Experiment Title: Rapamycin resistant diffuse large b-cell lymphoma cell lines

p-value: 0.05

Fold Change: 1.5

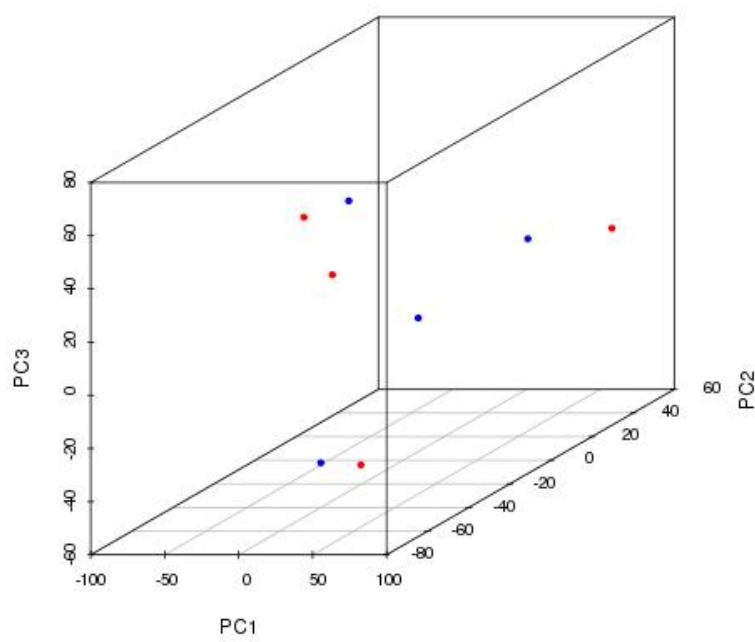**Control FDR: false**

Batch Corrected: true

Link to iReport: https://apps.ingenuity.com/ireport/data/report?reportid=2885

3D Principal Components Analysis Plot
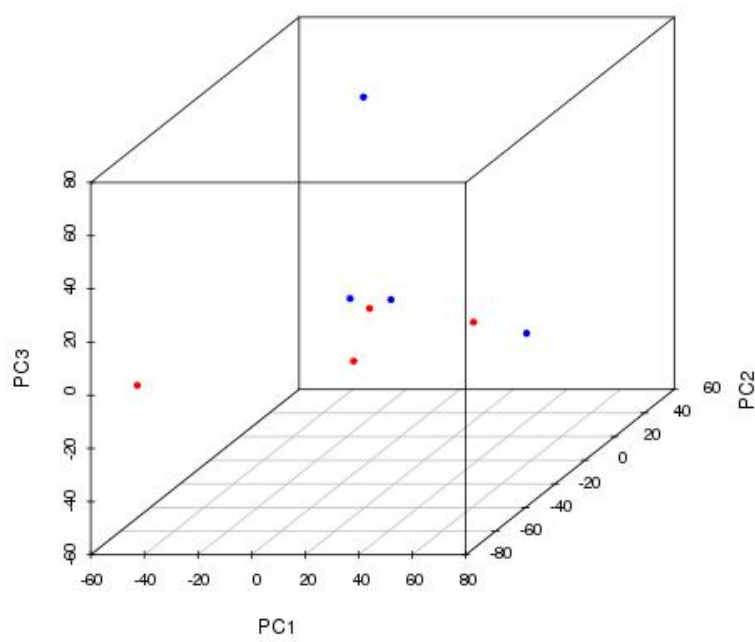
Data type: normalized expression values

The 3D PCA plot shows the same information as the 2D version
It is sometimes easier to evaluate the separation between groups in the 3D version

