Visualization of RNA-Seq Data

Data Visualizations

- Visualizations are useful for:
  - Illustrating relationships between variables
  - Identifying patterns/issues in the data
  - Summarizing results

Preprocessing of data

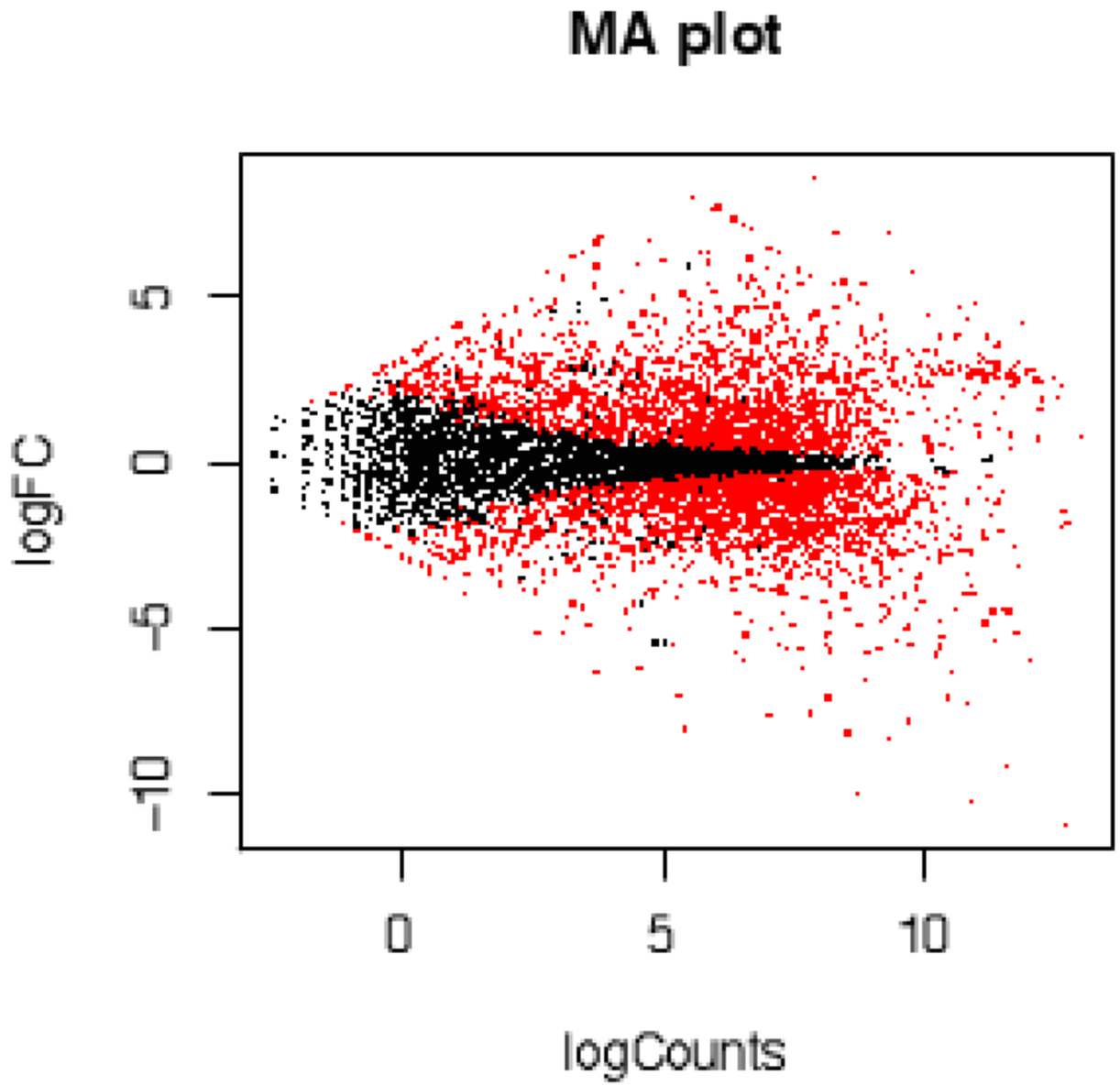
- Not Raw Read Counts
- Many visualizations (all of the ones in the following slides) work best on normalized, log transformed gene expression data.

MA Plots

- For visualizing differences in measurements (in this case, gene expression) between two groups.

