Quality Monitoring on Human 14K Oligo Chips at the University of Calgary

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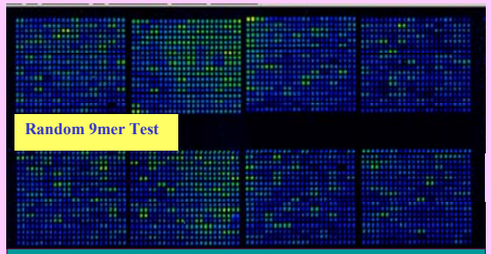
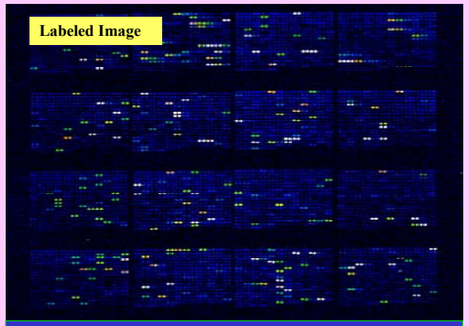
The production of microarrays needs to be carefully monitored and quality control tests done to track systematic effects and performance variations over time to maximize the possibility of getting high quality data.

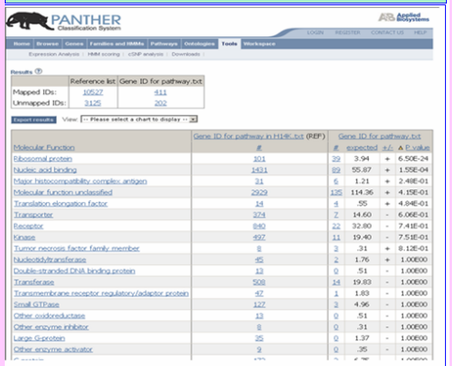


Morphology: **We test the quality of each printing run with a random Cy3-labeled 9mer hybridization to evaluate spot morphology (size, circularity, uniformity).**

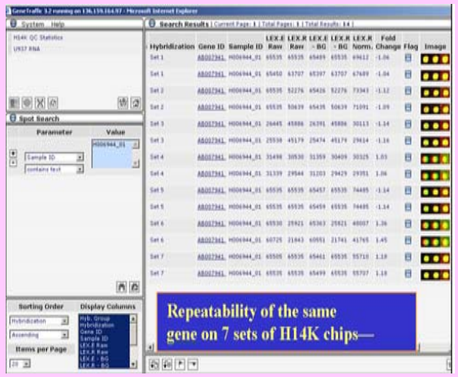


Labeling Efficiency: **We use U937 cell-line RNA to test array quality after each print run. Seven such sets of H14K chips have been analyzed to compare the consistency and variation from different production dates and different operators. Scanned images were quantified using *QuantArray* and further analysis was done with *Gene Traffic*. The variations from different printing dates and operators are compared by background and foreground intensities and presence of biological functional genes in each**

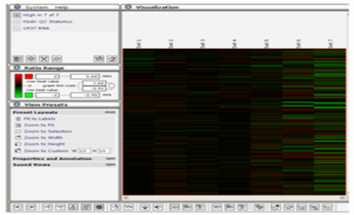
Consistency in H14K Chips



There are over 500 genes showed higher intensities in all sets analyzed which related to the biological functions of U937 cell line.



Variations by Operators

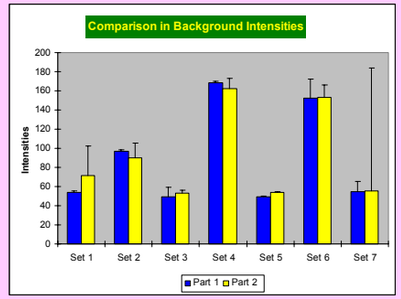


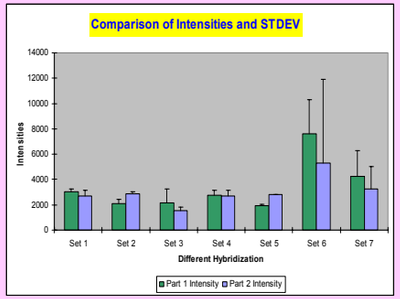
Since we have been using same cell line RNA samples labeled with Cy3/Cy5 to test the label efficiency on each print, it is reasonable that we don't have higher or lower ratio (fold changes). But there are intensities differences between the two different operators, set 6 and 7 show brighter and higher intensities, especially in Cy3-label channel.

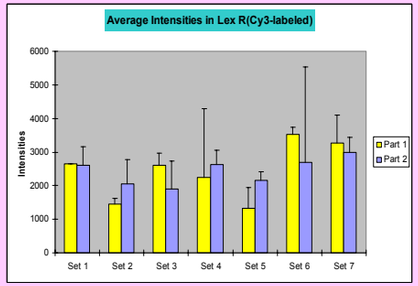
Expression Information:

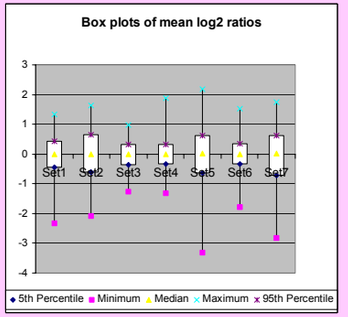
Box plots of the mean log 2 ratios show that 90% of the mean ratios fall within a tight range for each of the sets. The min and max whisker lines encompass the outliers. A total of 36 spots showed fold changes higher than 3 in the 7 hybridizations. After excluding dust and single spots, only 4 pairs of genes remained.

On the other hand, 186 spots showed fold change less than –3. Over half (95/186) of these spots were from set 6 and set 7, which may reflect operator variability.









Conclusions:

- **Morphology parameters remain consistent from print to print.**
- **The same genes (>500) are labeled with high intensity. These genes are related to the biological functions of the U937 cell line.**
- **Ninety percent of the mean log2 ratios stayed within a tight range for each of the hybridizations. However outliers were present.**