3D Principal Components Analysis Plot
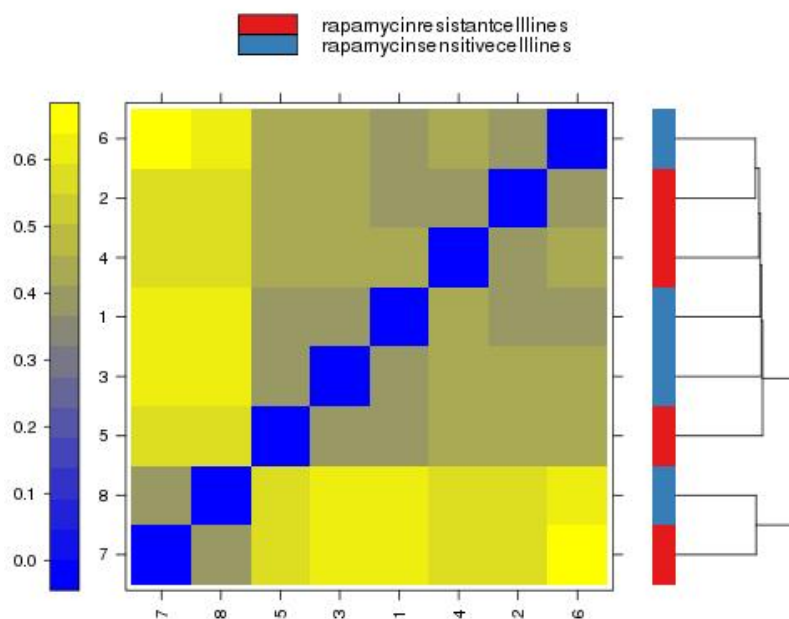
Data type: batch-corrected expression values

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Between-Sample Heatmap
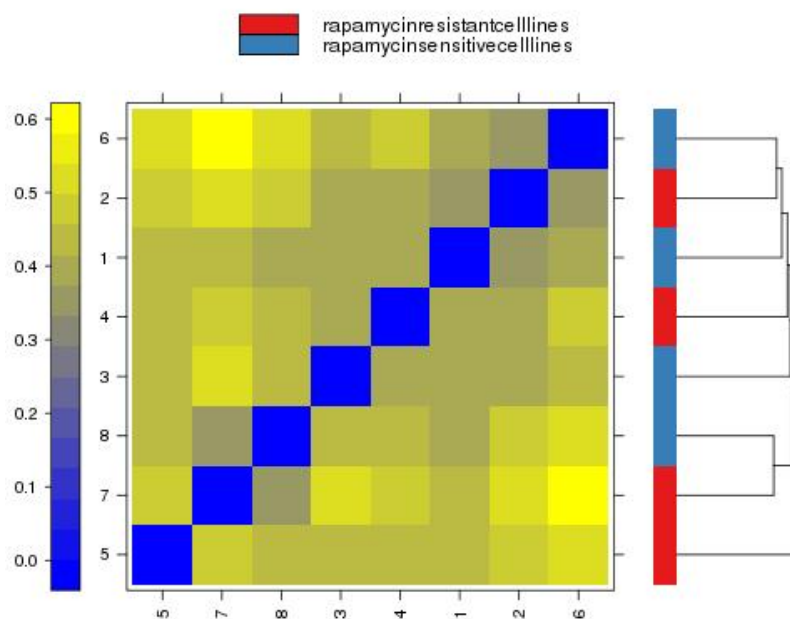
Data type: raw expression values

Each square represents the distance between two samples, where blue means the two samples are similar, and yellow means they are different
The distance is calculated as the mean absolute difference between the samples
Patterns in the heatmap can indicate intended biological differences or confounding sources of variance, such as batch effects

