Data Sheet

GeneChip® Exon Array System for Human, Mouse, and Rat

The GeneChip® Exon 1.0 ST Array enables you to look beyond the gene to see the real biology underlying key phenotypes and disease states.

By utilizing an unbiased, whole-transcript assay and array designs that feature probes across the entire length of the transcript, the GeneChip Exon Array System provides the most accurate and robust expression profiling of any array platform.

With the GeneChip Exon 1.0 ST Array, you'll be able to:

- **Detect changes and transcriptional events that you'd miss with other microarray platforms**

- **Measure expression of individual exons and entire genes, and detect alternative splicing information, all from a single experiment**

- **Get the most comprehensive coverage of the annotated genome, as well as predicted content for novel discovery, by interrogating more than 1 million exons**

Introduction

The GeneChip Exon Array is the most powerful whole-genome expression tool available today. With more than 5.5 million features on each array and the greatest single-array coverage of the transcriptome, including empirically supported and predicted transcripts, the Exon 1.0 ST Array maximizes your ability to identify known and novel alternative splicing events in addition to measuring expression of the entire transcriptome.

At the gene level, the Exon 1.0 ST Array summarizes approximately 40 probes from across the length of the gene into a single, expression-level data point that represents all transcripts derived from each gene. With the highest density of coverage for most genes compared to all other microarrays, gene-level analysis on the Exon 1.0 ST Array offers more sensitive measurement of gene expression and more statistically robust results than 3'-based approaches.

At the exon level, approximately four probes per exon enable you to measure the expression of individual exons and detect alternative splicing. The majority of genes express multiple isoforms and more than 80 percent are alternatively spliced, so incorporating exon-level analysis allows you to study a wealth of transcriptional variation that would be lost with 3'-biased approaches.

This alternative splicing and isoform variation affects susceptibility to, and severity of, a large number of human diseases, and helps account for the disparity between the hundreds of thousands of proteins that arise from the relatively low number of protein-coding genes. Changes in exon usage and alternative splicing are increasingly being shown to affect important pathways and phenotypes.

Ultimately, exon-level analysis provides hundreds to thousands more transcriptional events that you can associate with real biology.
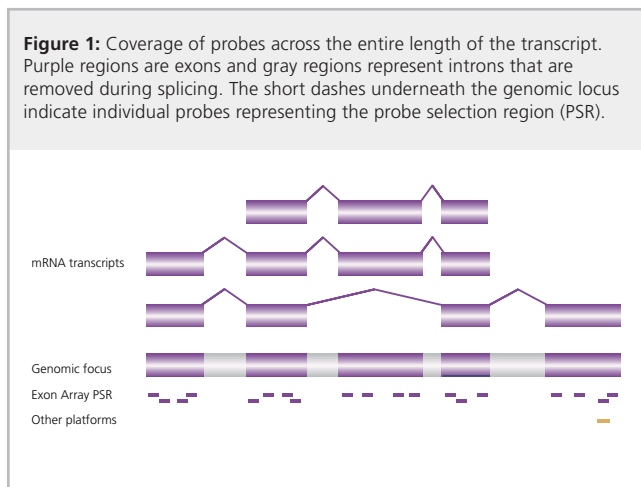
Array design

New information has shown that biologically significant transcription and alternative splicing events may not have been fully captured by the well-annotated sequences. Exon 1.0 ST Arrays support the most detailed survey of the human, mouse, and rat genomes and expand the discovery of novel transcript structures beyond the well-characterized and annotated genes.

The Exon 1.0 ST Array contains sequences from two primary sources:

- cDNA-based content, including the more established human RefSeq mRNAs, GenBank® mRNAs, and ESTs from dbEST; additional annotations were created by mapping syntenic cDNAs to the human, mouse, and rat genomes using genome synteny maps from the UCSC Genome Bioinformatics Group
- Predicted gene structure sequences from:
    - GENSCAN
    - Ensembl
    - Vega
    - geneid and sgp
    - TWINSCAN
    - Exoniphy
    - microRNA Registry
    - MITOMAP
    - structural RNA predictions

Most exons longer than 25 base pairs (bp), along the whole transcript, are represented with at least one probe set (Figure 1). The majority of the probe sets are comprised of four perfect match (PM) probes for each probe set to provide robust results. On average, a typical gene with 10 exons will be interrogated by 40 probes.

Figure 1: Coverage of probes across the entire length of the transcript. Purple regions are exons and gray regions represent introns that are removed during splicing. The short dashes underneath the genomic locus indicate individual probes representing the probe selection region (PSR).

Each probe on the array is designed from genomic sequence and annotated with its genome coordinates and the references to its relationship to the associated exon, exon cluster, and transcript cluster.

Projecting the design onto the genome facilitates the dynamic update of the design, reflecting the new knowledge of the genomic sequence and annotations. In addition, this design and annotation approach enables more convenient correlation of the expression array data with DNA sequence information and translated protein products. This makes it easier to dissect the mechanisms involved in transcription and alternative splicing regulation.

