

## Affymetrix<sup>®</sup> Gene 1.1 ST Array Strips for Human, Mouse, and Rat

Get the most complete view of the genome with whole-transcript expression array strips

**Affymetrix<sup>®</sup> Human, Mouse, and Rat Gene 1.1 ST Array Strips provide whole-transcript coverage in a convenient four-array strip format.**

**Whole-transcript microarrays, offered exclusively by Affymetrix, deliver the highest accuracy in gene expression profiling, the most complete view of cellular function, and detection of alternative splicing.**

**Designed for use with the GeneAtlas<sup>™</sup> System, Gene 1.1 ST Array Strips enable you to simplify parallel sample processing and increase productivity while leveraging the industry's most widely cited expression array designs.**

**The GeneAtlas System and array strips provide a complete, easy-to-use solution for processing microarrays and analyzing biological pathways.**

### Introduction

Affymetrix Human, Mouse, and Rat Gene 1.1 ST Array Strips offer the industry's highest quality expression technology and the ability to perform whole-transcript analysis by interrogating the entire gene for the discovery of alternative splicing events.

The GeneAtlas System enables you to process up to two strips per day or eight strips per week for maximum flexibility in low- to mid-throughput gene expression analysis studies. All array strips are supported by premium Affymetrix reagents and software and come with the necessary trays for hybridization, imaging, washing, and staining. Array strips demonstrate extremely high performance, with strong signal and fold change correlation between sample replicates.

Array strips provide:

- Maximum flexibility in a simplified workflow
- The ability to measure expression, across the entire gene, of more than 28,000 genes per sample
- Complete coverage of the annotated genome
- Accurate and reproducible data by using multiple independent measurements for each transcript

### Design and coverage

#### Human Gene 1.1 ST Array Strip

Each array is comprised of more than 750,000 unique 25-mer oligonucleotide probes that interrogate more than 28,000 genes. Discovery content, such as transcript regions supported by more speculative sources including expressed sequence tags (ESTs) and gene predictions, is not interrogated by the Human Gene 1.1 ST Array Strip.

The design is based on sequences and gene annotations obtained from several sources and used to group probes from the GeneChip<sup>®</sup> Human Exon 1.0 ST Array into new gene-level probe sets. In some cases, these sequences were used to select additional new probes. The sources were:

- March 2006 human genome sequence (UCSC hg18, NCBI v36)
- RefSeq NM (curated and provisional; not predicted) mRNA sequences (24,188 sequences) current to November 3, 2006
- GenBank<sup>®</sup> complete coding sequence mRNAs current to November 3, 2006 (56,249 sequences)
- Ensembl genome annotations from October 2006 (version 41.36c; 56,364 transcripts)

#### Mouse Gene 1.1 ST Array Strip

Each array is comprised of more than 770,000 unique 25-mer oligonucleotide probes that interrogate more than 28,000 genes. Discovery content, such as transcript regions supported by more speculative sources including expressed sequence tags (ESTs) and gene predictions, is not interrogated.

The design is based on sequences and gene annotations obtained from several sources and used to group probes from the GeneChip<sup>®</sup> Mouse Exon 1.0 ST Array into new gene-level probe sets. In some cases, these sequences were used to select additional new probes. The sources were:

- February 2006 mouse genome sequence (UCSC mm8, NCBI v36)
- RefSeq NM (curated and provisional; not predicted) mRNA sequences (19,719 sequences) current to April 3, 2007
- GenBank complete coding sequence mRNAs (35,257 sequences) current to November 13, 2006
- Mouse Ensembl transcripts current to April 3, 2007 (35,882 transcripts)
- Syntenically mapped full-length mRNAs and RefSeq NMs from human (68,820 sequences) and rat (20,409 sequences)

### Rat Gene 1.1 ST Array Strip

Each array is comprised of more than 720,000 unique 25-mer oligonucleotide probes that interrogate more than 27,000 genes. Discovery content, such as transcript regions supported by more speculative sources including expressed sequence tags (ESTs) and gene predictions, is not interrogated.

The design is based on sequences and gene annotations obtained from several sources and used to group probes from the GeneChip® Rat Exon 1.0 ST Array into new gene-level probe sets. In some cases, these sequences were used to select additional new probes. The sources were:

- November 2004 rat genome sequence (UCSC rn4, Baylor HGSC v3.4)
- RefSeq NM (curated and provisional; not predicted) mRNA sequences (10,084 sequences) current to April 3, 2007
- GenBank® complete coding sequence mRNAs (12,547 sequences) current to January 25, 2007
- Rat Ensembl transcripts current to April 3, 2007 (37,695 transcripts)
- Syntenically mapped full-length mRNAs and RefSeq NMs

### Performance

To demonstrate the performance of Human, Mouse, and Rat 1.1 ST Array Strips, cDNA targets were prepared from total RNA from various tissues using the protocols outlined in the *GeneAtlas™ WT Expression Kit User Manual* (Table 1). For human tissue samples, four tissue types with three biological replicates of each tissue type were used. For mouse and rat, three tissues with two biological replicates were tested.