Between-Sample Heatmap
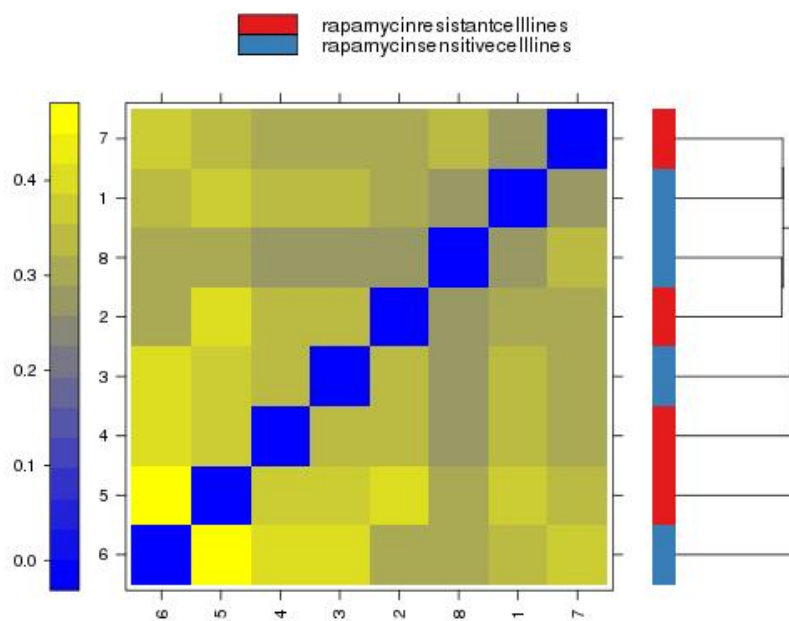
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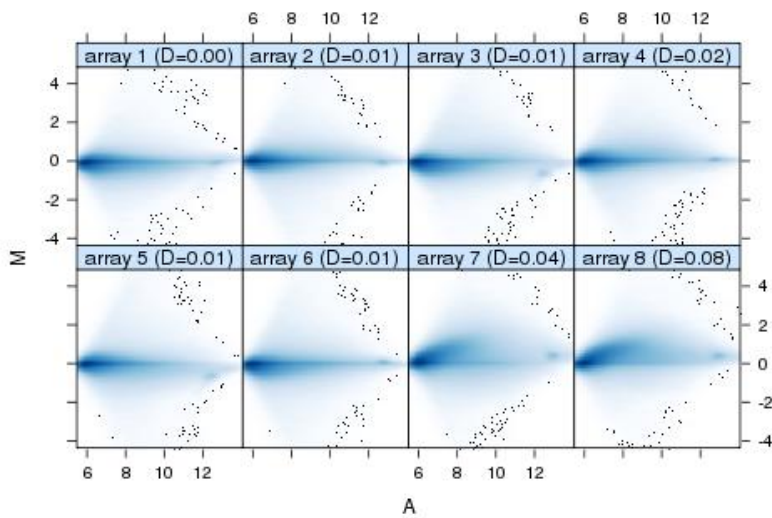
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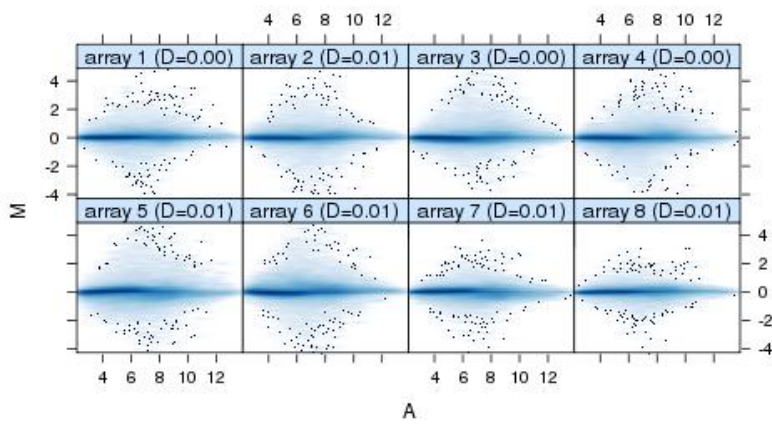
MA Plot

Data type: raw expression values

This plot compares the indicated array to a hypothetical 'ideal' array that is the average of all arrays in the experiment
M is the ratio of the intensity of indicated to ideal, and A is the average of the intensities of indicated and ideal
There is one point on the plot for every probeset
M and A are defined as: $M = log2(I1) - log2(I2)$, $A = 1/2 (log2(I1)+log2(I2))$, where I1 is the indicated array, and I2 is the ideal array
The plot should show no trend
A trend over low values of A can indicate different background intensities between arrays that haven't been properly corrected
A trend over high values may indicate saturation of measurements

MA Plot

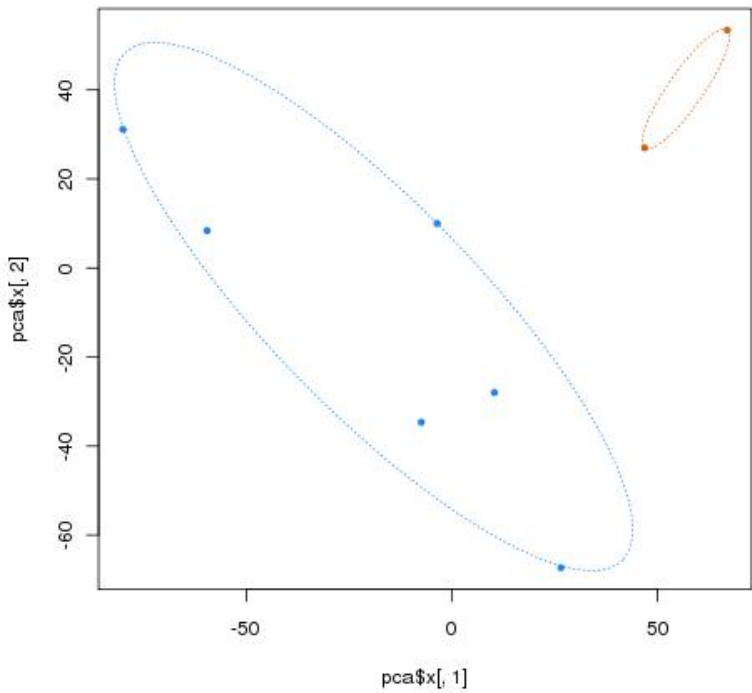## Data type: batch-corrected expression values

