DataSheet

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GeneChip® Mouse Gene 2.0 ST Array
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A whole-transcript design for the most comprehensive and accurate gene-level view of coding and long non-coding transcripts

Keeping pace with the research community's understanding of the transcriptome, Affymetrix has designed a whole-transcript array that includes probes to measure both messenger (mRNA) and long intergenic non-coding RNA transcripts (lincRNA).

This whole-transcript array design provides a complete expression profile of mRNA as well as a comprehensive view of the intermediary lincRNA that impact the mRNA expression profile.

Research over the past 20 years has predominantly focused on protein coding messenger RNA transcripts and their role in cellular processes, such as disease and development. Recently researchers have identified thousands of transcripts (>200 bases) with little or no protein coding potential. Only a small fraction of these non-coding RNAs has functional annotations to date.

There is, however, ample evidence that lincRNA play an important role in the genesis and progression of diseases, including cancer. Recent advancements in transcriptome profiling provided evidence of the association of lncRNAs in a diverse range of cellular functions such as:

- Regulation of mRNA transcription and transcriptional modifications

- Occlusion/recruitment of transcription factor binding

- Activation and transportation of transcription factors

- Interaction with accessory proteins

Benefits of these arrays are:

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

  - >30,000 coding and non-coding transcripts

  - >2,000 long intergenic non-coding transcripts

- 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	>26,500
NR and XR – RefSeq non-coding transcript, well-established and provisional annotations	>3,500
Total RefSeq transcripts	>30,000
RS (Entrez) gene count	>26,500
lincRNA transcripts	>2,000

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)
lncRNA db

Array design	
Total probes	>698,000
Exon-level probe sets	>263,000
Gene-level probe sets	>33,000
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
902462	GeneChip® Mouse Gene 2.0 ST Array and GeneChip® WT PLUS Reagent Kit	Sufficient for 10 samples
902463	GeneChip® Mouse Gene 2.0 ST Array and GeneChip® WT PLUS Reagent Kit	Sufficient for 30 samples
902120	Affymetrix® Mouse Gene 2.1 ST Array Strip	Contains one 4-array strip
902139	Affymetrix® Mouse Gene 2.1 ST 16-Array Plate and Trays	Contains one 16-array plate
902140	Affymetrix® Mouse Gene 2.1 ST 24-Array Plate and Trays	Contains one 24-array plate
902141	Affymetrix® Mouse 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