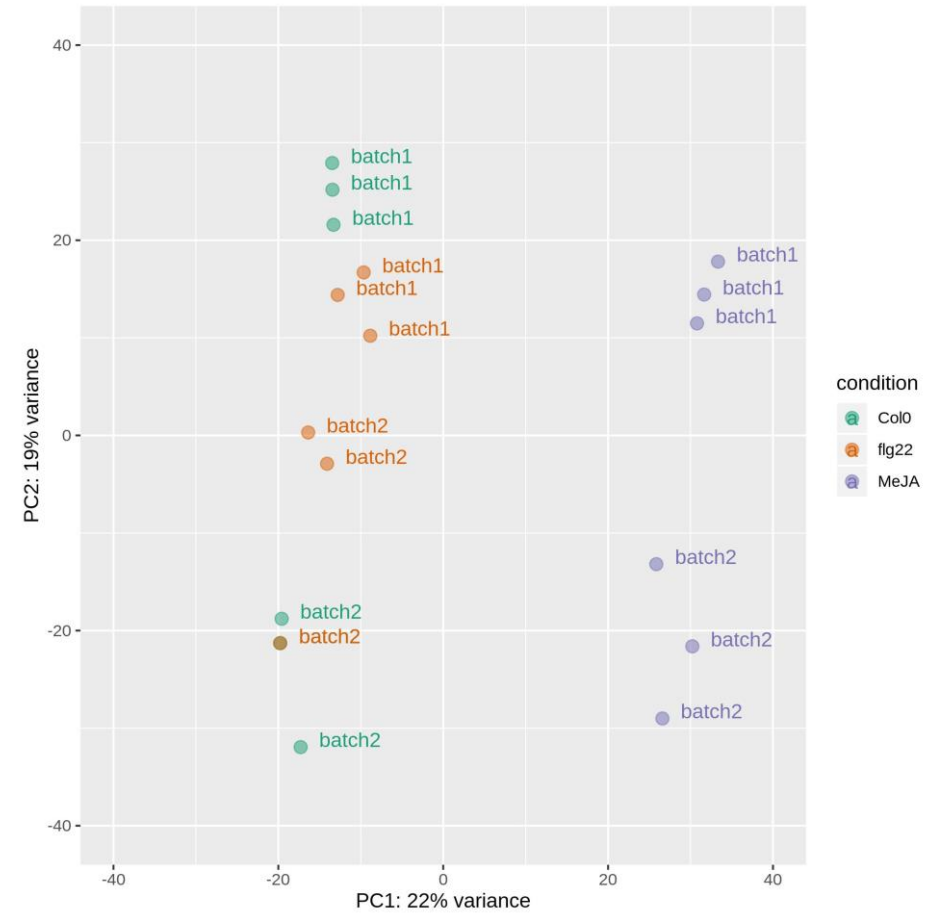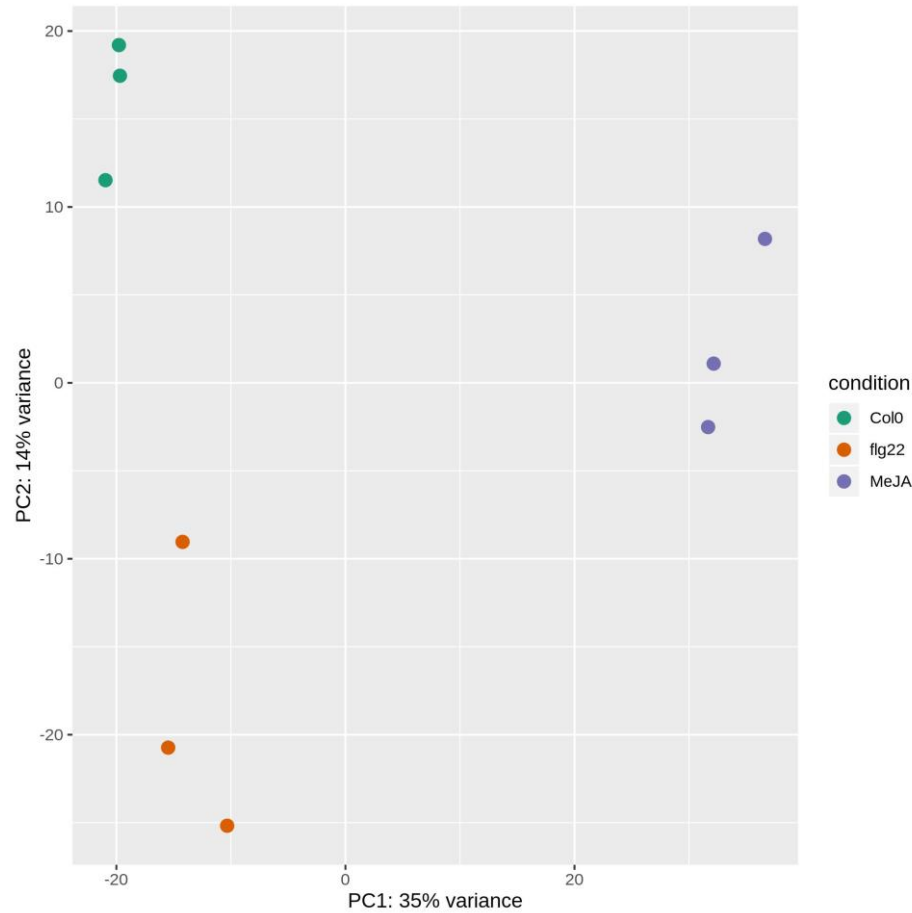# RNA-Seq data visualization