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PC1 vs. PC2 Batch Effect Analysis

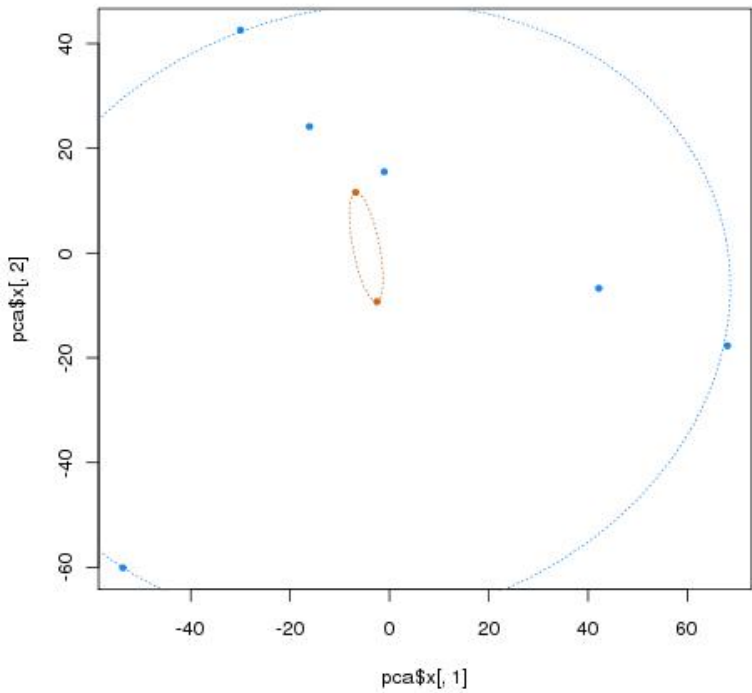**Data type: normalized expression values**

This plot illustrates the extent of the separation between batches in the first two principal components of the principal components analysis

PC1 vs. PC2 Batch Effect Analysis

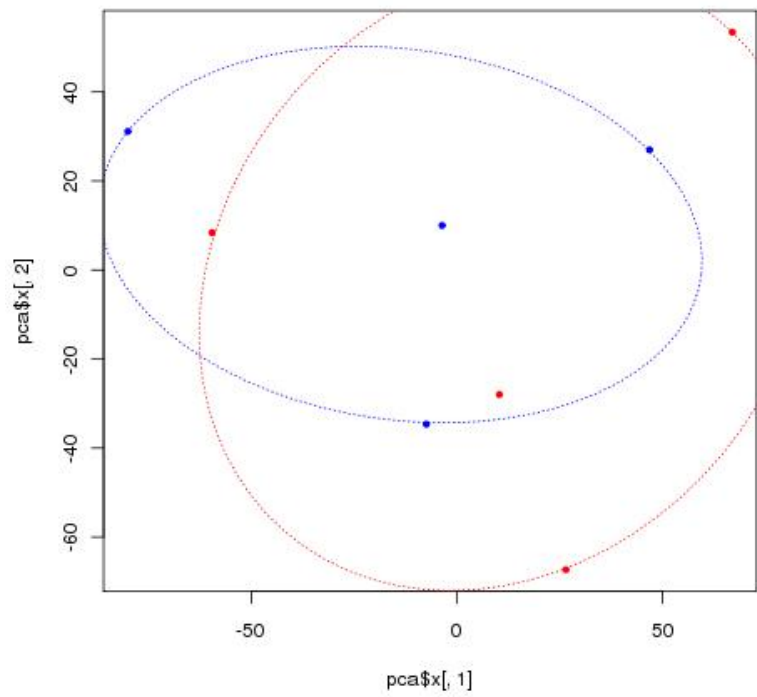**Data type: batch-corrected expression values**

