Data Sheet

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Almac Xcel™ Array for FFPE Profiling

Almac Xcel™ Array for the profiling of FFPE samples provides the only 3' gene expression array designed and optimized for use with formalin-fixed, paraffin-embedded (FFPE) tissues.

This array, offered exclusively through Affymetrix, was designed by Almac for optimal performance in these precious samples. The ability to profile FFPE samples enables researchers to access existing banks of stored retrospective samples containing known clinical outcomes. In addition, researchers can analyze newly collected tissue, as standard clinical protocols require clinicians to collect and store tumor and normal adjacent tissue using formalin fixation and paraffin embedding.

These sample sources enable the potential for retrospective biomarker and validation studies with significant reduction in biomarker development time and costs.

Introduction

Xcel Array generates robust data from RNA isolated from FFPE tissue, thus facilitating the discovery, validation, and commercialization of biomarker from clinical samples.

Containing significantly more data points than currently available from any other array platform, this additional content greatly increases the chances of successful biomarker discovery.

Xcel Array can be used to compare with historical Affymetrix® Human Genome U133 Plus 2.0 Array data—the most widely cited expression array—as 98% of the HG U133 Plus 2.0 Array content can be cross-mapped to Xcel Array, thus allowing fast validation with publicly available datasets.

Design and coverage

Almac Xcel Array

Almac Xcel Array is a high-density 3' array optimized for use with RNA isolated from FFPE material.

The array contains probe sets for over 97,000 transcripts, many of which are not represented on other arrays. Approximately 70% of the array is equivalent to GeneChip® Human Genome U133 Plus 2.0 Array content. A further 8% is updated, validated RefSeq information not contained on the U133 Plus 2.0 Array, with the remaining 22% being derived from high-quality in-house sequencing of cancer samples and filtered public data.

Performance

To demonstrate the performance of Xcel Array, Almac evaluated differential expression for tumor compared to normal adjacent tissue from a colorectal quad sample set: formalin-fixed, paraffin-embedded (FFPE) and matched fresh frozen (FF) tumor and normal tissues. Targets were prepared according to protocols outlined in the Genisphere® Sensation™ RNA Amplification Kit, (Genisphere SNSAT12) and Biotin Labeling Kit for 3' Arrays (Genisphere SS3BIO12). Three target preparation replicates of each sample were tested. (Xcel Array is currently being validated with the new Affymetrix® SensationPlus™ Reagents.)

Figure 1 shows that despite the poorer quality RNA isolated from FFPE samples compared to fresh frozen samples, it is possible to obtain useful data from FFPE samples using the Xcel Array. The first principal component demonstrates the variance contributed by sample type: FF and FFPE. The second principal component illustrates that the tumor samples can be distinguished from the normal adjacent tissue even when using poorer quality FFPE samples.

Figure 1: Principal components analysis of colon tumor and normal adjacent tissue in fresh frozen compared to FFPE samples. Principle Components Analysis (PCA) on RMA signal from the colon quad was carried out in the Partek® Genomic Analysis Suite. FFPE samples are represented by the red markers and FF samples by the blue markers. The ellipses indicate the boundaries that are two standard deviations from the centroid of each cluster.
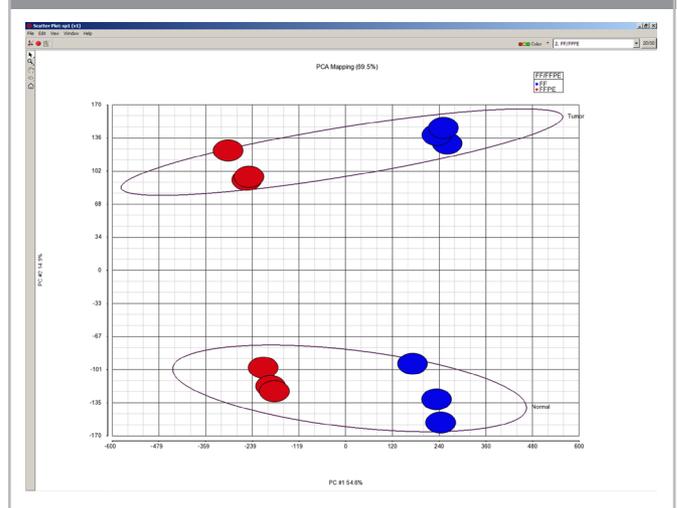
Volcano plots were generated to illustrate the magnitude of change and the statistical significance for colon tumor compared to normal samples in FF and FFPE samples. Only probe sets with an absolute $\log_2$ fold change of greater than or equal to 1 were plotted. Some loss of differential expression was observed for FFPE compared to FF samples. As expected, the FFPE samples had a little more than half the number of statistically significant changes observed in FF samples.

