Yang, H.-J., Brooks, M. J., Zelinger, L., KarakÃ¼lah, G., Gotoh, N., Boleda, A., Gieser, L., Giuste, F., Whitaker, D. T., Walton, A., Villasmil, R., Barb, J. J., Munson, P. J., Kaya, K. D., Chaitankar, V., Cogliati, T., & Swaroop, A. (2016). NRL-Regulated Transcriptome Dynamics of Developing Rod Photoreceptors. Cell Reports, 17(9), 2460-2473. https://doi.org/10.1016/j.celrep.2016.10.074
- van Schouwenburg, P. A., Davenport, E. E., Kienzler, A.-K., Marwah, I., Wright, B., Lucas, M., Malinauskas, T., Martin, H. C., WGS500 Consortium, Lockstone, H. E., Cazier, J.-B., Chapel, H. M., Knight, J. C., & Patel, S. Y. (2015). Application of whole genome and RNA sequencing to investigate the genomic landscape of common variable immunodeficiency disorders. Clinical Immunology (Orlando, Fla.), 160(2), 301-314. https://doi.org/10.1016/j.clim.2015.05.020