This plot illustrates the extent of the separation between batches in the first two principal components of the principal components analysis

PC1 vs. PC2 Quality

Data type: normalized expression values

This plot illustrates the quality of the separation between experimental groups in the first two principal components of the principal components analysis

PC1 vs. PC2 Quality

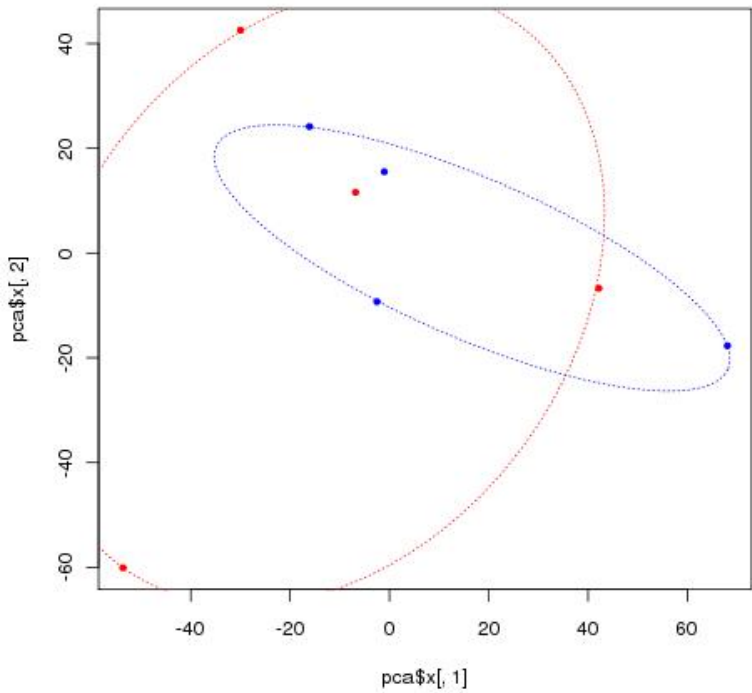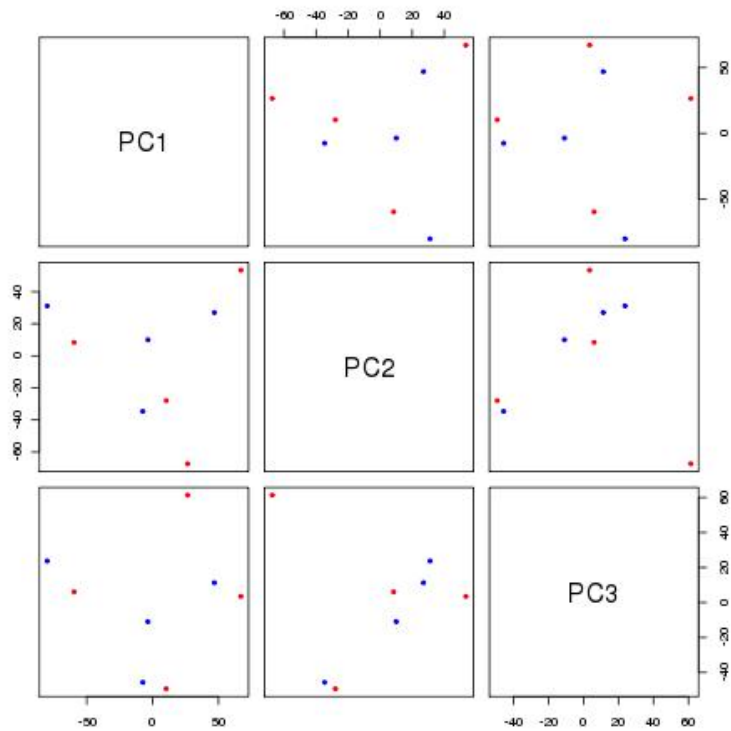**Data type: batch-corrected expression values**

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Principal Components Analysis Plot

