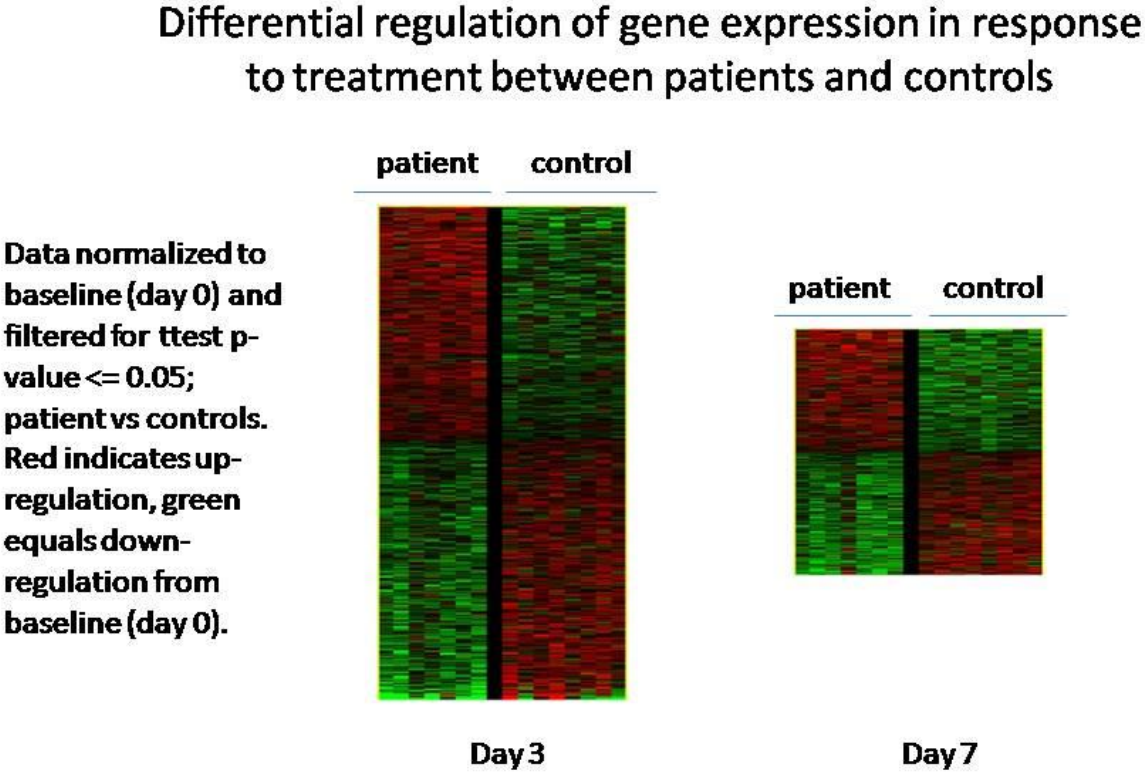
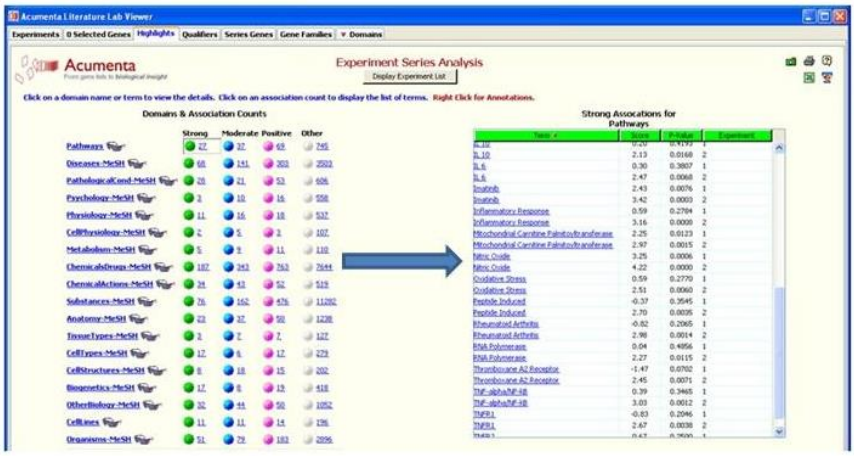
Literature Lab™ Use Case

