

WaferGen SmartChip Platform Produces Comparable Gene Expression Data to AB TaqMan® Microfluidic Card and Affymetrix GeneChip® Microarray

Customer Testimonial

Arul Chinnaiyan, M.D., Ph.D., *Professor of Pathology and Urology, University of Michigan
Howard Hughes Medical Institute Investigator, Director of Cancer Bioinformatics*

- Comparison of SmartChip, Taqman® and GeneChip® platforms yield similar results
- SmartChip Gene Expression Panels generate reproducible data when compared to other gene expression platforms
- SmartChip RT-PCR platform offers significant advantages over the two platforms in sensitivity, cost-effectiveness and ease of use

Summary

A comparison of gene expression analysis data using three different technology platforms was conducted by Arul Chinnaiyan, M.D., Ph.D., and colleagues at the University of Michigan (UM). Dr. Chinnaiyan, a Howard Hughes Medical Institute investigator, is also Director of Pathology Research Informatics and Director of Cancer Bioinformatics at the UM. The platforms from which results were compared were the WaferGen SmartChip Real-Time PCR System, the Applied Biosystems (AB) TaqMan® 384-Well Microfluidic Card, and the Affymetrix GeneChip® Human Genome U133A Array platform.

The newly obtained results from the SmartChip platform were compared with previously generated sample data sets obtained two to five years previously using the TaqMan and GeneChip platforms. In summary, the data indicated that the SmartChip results were highly comparable to those obtained using the other two platforms. These data demonstrate that the SmartChip system may be utilized as a platform for gene expression analysis, and that it yields similar results to those observed on other well known technology platforms. This is significant because when compared to the AB TaqMan and Affymetrix GeneChip platforms, the WaferGen SmartChip RT-PCR system offers a more flexible, cost-effective, and easier-to-use solution for quantitative gene expression analysis.

Comparison of gene signatures across technologies yields similar results

Dr. Chinnaiyan and colleagues compared gene expression levels (via fold-change) from disease patients with a poor prognosis (Group A) with gene expression levels from disease patients with a good prognosis (Group B). There were five patient samples in each group and the samples came from fresh frozen tissue extracted with TRIzol®.

A total of 44 genes overlapped on all three platforms (Figure 1). Thirty-eight of these 44 genes showed the same trends (up- or down-regulation) on all three platforms. 39 of 44 genes showed the same trends between the SmartChip Human Oncology Panel and the TaqMan microfluidic card, and 41 of 44 genes showed the same trends between the SmartChip Panel and the GeneChip array. 40 of the 44 genes showed the same trends between the TaqMan microfluidic