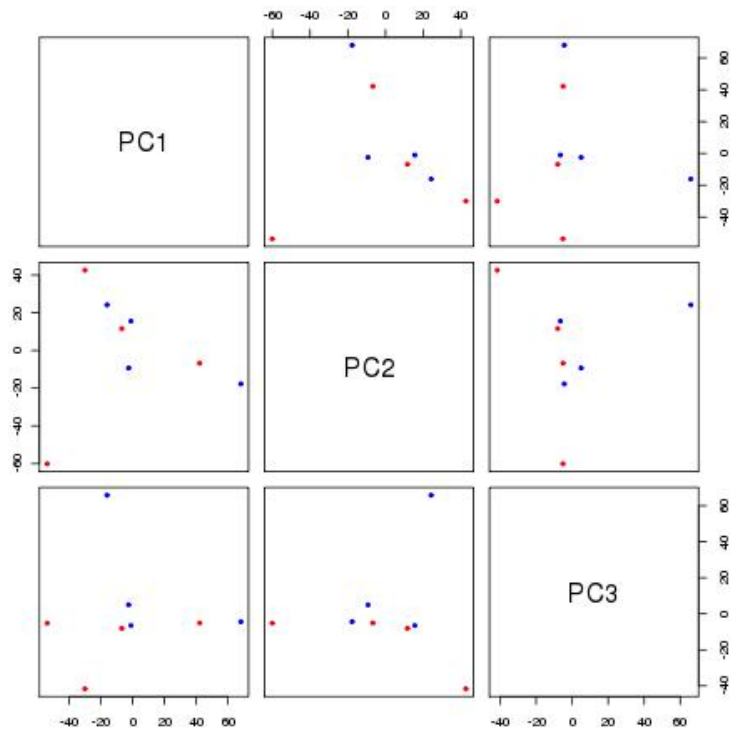## Data type: normalized expression values

The PCA plot splits out orthogonal components of variation in the data, starting with the largest (PC1)
Each point represents an array
In an experiment with low noise, the top center mini-plot (which shows PC1 versus PC2) will show strong clustering of and separation between the experimental groups (shown in different colors)
In a noisier experiment, the experimental groups may still be separable, but less strongly clustered (indicating that factors other than experimental group are significant)
In a very noisy experiment, the groups will be inseparable
The amount of separation in a PCA plot is a good indicator of the ability of the experiment to detect a meaningful biological effect

Principal Components Analysis Plot

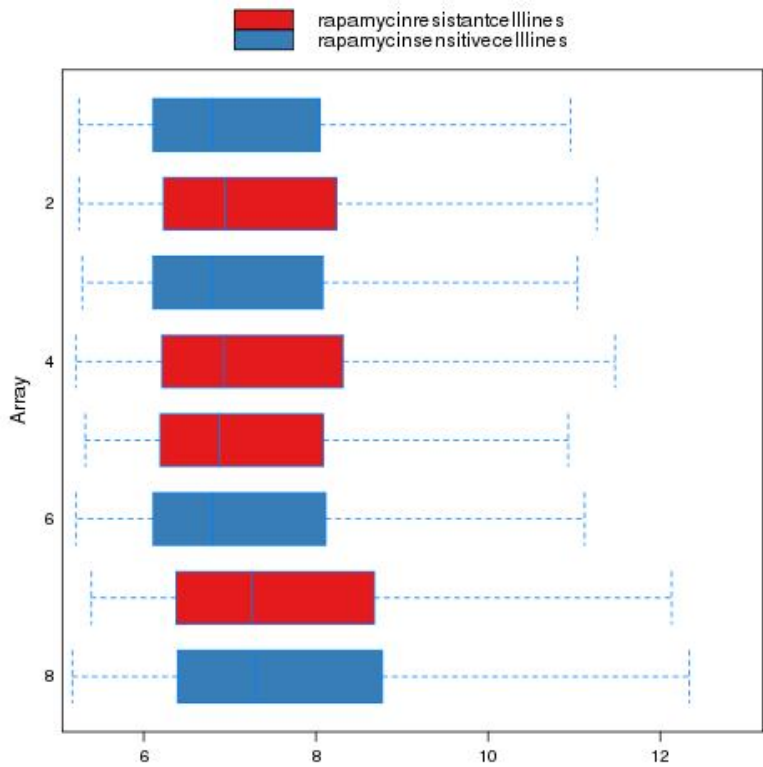## Data type: batch-corrected expression values

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Signal Box Plot

Data type: raw expression values

Each box represents the middle 50% of probe intensities from one array
The extents represent the minimum and maximum intensities
Typically, the intensity ranges are of similar size and have similar centers
Highlydissimilar ranges of intensities might be a problem for normalization