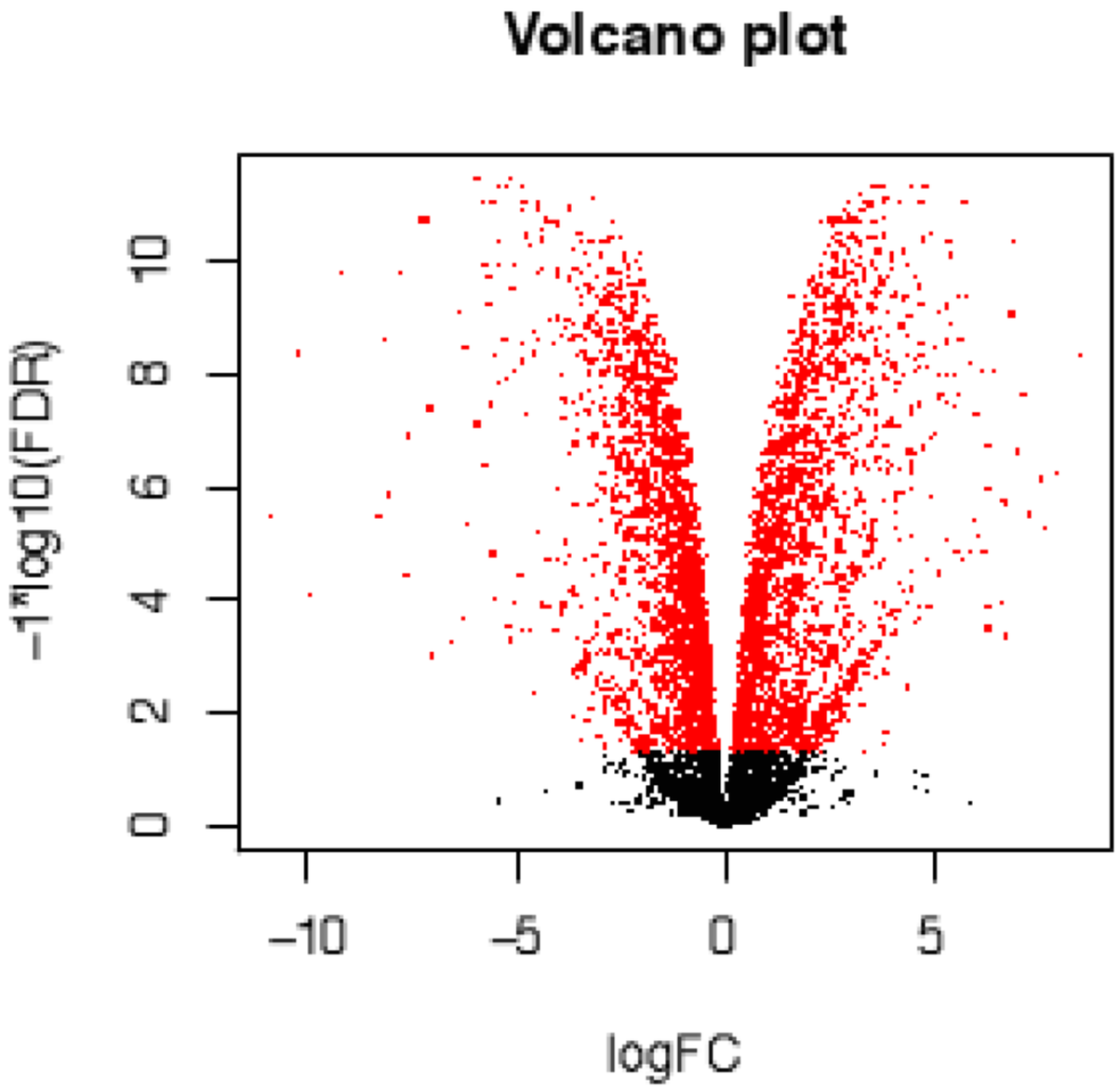
- M- log fold change (differences between two groups)

- A - mean gene expression (average value across samples)