Data analysis solutions
Gene-level analysis
Identifying and prioritizing gene-level expression changes using the Exon 1.0 ST Array is as simple as 3' expression analysis, and the workflows are similar. Use the GeneChip® Operating System (GCOS) or GeneChip® Command Console Software for initial image acquisition, and Affymetrix Expression Console™ Software provides an easy-to-use analysis workflow for quality control (QC) and probe set summarization to attain gene-level signal data.

Affymetrix also partners with a number of GeneChip-compatible™ software providers, which provide statistical analysis solutions for generating lists of differentially regulated genes. Several software providers offer solutions for pathway analysis—building and visualizing potential gene interactions by leveraging databases of published literature.

The NetAffx® Analysis Center, freely available from Affymetrix, enables you to correlate these results with array design and annotation information. The Integrated Genome Browser (IGB) provides visualization tools to further explore genomes and corresponding annotations from multiple data sources.

Exon-level analysis
Expression Console Software also enables you to compute exon-level signal estimates for Exon 1.0 ST Array data. To detect alternative splicing and isoform variation, several GeneChip-compatible software packages with simplified workflows are available, including Partek® Genomics Suite™, Biotique's XRay, JMP Genomics, Genomatix' ChipInspector, and GeneData's Expressionist. Pathway analysis, annotations from the NetAffx Analysis Center, and IGB analysis of exon array data can all be conducted using workflows similar to 3' expression array data.

GeneChip® Exon 1.0 ST Array design statistics summary

	Human	Mouse	Rat
Probe sets	1.4 million	1.2 million	1.0 million
Exon clusters	>1 million	~1 million	850,000
Supported by putative full-length mRNA	289,961 probe sets	266,200 probe sets	92,038 probe sets
Supported by Ensembl transcripts	306,583 probe sets	266,791 probe sets	195,943 probe sets
Supported by EST	665,175 probe sets	554,003 probe sets	211,451 probe sets
Supported by syntenic mRNA	220,262 probe sets[3]	214,763 probe sets[3]	272,061 probe sets[5]
Supported by gene prediction	883,105 probe sets	835,897 probe sets	875,666 probe sets
Probe selection region	Along the entire length of the transcripts		
Probes/probe selection region	4[1]		
Background subtraction strategy	Median fluorescence intensity of up to 1,000 background probes with the same GC content		
Total features per array	>5,500,000		
Interrogated strand	Sense[2]		

1. About 10 percent of the exon probe sets have fewer than four probes due to the probe selection region length and sequence constraints.
2. The probes tiled on the array are designed in the anti-sense orientation, requiring sense strand-labeled targets to be hybridized to the array. By convention, the array is called ST Array, representing the necessity of using sense targets (the labeled sample to be hybridized to the array).
3. Supported by mouse or rat mRNA.
4. Supported by human or rat mRNA.
5. Supported by human or mouse mRNA.

Ordering information

Part number	Product	Description
GeneChip® Exon 1.0 ST Array		
900651	GeneChip® Human Exon 1.0 ST Array	Contains 30 Arrays
900819	GeneChip® Mouse Exon 1.0 ST Array	Contains 30 Arrays
900822	GeneChip® Rat Exon 1.0 ST Array	Contains 30 Arrays
GeneChip® WT Sense Target Labeling and Control Reagents, 30 reactions		
900652	Includes:	
	GeneChip® WT cDNA Synthesis and Amplification Kit	30 reactions
	GeneChip® WT Terminal Labeling Kit	30 reactions
	GeneChip® Sample Cleanup Module	30 reactions
	GeneChip® IVT cRNA Cleanup Kit	30 reactions
	GeneChip® Eukaryotic Poly-A RNA Control Kit	~100 reactions
	GeneChip® Hybridization Control Kit	30 reactions
GeneChip® Exon 1.0 ST Array Starter Pack		
900654	GeneChip® Human Exon 1.0 ST Array Starter Pack	
900831	GeneChip® Mouse Exon 1.0 ST Array Starter Pack	
900848	GeneChip® Rat Exon 1.0 ST Array Starter Pack	
	Starter pack includes:	
	GeneChip® Exon 1.0 ST Array	30 arrays
	GeneChip® WT Sense Target Labeling and Control Reagents	30 reactions
	On-site training including the following arrays and reagents for the training:	
	GeneChip® Exon 1.0 ST Array	10 arrays
	GeneChip® WT cDNA Synthesis and Amplification Kit	10 reactions
	GeneChip® WT Terminal Labeling Kit	10 reactions
	GeneChip® Sample Cleanup Module	30 reactions
	GeneChip® Eukaryotic Poly-A RNA Control Kit	~100 reactions
	GeneChip® Hybridization Control Kit	30 reactions

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