SPP workshop
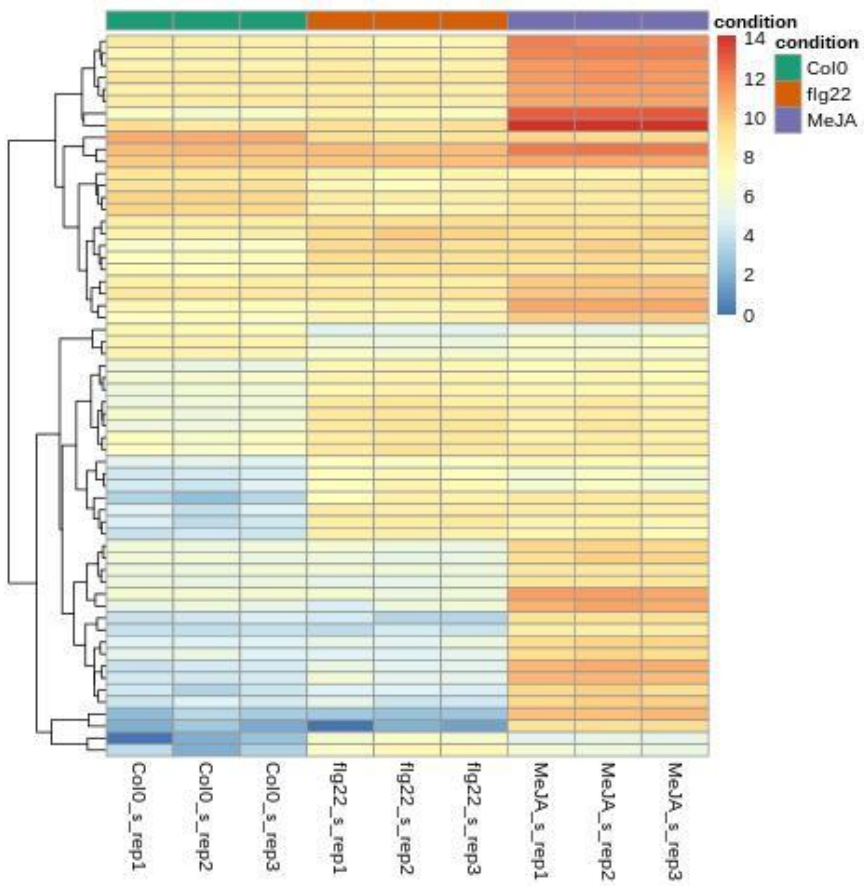**October 2019 | MPIPZ Cologne**

Yulong Niu

1. PCA plot

Use regularized **log–transformed data**, for example use *rld()* in the R/Bioconductor package DESeq2 to transform count table.

