Date	Presenter(s)	Location	Paper
Jan 19	Marietta Easterling, Hannah Marx	WSU Abelson 306	Cui P, Lin Q, Ding F, Xin C, Gong W, et al. (2010) A comparison between ribo-minus RNA-sequencing and polyA-selected RNA-sequencing. Genomics 96: 259–265.
Jan 26	Joe Crawford	UI 4th floor reading room Life Sciences South	Marioni, J.C., Mason, C.E., Mane, S.M., Stephens, M. & Gilad, Y. RNA-seq: an assessment of technical reproducibility and comparison with gene expression arrays. *Genome Res.* **18**,1509–1517 (2008).
Feb 2	Josh Brindley	WSU	Grabherr MG, Haas BJ, Yassour M, Levin JZ, Thompson DA, Amit I et al. Full-length transcriptome assembly from RNA-Seq data without a reference genome. *Nat Biotechnol*. 2011; 29:644-52.
Feb 9	Mark Smithson, Mason Linscott	UI	Trapnell C, Roberts A, Goff L, Pertea G, Kim D, Kelley DR, et al. Differential gene and transcript expression analysis of RNA-seq experiments with TopHat and Cufflinks. Nat Protoc. 2012;7:562–78.
Feb 16	Allison Kolbe	WSU	Rapaport F, Khanin R, Liang Y, Pirun M, Krek A, Zumbo P, Mason CE, Socci ND, Betel D. Comprehensive evaluation of differential gene expression analysis methods for RNA-seq data. Genome Biol. 2013;14(9):R95.
Feb 23	Anthony Brown	UI	Crowley JJ, Zhabotynsky V, Sun W, Huang S, et al. Analyses of allele-specific gene expression in highly divergent mouse crosses identifies pervasive allelic imbalance. Nat Genet. 2015 Apr;47(4):353-60. doi: 10.1038/ng.3222.
Mar 1	Wade Roberts	WSU	Conesa, A, Madrigal, P, Tarazona, S. et al. A survey of best practices for RNA-seq data analysis. Genome Biology 2016 17:13 DOI: 10.1186/s13059-016-0881-8
Mar 8	Marcus Hooker	UI	Smith S, Bernatchez L, Beheregaray LB (2013) RNA-seq analysis reveals extensive transcriptional plasticity to temperature stress in a freshwater fish species. BMC Genomics 14: 375. doi: 10.1186/1471-2164-14-375
Mar 15	Spring Break		
Mar 22	Christine Parent, Erica Crespi	WSU	Huang Y, Chain FJ, Panchal M, Eizaguirre C, Kalbe M, Lenz TL, et al. Transcriptome profiling of immune tissues reveals habitat-specific gene expression between lake and river sticklebacks. Mol Ecol. 2016 Jan 7. doi: 10.1111/mec.13520.
Mar 29	Michael Saxton	UI	Oldham, M.C., Horvath, S. & Geschwind, D.H. Conservation and evolution of gene coexpression networks in human and chimpanzee brains. *Proc. Natl Acad. Sci. USA* **103**,17973–17978 (2006).
Apr 5	Amanda Staheke	WSU	Renaut S, Grassa CJ, Yeaman S, Moyers BT, Lai Z, Kane NC, Bower s JE, Burke JM, Rieseberg LH. 2013. Genomic islands of divergence are not affected by geography of speciation in sunflowers. Nat Com. 4: 1827. doi:1810.1038/ncomms2833

Apr 12	Derek Denney	UI	A. Necsulea, H. Kaessmann, Evolutionary dynamics of coding and non-coding transcriptomes. Nat. Rev. Genet. **15**, 734–748 (2014).
Apr 19	Austin Patton	WSU	Yu Y, Fuscoe JC, Zhao C, Guo C, Jia M, Qing T et al.. A rat RNA-Seq transcriptomic BodyMap across 11 organs and 4 developmental stages. *Nat Commun.* 2014; 5:3230
Apr 26	Alex Fraik	UI	Narum SR, Campbell NR (2015) Transcriptomic response to heat stress among ecologically divergent populations of redband trout. BMC Genomics 16, 103.
May 3	Johnathan Kaiser, CJ Jenkins	WSU	Lappalainen T, Montgomery SB, Nica AC, Dermitzakis ET. Epistatic selection between coding and regulatory variation in human evolution and disease. Am J Hum Genet. 2011 Sep 9;89(3):459-63. doi: 10.1016/j.ajhg.2011.08.004.

The paper that was removed from the list:
Piskol R, Ramaswami G, Li JB (2013) Reliable Identification of Genomic Variants from RNA-Seq Data. American Journal of Human Genetics, 93:641-651 .
Other interesting papers and websites:

Knowles D, Davis JR, Raj A, et al (2016) Allele-specific expression reveals interactions between genetic variation and environment. http://biorxiv.org/content/biorxiv/early/2015/09/13/025874.full.pdf

Saletore, Yogesh; Meyer K; Korlach J; Vilfan ID; Jaffrey S; Mason CE. (31 Oct 2012). "The birth of the Epitranscriptome: deciphering the function of RNA modifications.". *Genome Biol* **13** (10): 175. doi:10.1186/gb-2012-13-10-175

http://www.rna-seqblog.com/

http://nextgenseek.com/2015/03/three-papers-on-new-rna-seq-methods-offer-a-new-way-to-do-rna-seq-analysis/

http://nextgenseek.com/2014/08/nature-biotechnology-goes-nature-rna-seq-with-5-rna-seq-papers/

https://www.biostars.org/p/52152/