qPCR Array data analysis web portal

For quick and simple analysis of any qPCR data

QIAGEN's qPCR data analysis web portal provides the capability to analyze **any qPCR data**. Starting with raw C_T values from any SYBR® Green or hydrolysis-probe based qPCR assay, scientists can quickly upload data, normalize, and export biologically relevant fold-change data and multiple graphs in as little as 15 minutes.

Visit the web portal here:

http://pcrdataanalysis.sabiosciences.com/pcr/arrayanalysis.php

Benefits of using QIAGEN's qPCR data analysis web portal:

- Reliable conversion of any qPCR C_T values into fold changes
- Fold changes include p-value and 95% confidence intervals
- Automatic housekeeping gene recommendation and selection
- Multiple graph formats to visualize data
- Suggestions for future experiments

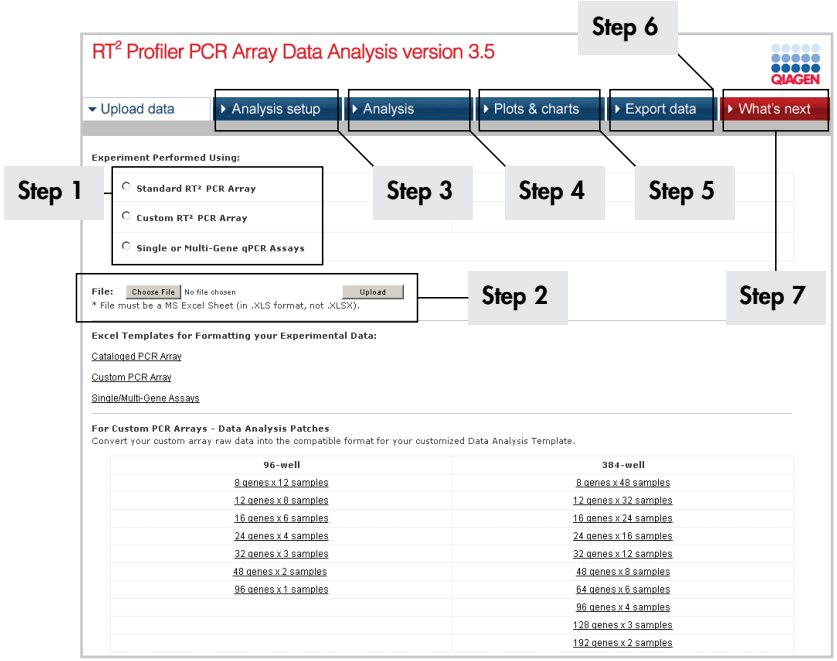

Figure 1. QIAGEN's data analysis tool. This screenshot shows the "Upload data" screen of the web-based data analysis tool at the SABiosciences website. SABiosciences is a QIAGEN company.

Seven steps to easier analysis

1. Choose experiment that was performed (Figure 1).
2. Upload the Microsoft® Excel® file containing your PCR data with a maximum number of 100 samples.
3. Input information into the "Analysis setup" page.
4. See the "Average ΔC_T", "2^(–ΔC_T)", "Fold Change", "p-value", and "Fold Regulation" sections for the results processed by the software from your data.
5. Create the plots and charts you need (Figures 2–4), including:
   - Heat map
   - Scatter plot and volcano plot
   - Clustergram
   - Multigroup plot
6. Click "Export data" to download a Microsoft Excel file containing all raw and processed data from the "Readout" and "Analysis Results" sections.
7. On the "What's Next" page, explore experimental solutions for identifying the mechanisms behind the observed changes in gene expression.