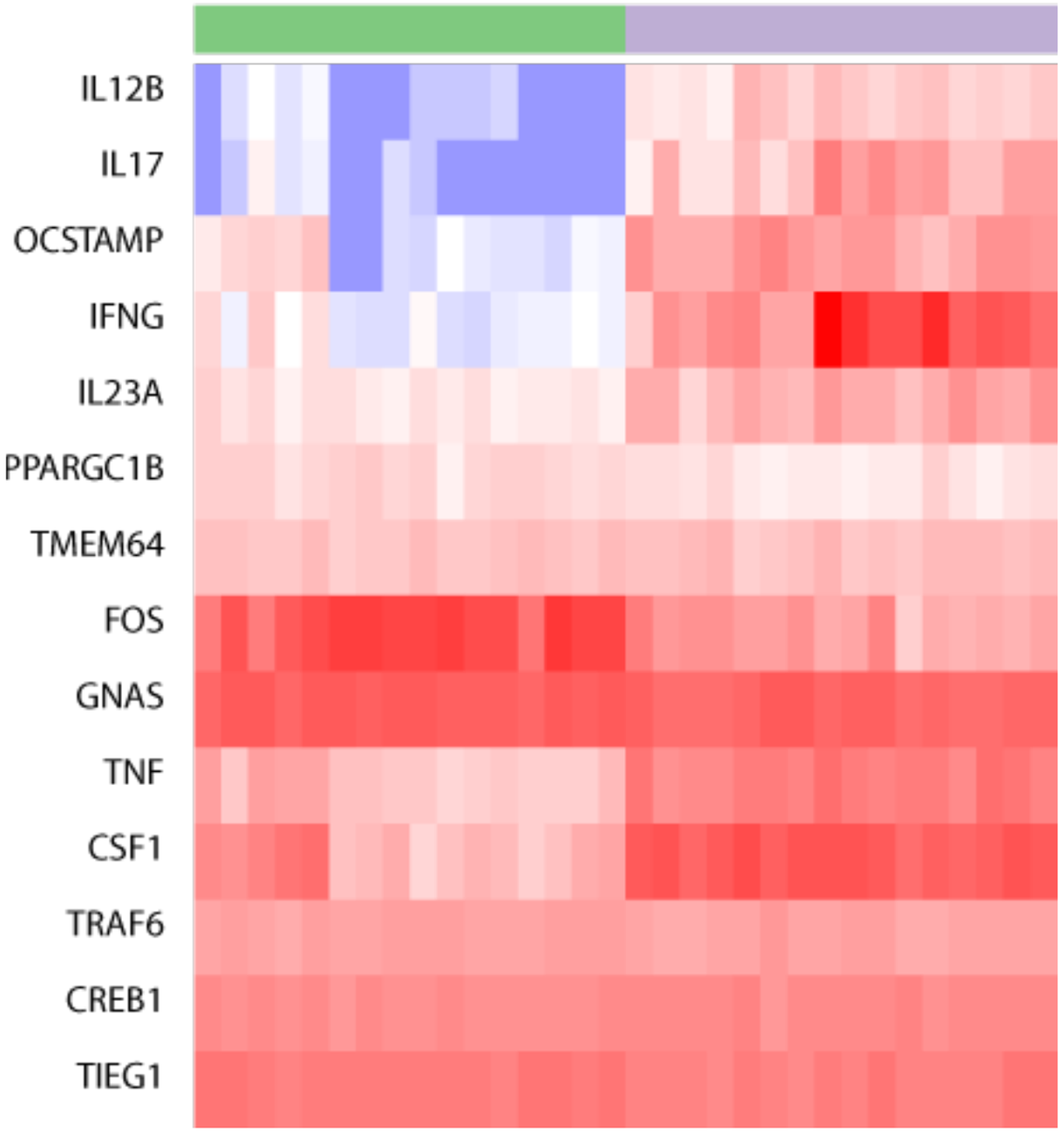
Volcano Plots

- Plots fold change vs significance value for all genes.
- Helps quickly see how many significantly differentially expressed genes are present.



