

GeneChip[®] Human Gene 2.0 ST Array Affymetrix[®] Human Gene 2.1 ST Array Strip Affymetrix[®] Human Gene 2.1 ST Array Plate

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 more than 10,000 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 lincRNAs 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:
 - >33,500 coding transcripts
 - >11,000 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 21 unique probes per transcript. Each unique probe is 25 bases in length, which means that the array measures a median of 525 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 | >33,500 |
| NR and XR – RefSeq non-coding transcript, well-established and provisional annotations | >6,500 |
| Total RefSeq transcripts | >40,000 |
| RS (Entrez) gene count | >25,000 |
| lincRNA transcripts ¹ | >11,000 |

¹ Derived from the Broad Institute's Human Body Map lincRNAs and TUCP (transcripts of uncertain coding potential) catalog and lincRNA db

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 | |
| Broad Institute, Human Body Map lincRNAs and TUCP (transcripts of uncertain coding potential) catalog | |

| 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.

| Array design | |
|------------------------------|-------------------------------|
| Total probes | >1.35 million |
| Exon-level probe sets | >418,000 |
| Gene-level probe sets | >48,000 |
| ERCC probe sets ¹ | 92 |
| 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) | 21 |
| Target RNA orientation | Sense target |

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 |
|-------------|---|-----------------------------|
| 902458 | GeneChip® Human Gene 2.0 ST Array and GeneChip® WT PLUS Reagent Kit | Sufficient for 10 samples |
| 902459 | GeneChip® Human Gene 2.0 ST Array and GeneChip® WT PLUS Reagent Kit | Sufficient for 30 samples |
| 902476 | GeneChip® Human Gene 2.0 ST Array and SensationPlus™ FFPE Amplification and WT Labeling Kit | Sufficient for 12 samples |
| 902477 | GeneChip® Human Gene 2.0 ST Array and SensationPlus™ FFPE Amplification and WT Labeling Kit | Sufficient for 24 samples |
| 902114 | Affymetrix® Human Gene 2.1 ST Array Strip | Contains one 4-array strip |
| 902136 | Affymetrix® Human Gene 2.1 ST 16-Array Plate and Trays | Contains one 16-array plate |
| 902137 | Affymetrix® Human Gene 2.1 ST 24-Array Plate and Trays | Contains one 24-array plate |
| 902138 | Affymetrix® Human 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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