Comparison of Gene Expression Data from Three Platforms

Customer testimonial

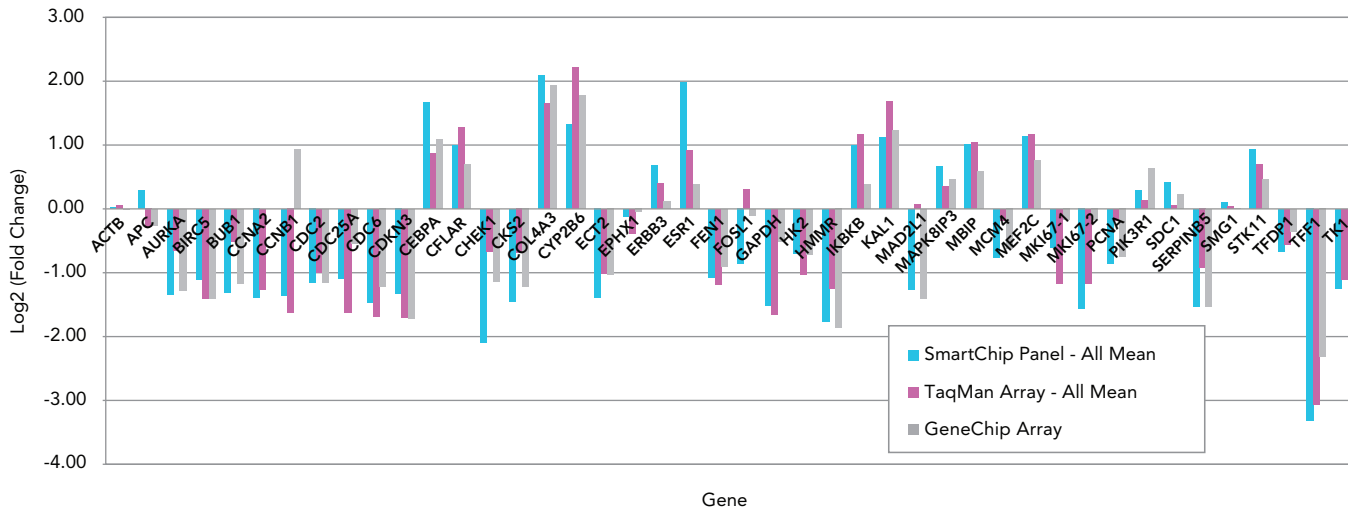


Figure 1. Comparison of fold-change data for the 44 genes overlapping on all three platforms. This graph shows the fold-change data for the 44 genes that overlapped on all three platforms. For the SmartChip data, the mean value of all genes was used for normalization. For the TaqMan data, the mean value of all genes was used for normalization.

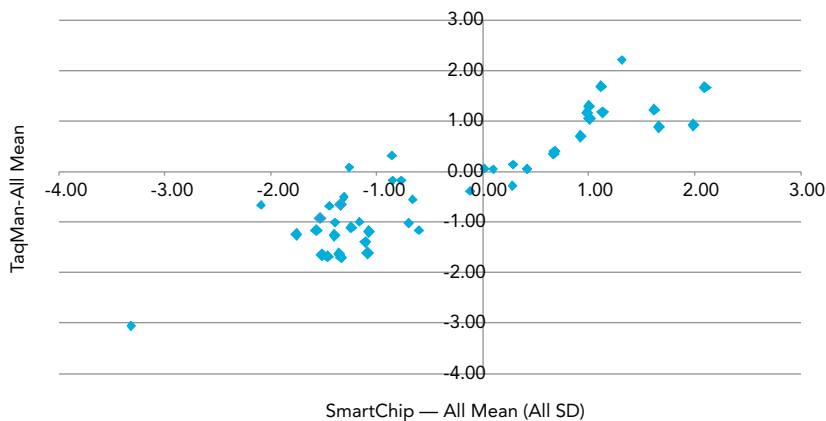


Figure 2. delta-delta Ct plot correlating SmartChip fold-change data versus TaqMan fold-change data for the 44 genes overlapping on all three platforms. Graph shows delta-delta Ct plot of SmartChip all-mean fold-change data versus TaqMan all-mean fold-change data. All-mean indicates that the mean value for all genes was used for normalization.

