FINAL PROJECT—Qiong ZHANG

Transcript level Differential Expression Heatmap in different tissues

Method

*Kallisto* was used to build transcript index file, quantified RNA-Seq to obtain 10 bootstraps samples, which output including HDF5 files and the estimation of transcript abundance. Differential transcript expression heatmap was produced from *sleuth 0.30.1* in R Studio using covariate models by grouping samples as replicates of one type of tissue. The likelihood ratio test with a <5% false-discover rate.

Result

Different tissues expressed gene differently. Leaf tissue expressed geneDAnjou\_Chr17v0.1\_45598.1 the most than other tissues. In fruitlet and bud tissue, gene DAnjou\_Chr90.1\_21164.1 expressed the most than leaf tissue. Some gene showed better expression in fruitlet and bud tissue than leaf tissue, such as DAnjou\_Chr13v0.1\_32788.1, DAnjou\_Chr17v0.1\_43986.1, DAnjou\_Chr2v0.1\_04302.1. Also, Gene expression was similar in same type of tissue. For an instance, budding leaves showed similar gene expression with expanding leaves. For fruitlet tissue, gene DAnjou\_Chr90.1\_21164.1 expressed the most and similarly in both stage1 and stage2.

Figure. XX Cluster analysis of transcript level differential expression heatmap of different tissues from RNA-Seq