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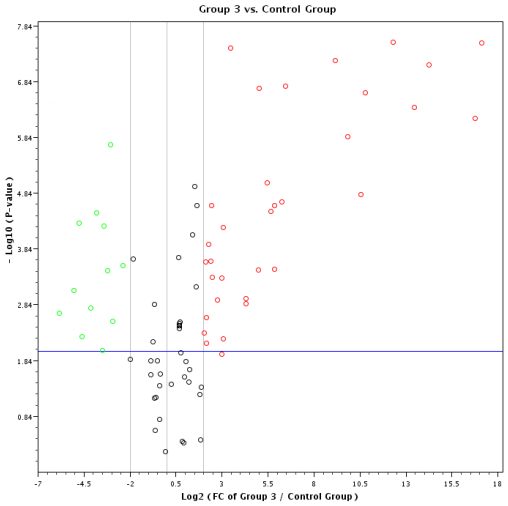

Figure 2. Volcano plot of 84 common cytokine assays reveals 23 upregulated and 6 downregulated genes following PMA and ionomycin treatment. Log_2 fold changes in gene expression between stimulated and resting PBMCs are plotted against t-test p-values. Thresholds for fold change (vertical lines, 5 fold) and significance (horizontal line, p<0.005, n=3 per group) were used in this display.

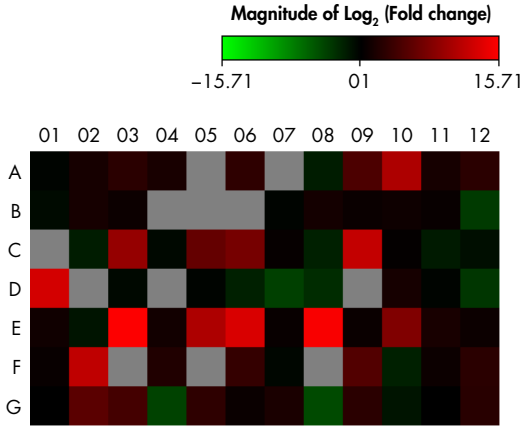

Figure 3. Heat map generated from PCR array data reflecting gene expression values in treated versus untreated conditions. This graph represents fold-regulation data from two sample groups on a 96-well plate layout.

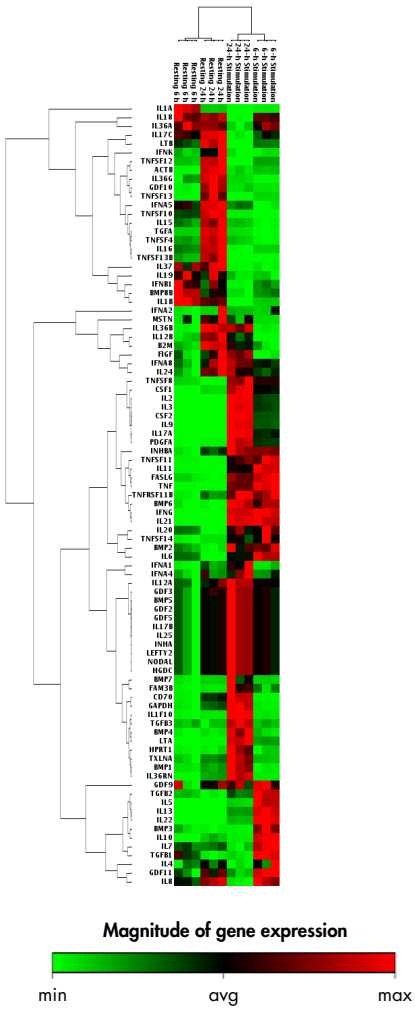

Figure 4. Clustergram of 84 common cytokines grouped by sample type. Non-supervised hierarchical clustering was used to display common cytokine gene expression by heat map visualization, with dendrograms indicating coregulated genes across groups or individual samples.

For up-to-date licensing information and product-specific disclaimers, see the respective QIAGEN kit handbook or user manual. QIAGEN kit handbooks and user manuals are available at www.qiagen.com or can be requested from QIAGEN Technical Services or your local distributor.

Take a test run today at http://pcrdataanalysis.sabiosciences.com!

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