

## GeneChip® CHO Gene 2.0 ST Array Affymetrix® CHO Gene 2.1 ST Array Strip Affymetrix® CHO 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

The Chinese hamster ovary (CHO) cell lines were introduced in the 1960's and have become an extremely important tool for the research community and in biomedical manufacturing. Their rapid growth, stable gene expression profiles, and high protein production makes them ideal for both research studies and for the production of therapeutic proteins.

To help further your research and improve manufacture yield, Affymetrix has introduced the CHO gene 2.0 and 2.1 ST arrays. Affymetrix® gene ST expression array designs provide the highest coverage of the transcribed genome. We use a comprehensive collection of information sources to design probes that interrogate up to 26 unique sequences of each 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.

These organisms are the latest additions to the growing family of Affymetrix gene expression microarrays offering whole-transcript coverage. These unique designs are based on the most recent genome content and offer the highest probe coverage (up to 26 probes across the full length of the gene). This yields accurate detection for genome-wide transcript expression changes and provides higher resolution and accuracy than other classical 3'-biased microarray solutions on the market. The whole-transcriptome 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.

#### Key benefits:

- 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:
  - >16,900 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  $\geq 0.99$

#### 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 23 unique probes per transcript. Each unique probe is 25 bases in length, which means that the array measures a median of 575 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	
XM and NM – RefSeq coding transcripts, well-established and provisional annotations	>16,900
XR and NR – RefSeq non-coding transcripts, well-established and provisional annotations	>300
Total RefSeq transcripts	>17,200
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](http://www.affymetrix.com) to access this content.

Data sources used to design the array	
RefSeq (release 51)	
www.chogenome.org	

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

<sup>1</sup> 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.

Array design	
Total probes	>644,000
Exon-level probe sets	>135,000
Gene-level probe sets	>26,000
ERCC probe sets <sup>1</sup>	95
Background probes	Antigenomic set
Poly-A controls	<i>dap, lys, phe, thr</i>
Hybridization controls	<i>bioB, bioc, bioD, creX</i>
Total RNA input required	50–500 ng
Probe feature size	5 μm
Probe length	25-mer
Probes per gene (median)	23
Target RNA orientation	Sense target

<sup>1</sup> 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
902130	GeneChip® CHO Gene 2.0 ST Array	Contains 6 arrays
902131	GeneChip® CHO Gene 2.0 ST Array	Contains 30 arrays
902132	Affymetrix® CHO Gene 2.1 ST Array Strip	Contains one 4-array strip
902146	Affymetrix® CHO Gene 2.1 ST 24-Array Plate and Trays	Contains one 24-array plate
902147	Affymetrix® CHO 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

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