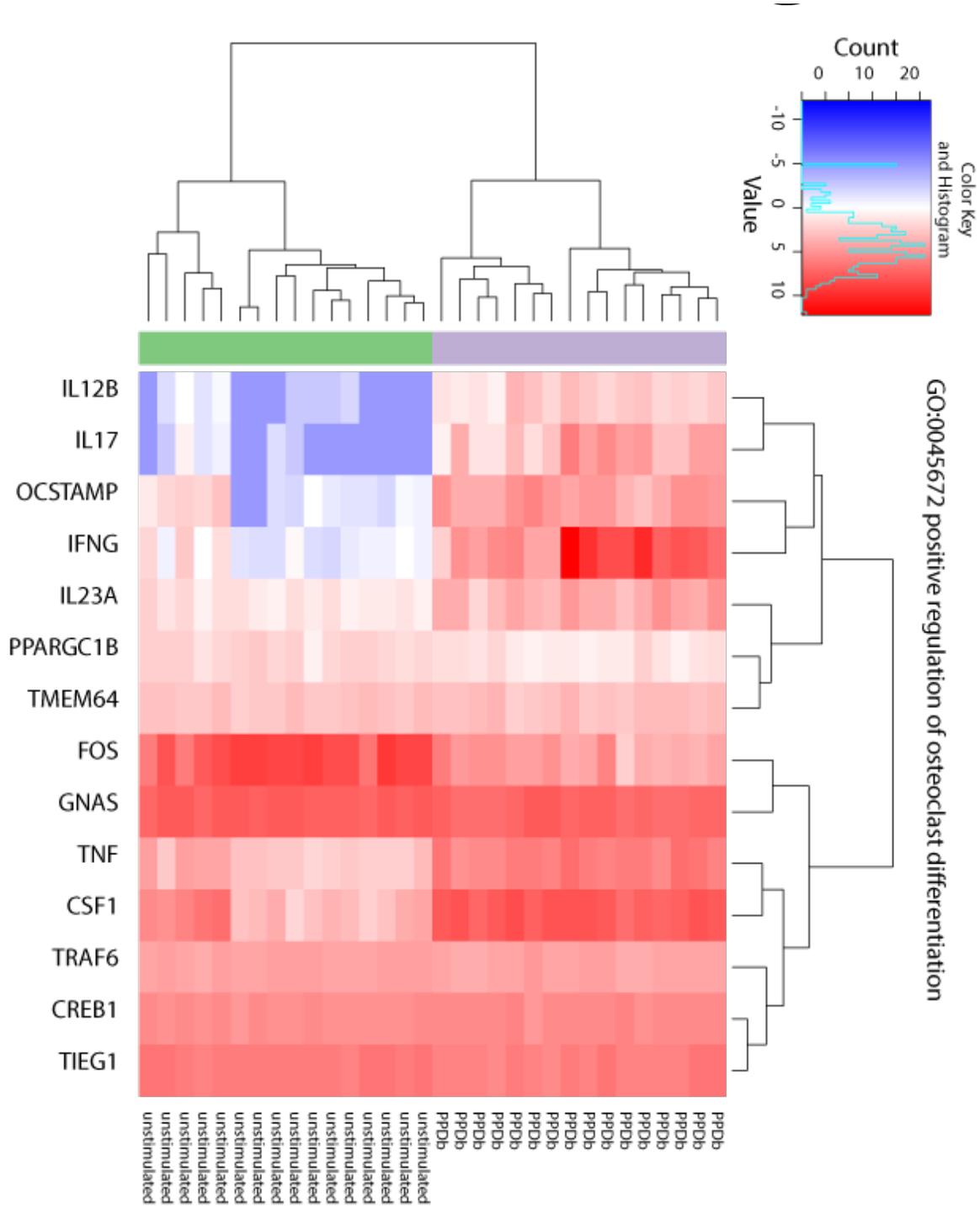
Heatmaps

- Heat Maps represent gene expression by colors.
- For visualizing how gene expression changes in different samples.
- Columns are genes
- Rows are Samples