Labeled target from each sample was pooled and hybridized to Human, Mouse, or Rat Gene 1.1 ST Array Strips, CEL files were

sketch-quantile normalized in Expression Console™ Software, and the RMA algorithm was used for probe set signal summarization. The Pearson correlation coefficient was calculated for comparisons of signal from replicate arrays within a strip or from the median signal for arrays from different strips.

Correlation coefficients were calculated using detected probe sets (DABG < 0.01). RMA signal was converted from log to linear scale to calculate the coefficient of variation (CV) for each probe set. The median CV was calculated from all probe sets. Affymetrix observed a median CV of less than 10 percent and a Pearson correlation coefficient for replicate arrays of greater than 0.990 (Tables 2 and 3, Figure 1).

**Table 1: Human, mouse, and rat total RNA samples.**

RNA	Supplier	Part number
Human brain	Ambion	AM7962
Human heart	Ambion	AM7966
Human prostate	Ambion	AM7988
Human testes	Ambion	AM7972
MAQC A (Universal Human Reference RNA)	Stratagene	740000
MAQC B (Human Brain Reference RNA)	Ambion	AM6050
Mouse brain	Stratagene	736001-41
Mouse heart	Ambion	AM7816
Mouse liver	Ambion	AM7810
Rat brain	Stratagene	737001-41
Rat heart	Ambion	AM7916
Rat liver	Ambion	AM7910

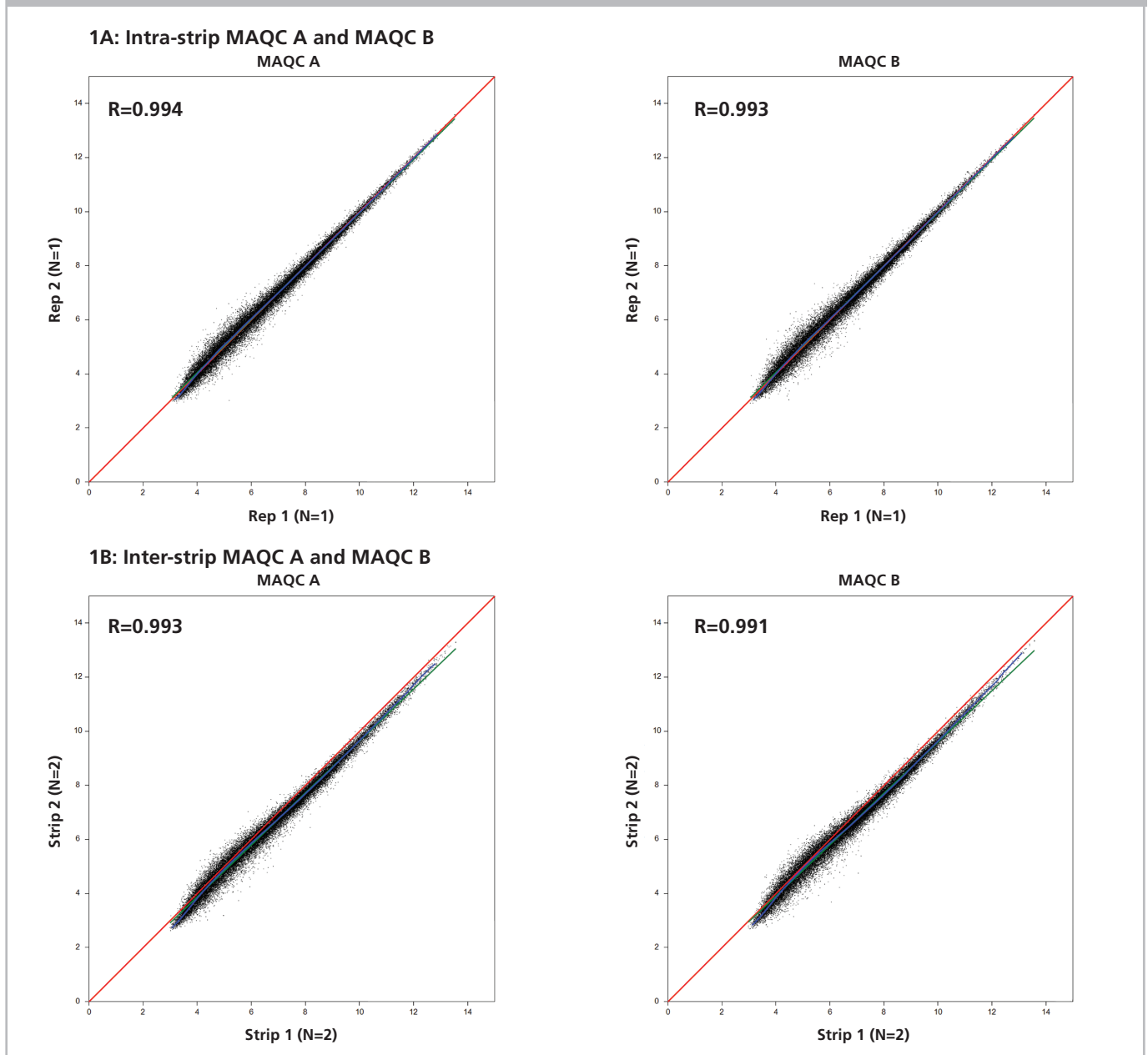
**Table 2: CV for human, mouse, and rat tissues.** Pooled, labeled target from the samples shown was hybridized in quadruplicate to Human, Mouse, or Rat Gene 1.1 ST Array Strips. RMA signal was converted from log to linear scale and the CV for each probe set was calculated from all replicates (N = 4). Median CV was calculated from all probe sets. Each sample represents a different biological replicate of the same tissue type.