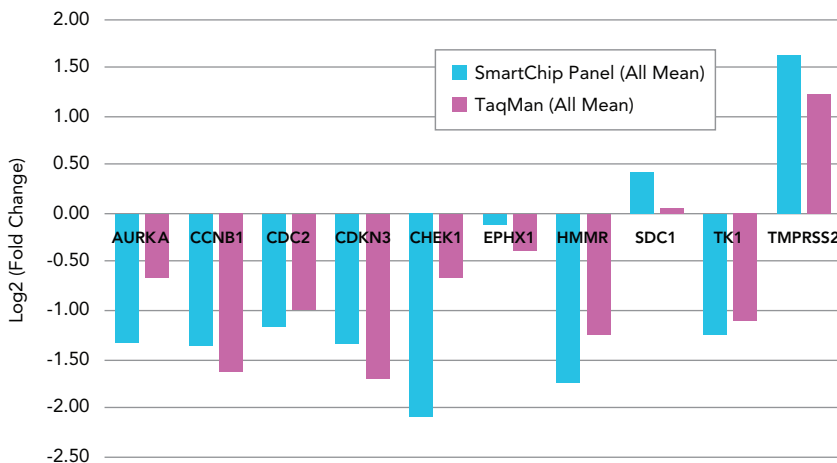


Figure 3. SmartChip versus TaqMan fold-change data for the 10 of 44 overlapping genes with matching exon target regions. This graph shows fold-change data for the 10 gene targets that were designed with primers targeting the same exon areas in both the SmartChip and TaqMan assays. There is strong consistency in the expression levels of the 10 genes between both SmartChip and TaqMan fold-change data even though several of these targets had small log2 fold changes. All-mean indicates that the mean value for all genes was used for normalization.

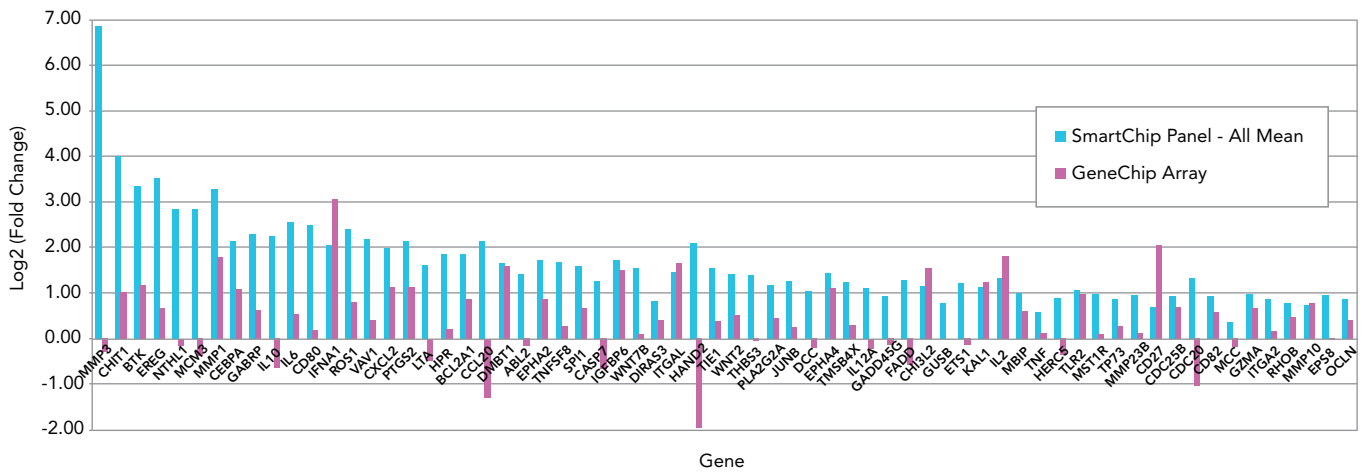


Figure 4. Comparison of fold-change data for 66 up-regulated genes (SmartChip versus GeneChip data). This graph shows the fold-change data for 66 genes up-regulated by at least 2-fold on the SmartChip platform compared to the fold-change data for the same genes on the GeneChip platform. SmartChip data is shown both as Ave2 data (an average of the two least variable genes was used for normalization) and as all-mean data (the mean value for all genes was used for normalization).

card and the GeneChip array. Of the few genes that showed inconsistent data, small changes (less than 2-fold) were detected on all three platforms.

A delta-delta Ct plot of all-mean data from the SmartChip panel versus all-mean data from the TaqMan microfluidic card showed significant correlation between gene expression results on the two platforms for the 44 genes overlapping on all three platforms (Figure 2). The r_s value (Spearman's Rank Correlation

Coefficient) for this comparison was 0.85 ($p < 0.0001$) and the r value (Pearson's Product Moment Correlation Coefficient) was 0.90.

A plot of gene expression levels for the 10 of the 44 overlapping genes for which primers were designed for the same exon region, showed consistent correlation in the up or down trends for the data generated from the SmartChip and TaqMan platforms (Figure 3).