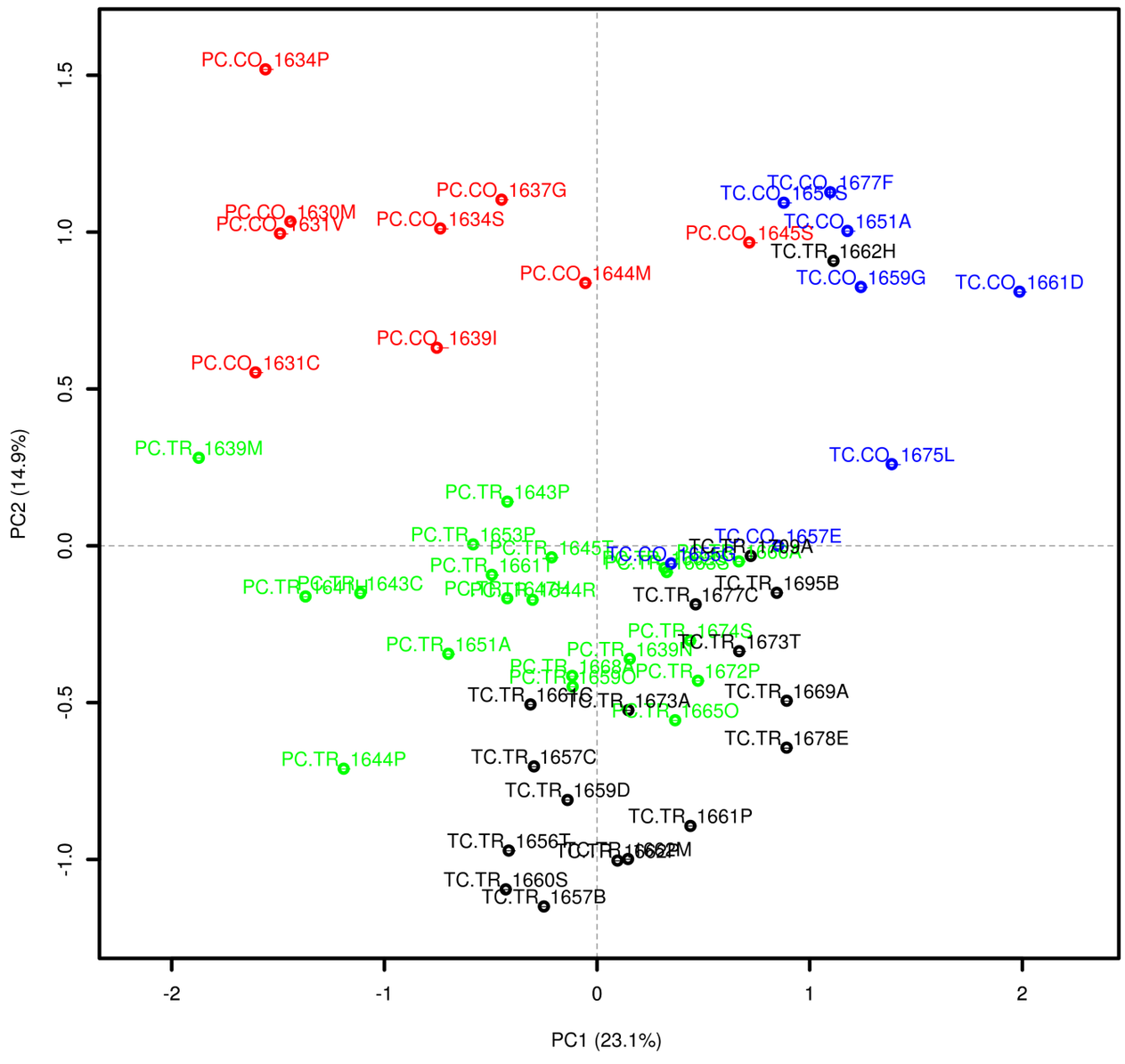
Heatmaps/Clustering

- Dendograms can be added to heat maps
- Samples can be clustered by gene expression
- Genes can be clustered by gene expression
  - time consuming for large number of genes

