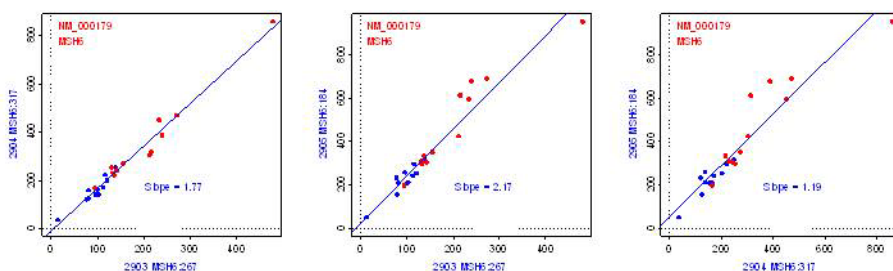


Biomarker Translation from Global Expression Arrays to Focused Arrays

Gene expression signatures are typically discovered with global expression arrays. In order to validate and advance these biomarker signatures into routine testing for clinical research, an alternative platform is required that uses different probes for well-defined targets, enables high throughput processing of a large number of biological samples, and faithfully captures the biologically relevant aspects of the signature. To demonstrate the Zplex® System as a powerful tool for routine gene expression analysis, 93 genes relevant to ovarian cancer were translated from an Affymetrix platform to the Zplex® System.

Probe Design

Three oligonucleotide probes were designed to hybridize to the 3' ends of the transcripts corresponding to the 93 selected genes and then screened against 23 different RNA samples from normal and cancerous ovarian cells. A single optimal probe was then selected based on maximum signal intensity, minimum distance from the 3' end of the target sequence, differences between samples, and correlation between different probe designs (see example below).



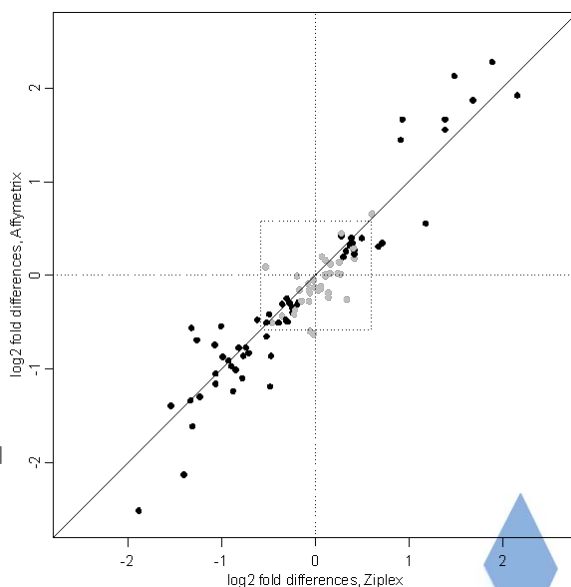
Good correlations between signal intensities of all three probes for a given target indicate that the probes were most likely hybridized to the same transcript, as shown for samples from normal (blue) and tumor cells (red). All three probes for this particular target also show discrimination between the two samples.

Concordance between platforms

High concordance was shown between the Affymetrix and Zplex platforms in the fold differences in signal intensities for 93 genes in both sets of samples (right).

Highlights:

- Straight forward and reliable translation of expression signatures between global expression arrays and the Zplex® System.
- Quantification of gene expression equivalent to that of discovery platforms can be realized with additional the speed and automation of flow-thru chip technology.



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