Figure 2: Volcano Plots. Median fold change was calculated from 3 replicates each for colon tumor compared to normal adjacent tissue using FF and FFPE samples. In addition, the p-values were calculated using a paired T-Test with equal variance. **X-axis:** $\log_2$ fold change. **Y-axis:** Negative $\log_{10}$ p-value. Points above a negative $\log_{10}$ p-value of 2 (p-value = 0.01) are considered to be statistically significant.
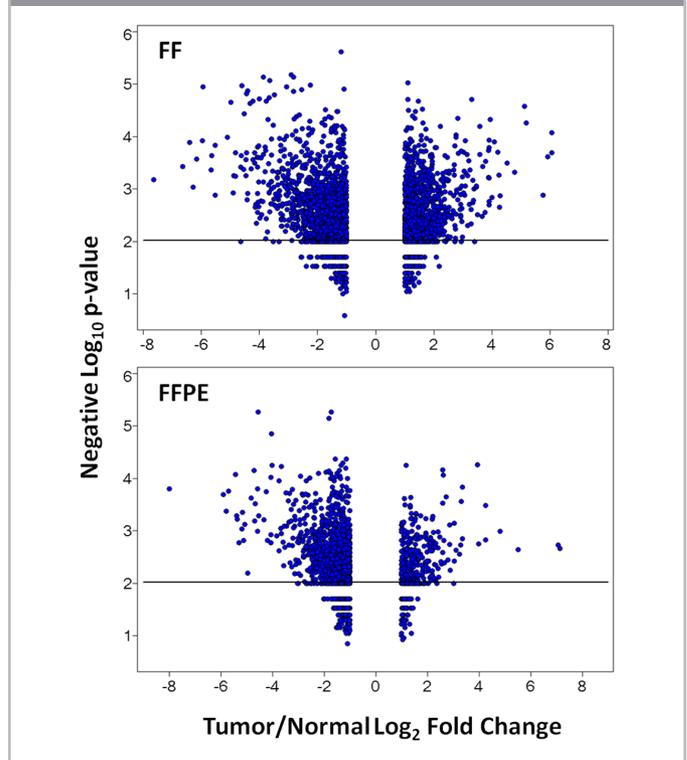
Ordering information

Part number	Description	Details	Supplier
902016	Almac Xcel™ Array	Contains 6 arrays	Affymetrix
SNSAT12	Sensation™ One-Round Amplification Kit	Sufficient for 12 reactions	Genisphere
SS3BIO12	Biotin Labeling Kit for 3' Arrays	Sufficient for 12 reactions	Genisphere
SENSE-3PR	Sensation™ 3' Amplification and Labeling for 3' IVT Expression Arrays	Sufficient for 12 reactions	Genisphere
901285	Affymetrix® Gene Profiling Reagents – RNA Control Kit (IVD Kit 1)	Sufficient for 64 reactions	Affymetrix
901286	Affymetrix® Gene Profiling Reagents – Transcript Synthesis and Labeling Kit (IVD Kit 3)	Sufficient for 32 reactions	Affymetrix
901299	Affymetrix® Gene Profiling Reagents – Transcript Detection Kit (IVD Kit 3)	Sufficient for 32 reactions	Affymetrix

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