1. What is principal component analysis? by Lior Pachter
2. Ringnér M 2008
3. Raw data from Castrillo G, Teixeira PJ, Paredes SH et. al., 2017, replot by Yulong Niu

2. Heatmap

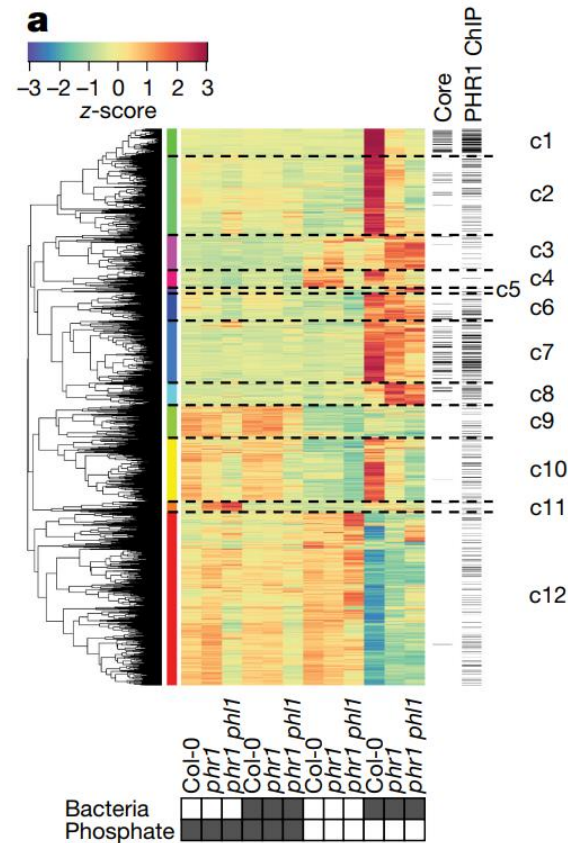Raw data from Castrillo G, Teixeira PJ, Paredes SH et. al., 2017, replot by Yulong Niu

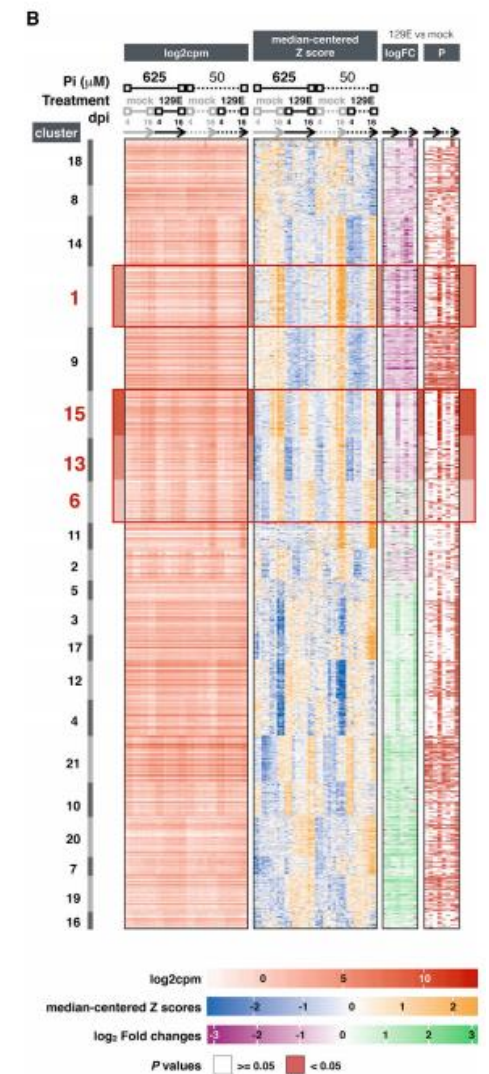Fig. 3a from Castrillo G, Teixeira PJ, Paredes SH et. al., 2017

