DataSheet

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Biology for a better world

GeneChip® Rat Gene 2.0 ST Array
Affymetrix® Rat Gene 2.1 ST Array Strip
Affymetrix® Rat Gene 2.1 ST Array Plate

A whole-transcript design for the most comprehensive and accurate gene-level view of coding and non-coding transcripts

Affymetrix understands that rats are an important model organism commonly used for studying human disease. In order to keep your experiments relevant to the understanding of the transcriptome, Affymetrix has designed an array based on the most recent genome content for generating genome-wide expression profiles.

The gene ST family of arrays offers a unique feature not available in other microarrays. Unlike traditional array designs that rely on a probe(s) designed to the first exon of the gene's 3' end, the hundreds of thousands of probes on each gene ST array is designed to every exon of every transcript represented on the array.

The high-transcript coverage (median of 22 probes per gene) yields accurate detection for genome-wide transcript expression changes. These arrays provide higher resolution and accuracy than many of the classical 3'-biased microarray solutions available. The whole-transcript analysis approach enables researchers to detect multiple transcript isoforms from a given gene, including those that could be missed using a 3'-biased expression design, such as splice variants, non-polyadenylated transcripts, transcripts with alternative polyadenylation sites, and truncated transcripts.

Benefits of these arrays are:

- Whole-transcript analysis enables the capture of transcript isoforms you may miss with 3'-biased expression designs

- Comprehensive transcriptome coverage provides the best opportunity to discover interesting biology:

  - >13,900 protein coding transcripts

  - >17,000 Entrez genes

- Measure alternative splicing events/transcript variants with probes designed to maximize coverage of exons

- Reproducible: signal correlation coefficient ≥0.99

Array design strategy and coverage

These expression arrays are designed to provide extremely high coverage of the transcribed genome. We have used a comprehensive collection of information sources to design probes to interrogate multiple loci on every exon of every transcript.

These expression arrays have been designed with a median of 22 unique probes per transcript. Each unique probe is 25 bases in length, which means that the array measures a median of 550 bases per transcript.

This design strategy provides you with the ability to evaluate whole-transcriptome gene expression at the gene and exon levels, which allows the study of transcript variants and alternative splicing events.

This high coverage across the entire transcript results in superior performance and data confidence.

Specifications

Transcript coverage of the array	
NM and XM – RefSeq coding transcript, well-established and provisional annotations	>13,900
NR and XR – RefSeq non-coding transcript, well-established and provisional annotations	>500
Total RefSeq transcripts	>14,400
RS (Entrez) gene count	>17,000

Detailed information on content of this array can be obtained on NetAffx using the Expression Array Comparison tool (http://www.affymetrix.com/analysis/compare/index.affx). Please note that you will need to log on to www.affymetrix.com to access this content.

Data sources used to design the array
RefSeq (release 51)
Ensembl (release 65)

Array design	
Total probes	>610,400
Exon-level probe sets	>214,300
Gene-level probe sets	>29,400
ERCC probe sets[1]	92
Background probes	Antigenomic set
Poly-A controls	*dap, lys, phe, thr*
Hybridization controls	*bioB, bioc, bioD, creX*
Total RNA input required	50–500 ng
Probe feature size	5 µm
Probe length	25-mer
Probes per gene (median)	22
Target RNA orientation	Sense target

Performance specifications	
Sensitivity[1]	≥1:100,000 (≥1.5 pM)
Signal correlation coefficient	≥0.99
Detectable fold change[1]	2-fold for 1:100,000 vs. 1:50,000
Dynamic range	~3 logs

[1] Sensitivity and dynamic range were determined using a Latin square experimental design with 61 full-length, *in vitro* transcribed RNAs spiked into HeLa total RNA. For this experiment, four samples comprising four different relative abundances were tested. Sensitivity to detect a 2-fold change was defined as significant based on a t-statistic meeting a threshold set for three replicates and 95% confidence.

[1] Probe sets interrogating external RNA controls present in the Ambion® ERCC RNA Spike-In Control Mixes, P/N 4456740 and 445673

Ordering information

Part number	Description	Details
902466	GeneChip® Rat Gene 2.0 ST Array and GeneChip® WT PLUS Reagent Kit	Sufficient for 10 samples
902467	GeneChip® Rat Gene 2.0 ST Array and GeneChip® WT PLUS Reagent Kit	Sufficient for 30 samples
902126	Affymetrix® Rat Gene 2.1 ST Array Strip	Contains one 4-array strip
902142	Affymetrix® Rat Gene 2.1 ST 16-Array Plate and Trays	Contains one 16-array plate
902143	Affymetrix® Rat Gene 2.1 ST 24-Array Plate and Trays	Contains one 24-array plate
902144	Affymetrix® Rat Gene 2.1 ST 96-Array Plate and Trays	Contains one 96-array plate

Related products

Part number	Description	Details
902280	GeneChip® WT Plus Reagent Kit	Sufficient for 10 reactions
902281	GeneChip® WT Plus Reagent Kit	Sufficient for 30 reactions (manual) or 24 reactions (automated)
902414	GeneChip® HT WT Plus Reagent Kit	Sufficient for 96 reactions
900720	GeneChip® Hybridization, Wash, and Stain Kit	Sufficient for 30 reactions
901667	GeneAtlas® Hybridization, Wash, and Stain Kit for WT Array Strips	Sufficient for 60 reactions
901622	GeneTitan® Hybridization, Wash, and Stain Kit for WT Array Plates	Sufficient for 96 reactions