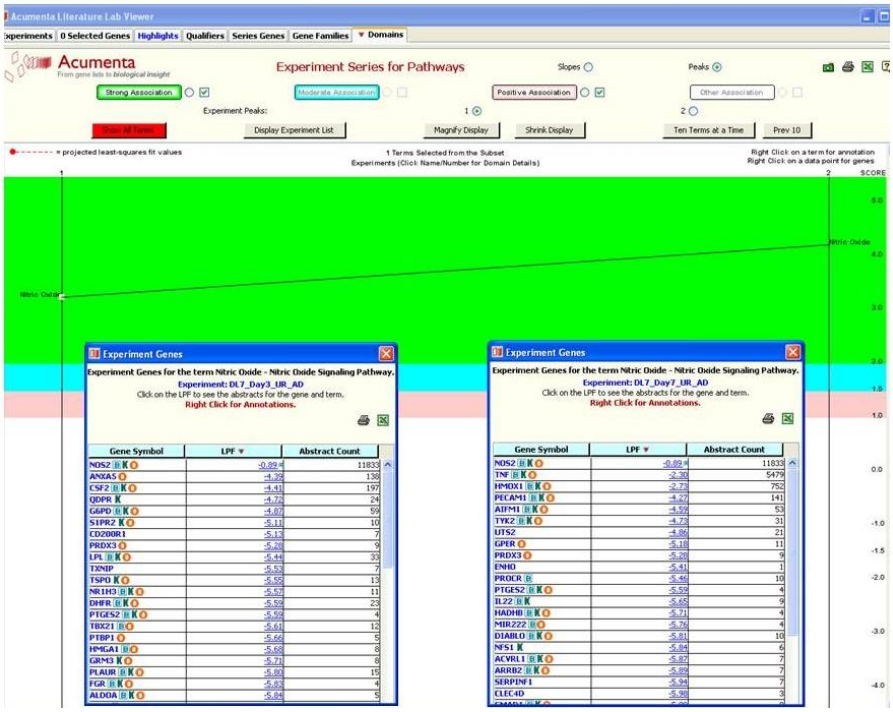
Situation: A bioinformatics expert at a major research university was asked to analyze data from a time course experiment on 7 patients. The scientist needed to "push" the data in order to see differential gene expression activity. The data proved to be uniform, and many small changes were observed to be operating in a coordinated fashion. However, standard enrichment analysis tools were unable to provide useful information about the funtional roles of the gene sets.



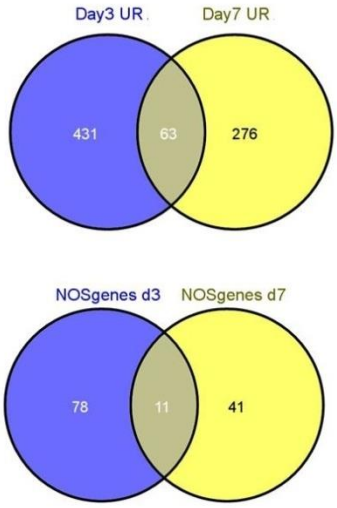
Functional Analysis: Literature Lab™ was used to compare the data from days 3 and 7. The Nitric Oxide Signaling pathway was immediately shown to be strongly associated with both data sets, and Inflammatory Response was strongly associated with day 7. These findings were highly relevant to the biology under analysis.



Results: The view below is a composite of several Literature Lab screens showing the NOS pathway associations on both days 3 and 7. The insets list the genes driving the association at each time point, and indicate that the gene sets are not highly overlapping.



There is some overlap, but the gene sets are distinctly different.

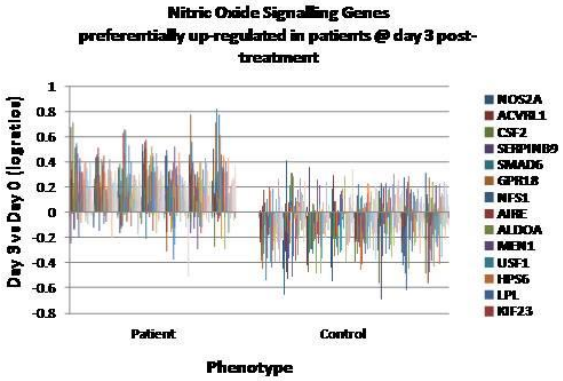


Plotting the expression of the genes elevated in the patients vs control between days 3 and day 7 clearly illustrates the differential regulation between the two phenotypes and that the drivers are the NOS signaling genes.

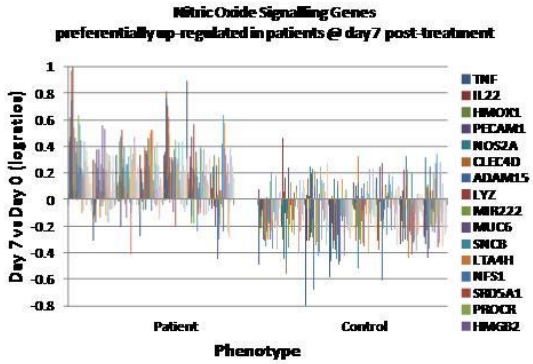
Genes from the nitric oxide signaling pathway are up-regulated in patients at day 3 and day 7 post-treatment, (a logratio of one equals a two-fold change).

These changes are relatively small for individual genes but become significant when considered as a group; day 3 (p< 6E-04) and day 7 (p< 1E-05).

A



B



In this Case Study the data sets from the two days had significant non-overlap, but each one uniquely had a statistically significant association with the Nitric Oxide pathway, along with the Inflammatory Response pathway on day seven. Each list had genes that were associated with these pathways in the literature, but there were not enough canonical genes or other data in these lists to enable enrichment by conventional gene list-and ontology-based tools.
Analysis of the metabolites in the patients confirmed the associations revealed by Literature Lab™.