Signal Box Plot

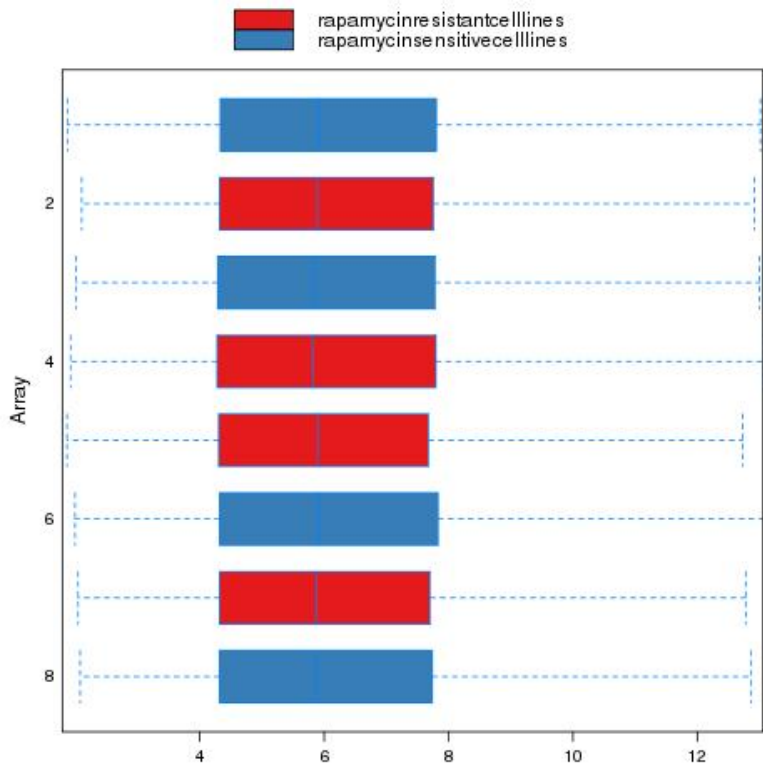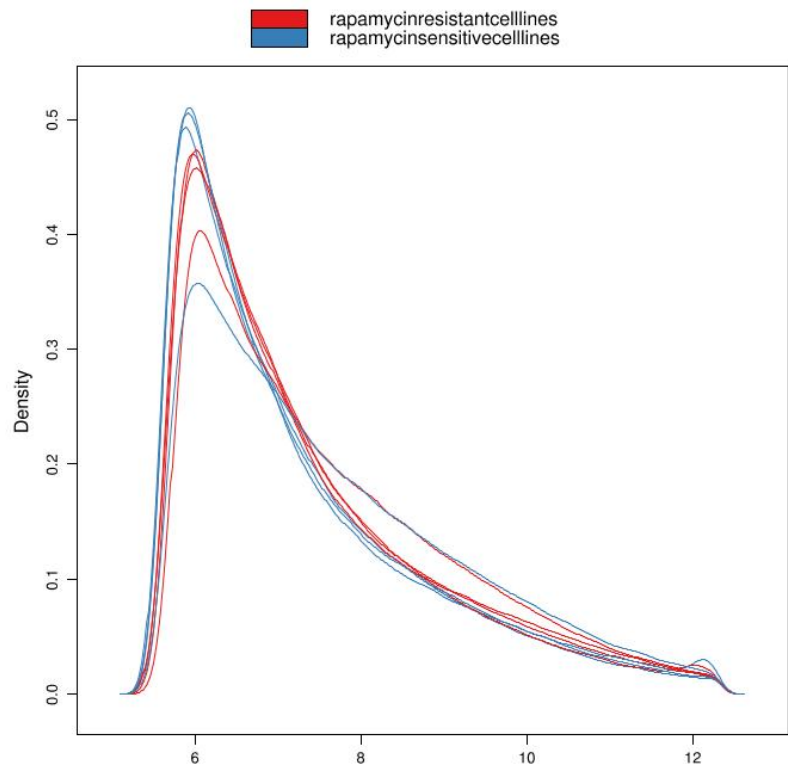**Data type: batch-corrected expression values**