Fig. 5B from Garrido-Oter R, Nakano RT, et. al., 2018

3. Other visualizations
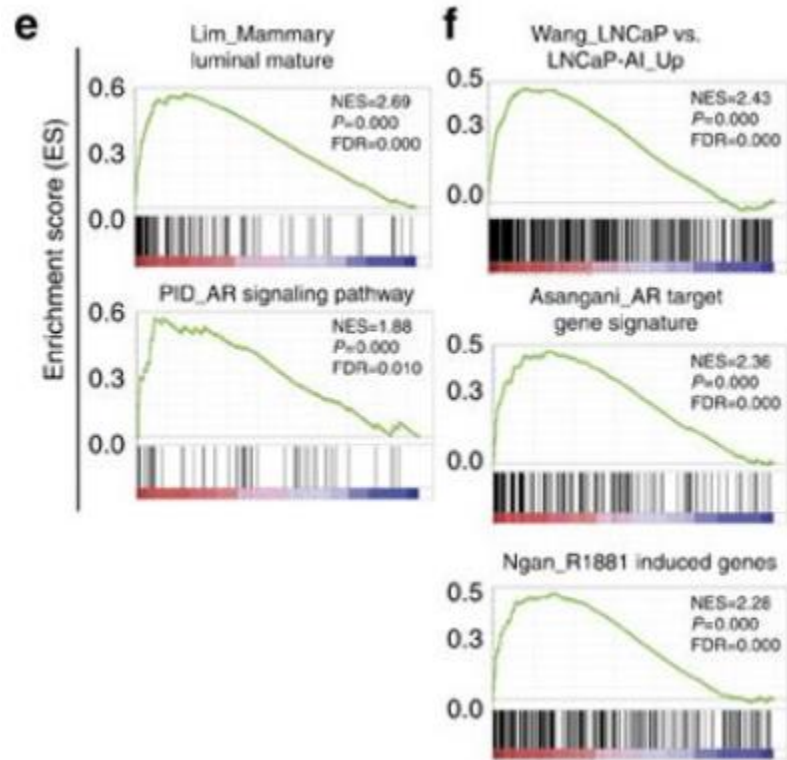
gene-set enrichment analysis

co-expression network
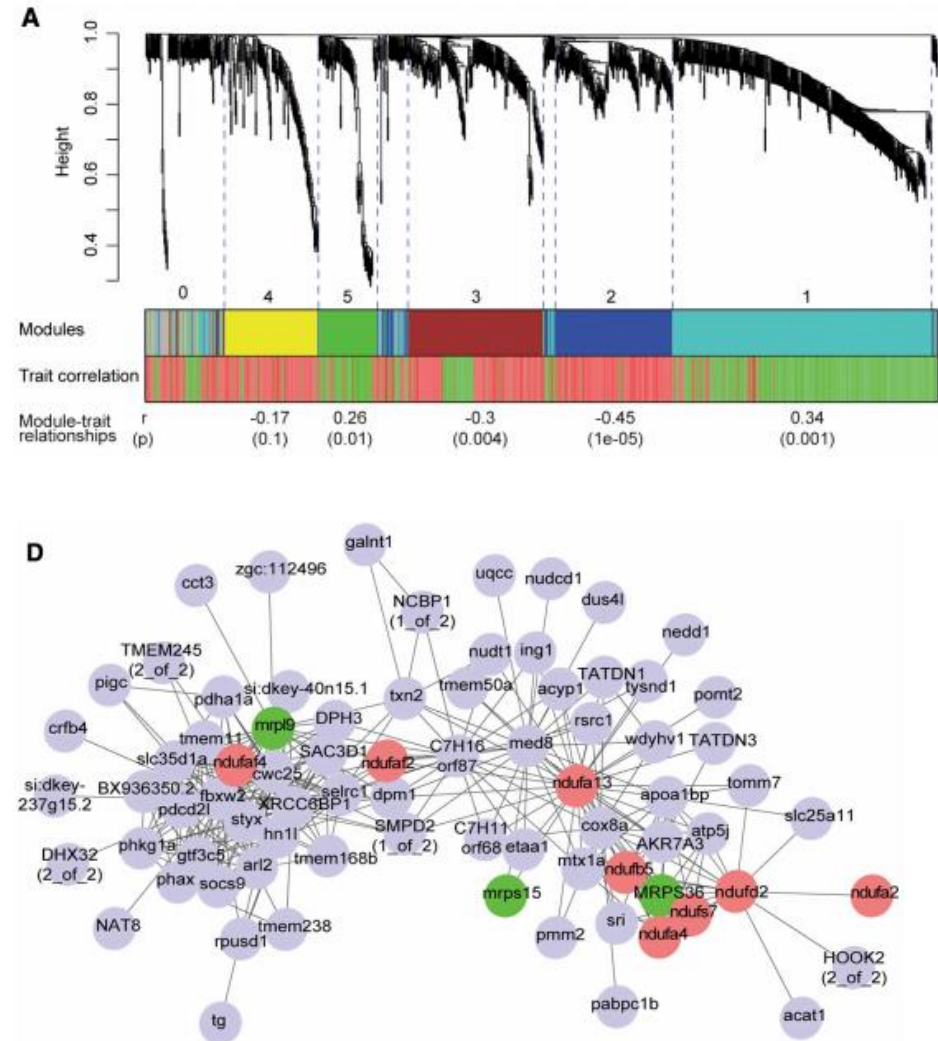

Fig. 1e and 1f from Zhang D, et.al., 2016

Fig. 4A and 4D from Baumgart M, Priebe S, Groth M, Hartmann N et.al., 2016

Hands-on session: : Expression data visualization in R

https://github.com/YulongNiu/MPIPZ_SPP_workshop/blob/master/RNA-Seq/tutorials/RNA-Seq_visual.md