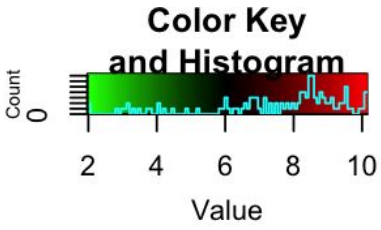
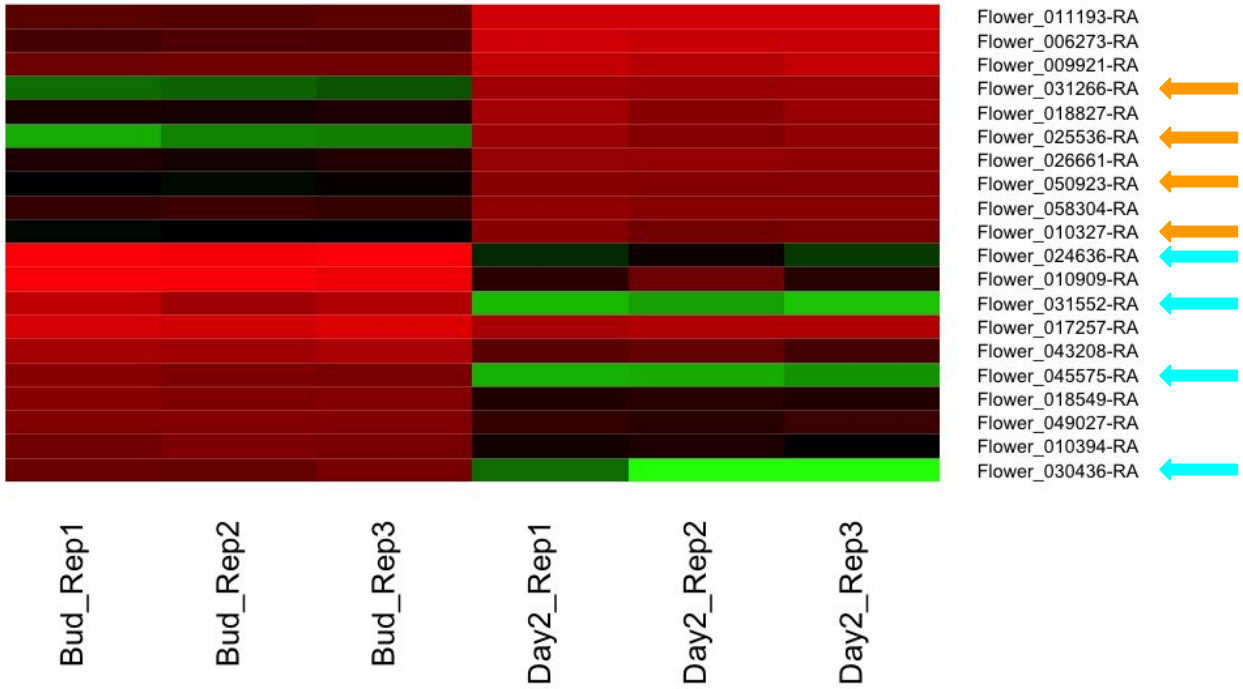
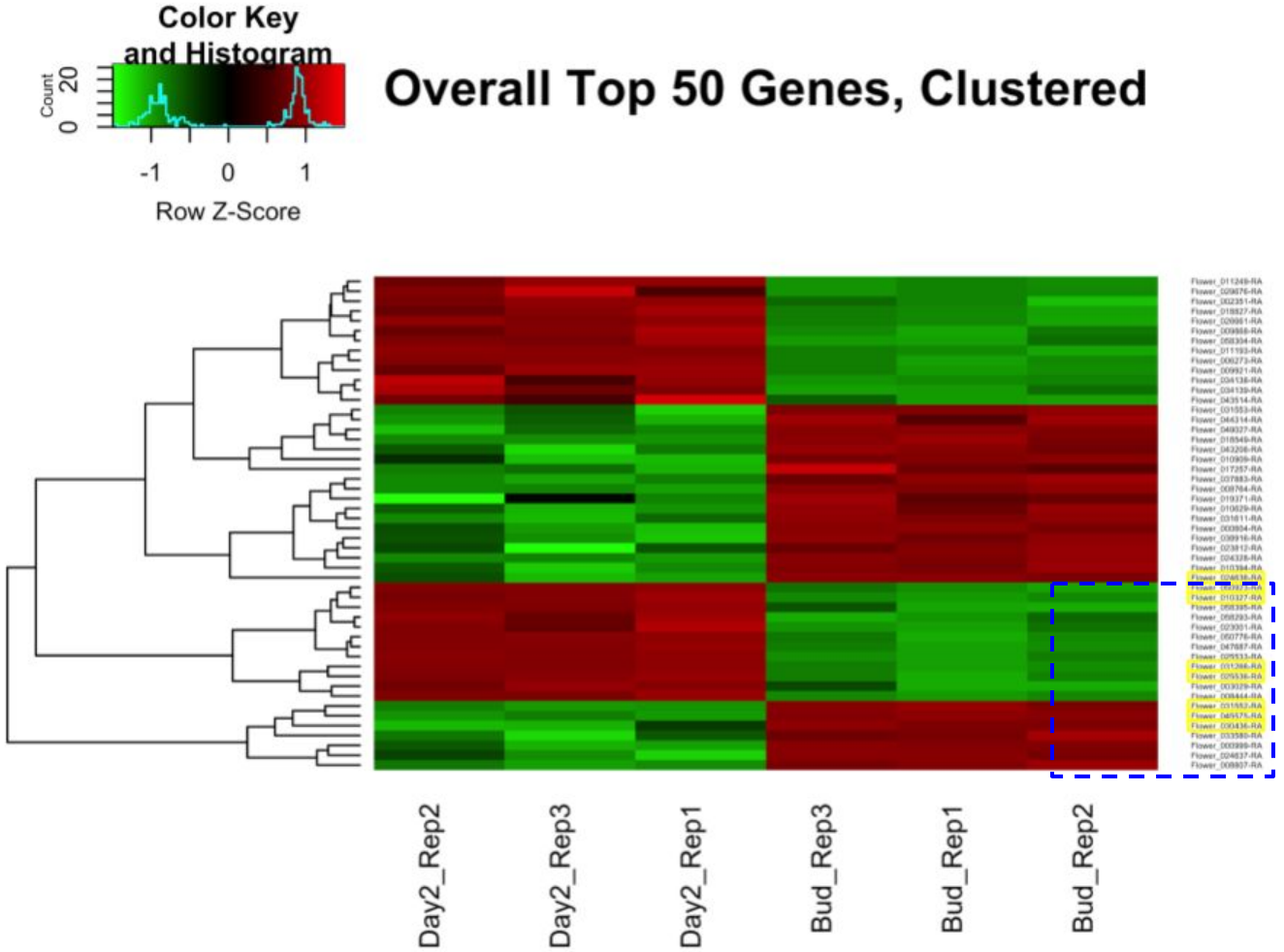


Overall Top 20 Genes

- 20 genes showing a high level of variance between Bud and Day2 replicates, 10 showing an increase in expression and 10 showing a decrease in expression
- Targets for further investigation are labeled on the right



Overall Top 50 Genes, Clustered



- Here are the top 50 genes clustered by similarity in expression profiles across all of the replicates.
- Gene targets from the previous slide are highlighted in yellow
- Adjacent genes within the same cluster are also potential candidates for further analysis (shown below)

As for explaining these results to a non-technical audience, I would use these slides to explain that the top 20 genes were found by finding the genes that showed the greatest amount of change in expression. (subtracting beginning expression from outcome expression)

In explaining the procedure for the clustering algorithm (agglomerative hierarchical clustering): In the beginning, each gene is assigned it's own cluster, and similar clusters are subsequently combined based on a distance function. This continues until there is only one cluster.

In this example, the clusters that contain the "top" genes do not converge with the remaining genes (or each other) until there are 1 or 2 clusters remaining. The most similar targets for investigation would therefore be those that remain within the same cluster as our "top" genes as we move in the direction of a higher number of diverging clusters (i.e. 003029, 008444, and 033580).