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Signal Density Plot
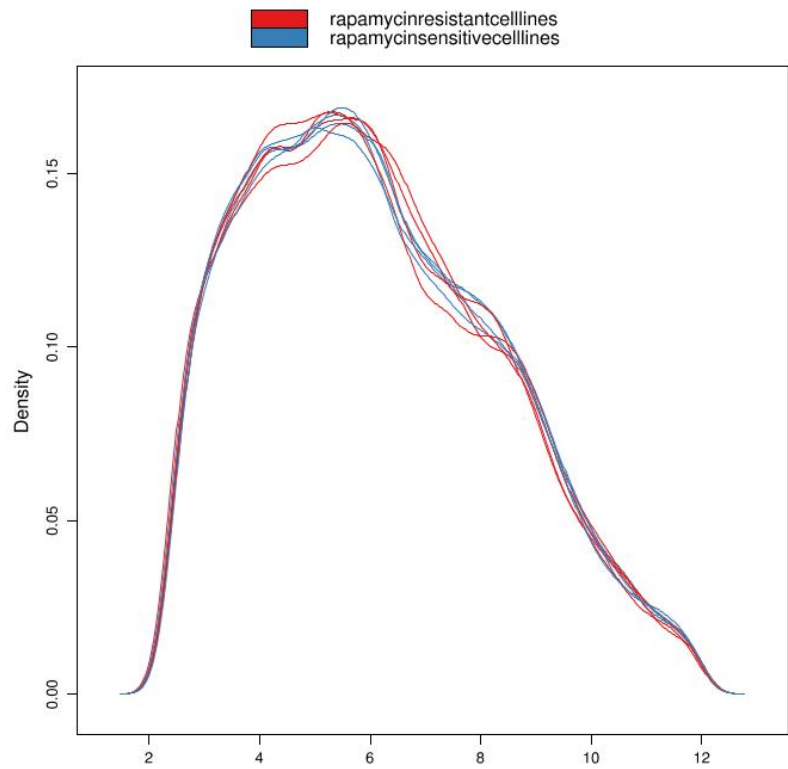
Data type: raw expression values

The x-axis is the signal (Perfect Match) intensity, the y axis is the prevalence of that signal level (a smoothed histogram), and each array is plotted individually
The expectation is that all arrays will have similarly shaped curves
Highly dissimilar curves might be a problem for normalization

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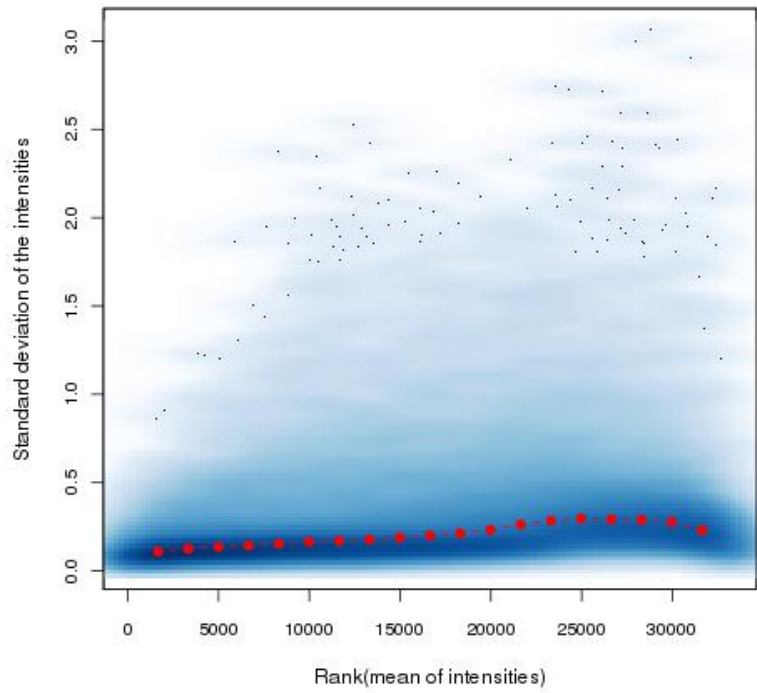
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Highly dissimilar curves might be a problem for normalization

Variance Mean Plot

Data type: batch-corrected expression values

All probes are ranked by their intensity value (the average across all arrays for that probe) on the x-axis, and the y-axis is the standard deviation for that probe
There should be no trend (flat) in the red dotted line drawn through the plot
A trend on the right-hand side may indicate measurement saturation (like an overexposed photo)

Volcano Plot (Fold Change vs. Statistical Significance)

Data type: fold change and p-values

This plot compares the statistical likelihood of differential expression (y-axis) against foldchange (x-axis)
A higher y value indicates a greater likelihood of expression (thisis the opposite of p-values)