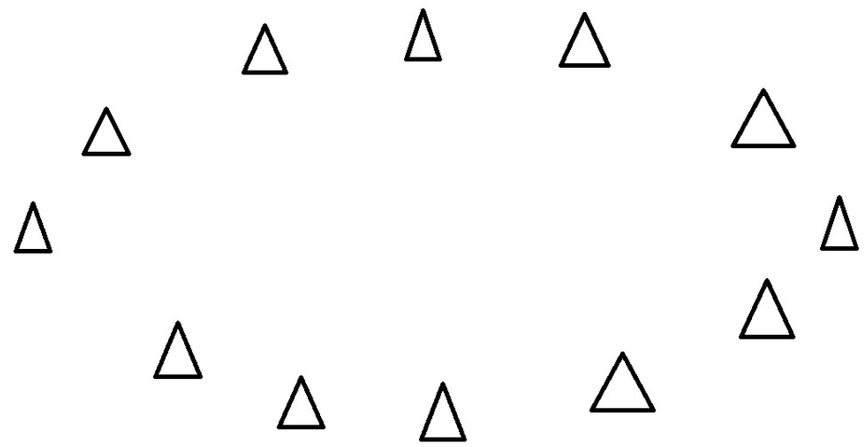


Principal Component Analysis

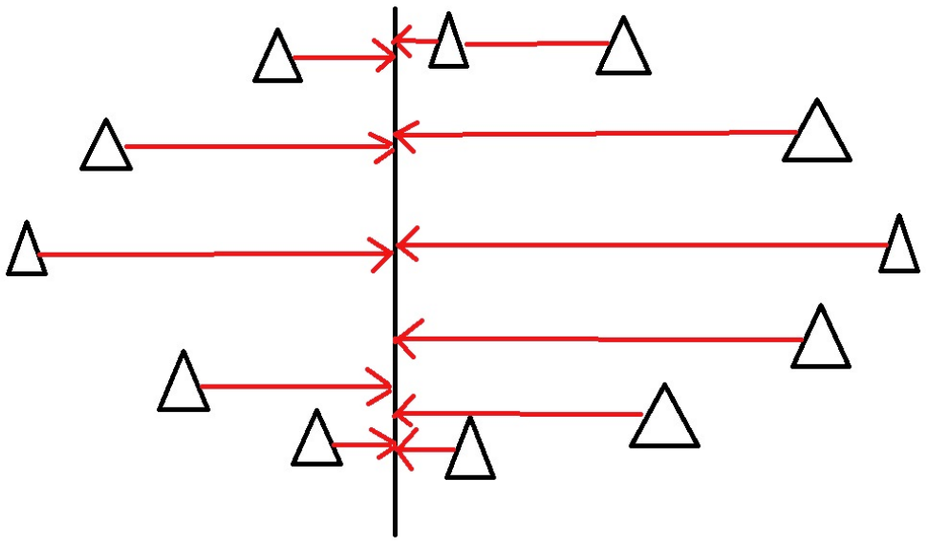
- Each principal component is one dimension in the data.
- Illustrates how the data groups based on the dimensions that represent the highest variability.



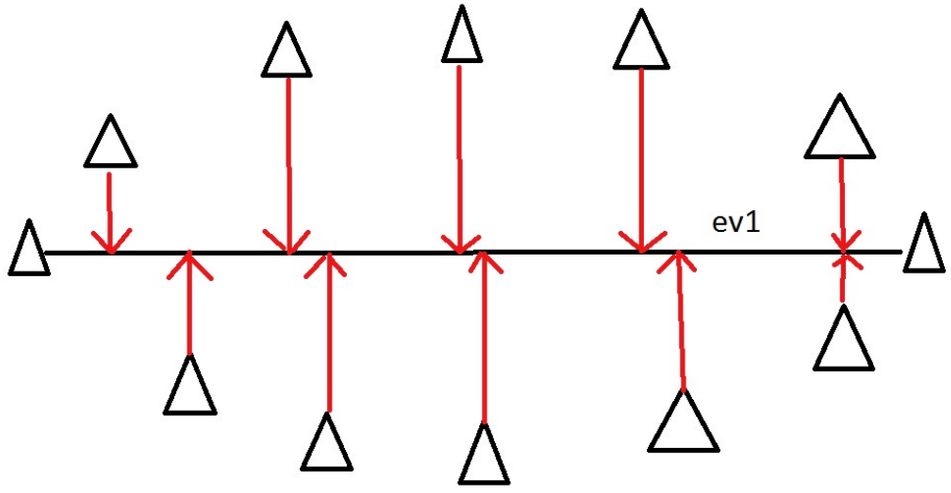
Principal Component Analysis



- What are the Principal components of this data?
  - Directions where there is most variance



- When data is projected onto a straight line, the data is most spread out.