A total of 399 genes containing a single GeneChip target region per gene overlapped with SmartChip and were compared. 66 of these genes were up-regulated by at least a 2-fold change on the SmartChip platform and the data was plotted (Figure 4), while 55 of the genes were down-regulated by at least a 1.6-fold change on the SmartChip platform and this data was also plotted (Figure 5). Of the 66 up-regulated genes, 47 (71%) were also up-regulated on the GeneChip

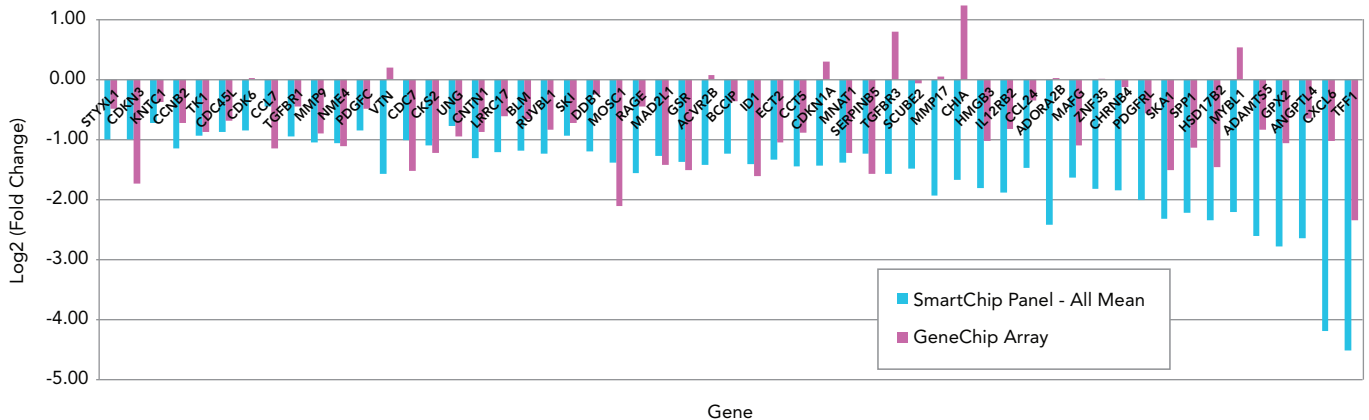


Figure 5. Comparison of fold-change data for 55 down-regulated genes (SmartChip versus GeneChip data). This graph shows the fold-change data for 55 genes down-regulated by at least 1.6-fold on the SmartChip platform compared to the fold-change data for the same genes on the GeneChip platform. SmartChip data is shown and as all-mean data (the mean value for all genes was used for normalization).

platform. In general, greater changes were observed with SmartChip (real-time PCR) when compared to GeneChip (hybridization), which is to be expected. Of the 55 down-regulated genes, 45 (~82%) were down-regulated on the GeneChip platform.

It should be noted that 392 genes contained two or more target regions per gene on the GeneChip array. 83 (~21%) of these 392 genes exhibited at least a 0.5 log₂ change (1.4-fold) that shifted the interpretation from up- to down-regulation in the same gene.

Conclusion

In conclusion, all three platforms showed similar trends for up- versus down-regulation. And, as expected, both real-time PCR platforms were able to detect larger-fold changes when compared to the GeneChip platform. Most variability in the platforms in up- versus down-regulation was seen in genes that showed less than 2-fold changes.

Trends between SmartChip and TaqMan data, when compared to GeneChip data, were similar, with SmartChip data matching 41 of 44 genes and TaqMan data matching 40 of 44 genes.

To reiterate, results obtained with the SmartChip platform were highly comparable to those obtained with the TaqMan and GeneChip platforms. These results further demonstrate that the SmartChip platform can be used for gene expression analysis in applications and samples which are currently run on the two comparison platforms. This is significant because the SmartChip platform offers significant advantages over the other platforms in flexibility, cost-effectiveness and ease of use.