https://georgemdallas.wordpress.com/

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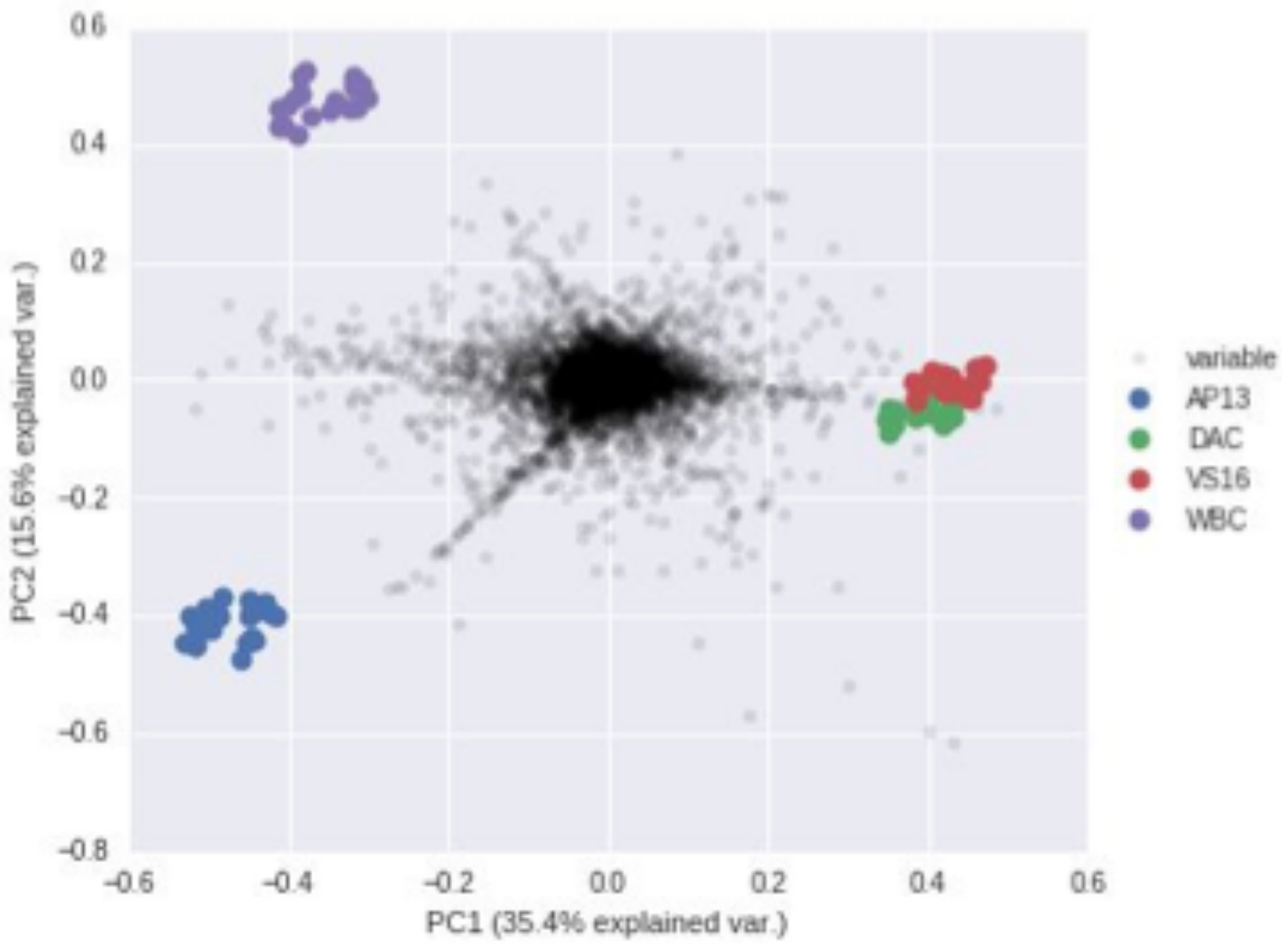
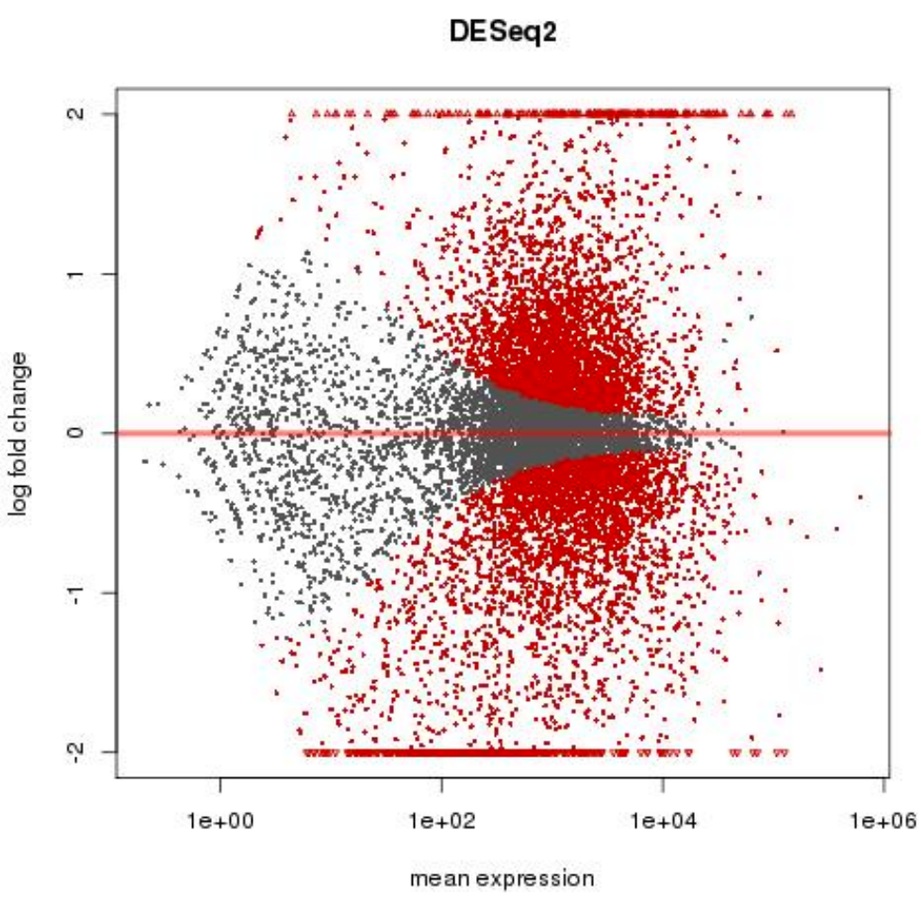
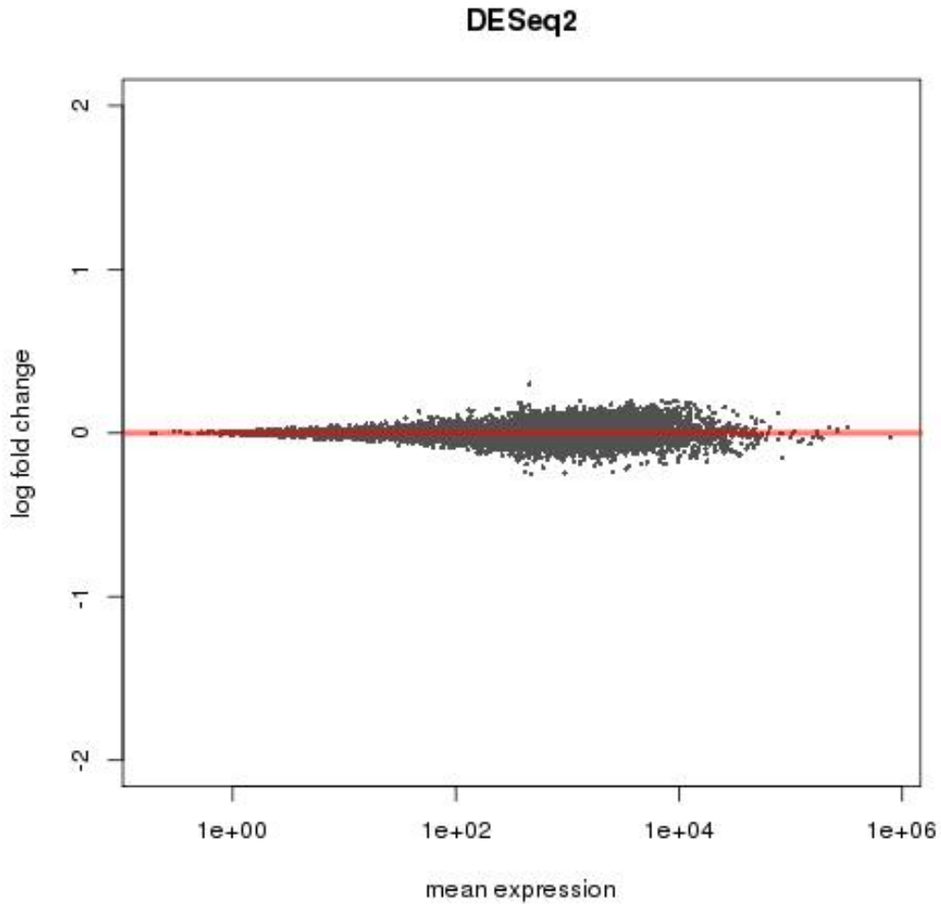


Contributed by Nick Dawes

Looking at Some Real Data

- **Mysterious results for an experiment with 6 samples across:**
  - 2 different time points, 2 different conditions: control vs treated. 3replicates each.





Looking at Some Real Data

- **Can these plots inform us about what might be going on?**