Human Gene 1.1 ST Array Strip	Sample 1	Sample 2	Sample 3
Brain	6.1%	5.6%	8.3%
Heart	5.8%	5.8%	7.5%
Prostate	7.0%	5.6%	8.2%
Testes	4.6%	5.3%	8.0%
Mouse Gene 1.1 ST Array Strip			
Brain	6.4%	6.6%	N/A
Heart	6.2%	6.7%	N/A
Liver	6.7%	6.5%	N/A
Rat Gene 1.1 ST Array Strip			
Brain	6.2%	6.2%	N/A
Heart	8.0%	6.7%	N/A
Liver	5.6%	6.4%	N/A

**Table 3: Correlation coefficient for intra- and inter-array strips.** Pooled, labeled target from MAQC A and B was hybridized in duplicate to two Human Gene 1.1 ST Array Strips. Intra-array strip correlation coefficients were calculated from the RMA signal from two replicate arrays within each of the two strips. Inter-array strip correlation coefficients were calculated from the median RMA signal of duplicate arrays between strips.

Intra-strip	No. of replicates	MAQC A	MAQC B
Strip 1	1	0.994	0.993
Strip 2	1	0.993	0.991
Inter-strip	No. of replicates	MAQC A	MAQC B
Strips 1 and 2	2	0.993	0.991

**Figure 1: Signal correlation.** Scatter plots of RMA probe set signal comparing replicate hybridizations of MAQC A and MAQC B samples. The Pearson coefficient correlation (R) is calculated for each comparison (not all data shown).



## Specifications

	Human Gene 1.1 ST Array Strip	Mouse Gene 1.1 ST Array Strip	Rat Gene 1.1 ST Array Strip
Feature size	5 µm	5 µm	5 µm
Total number of distinct probes	764,885	770,317	722,254
Oligonucleotide probe length	25-mer	25-mer	25-mer
Required orientation of labeled targets to be hybridized to the array	Sense target	Sense target	Sense target
Resolution (number of probes per gene)	26 (median)	27 (median)	26 (median)
Estimated number of genes	28,875	28,853	27,342
Gene-level probe sets with Ensembl support	28,132	27,543	26,008
Gene-level probe sets with putative full-length transcript support (GenBank® and RefSeq)	19,734	19,434	9,916
Hybridization volume	120 µL	120 µL	120 µL
Positive controls (constitutively expressed genes)	1,195 putative exon-level probe sets from putative constitutive genes	1,324 putative exon-level probe sets from putative constitutive genes	399 putative exon-level probe sets from putative constitutive genes
Negative controls	2,904 putative intron-level probe sets from putative constitutive genes	5,222 putative intron-level probe sets from putative constitutive genes	1,153 putative intron-level probe sets from putative constitutive genes
Hybridization controls	<i>bioB</i> , <i>bioC</i> , <i>bioD</i> , <i>creX</i>	<i>bioB</i> , <i>bioC</i> , <i>bioD</i> , <i>creX</i>	<i>bioB</i> , <i>bioC</i> , <i>bioD</i> , <i>creX</i>
Background probes	Antigenomic set	Antigenomic set	Antigenomic set
Poly-A controls	<i>dap</i> , <i>lys</i> , <i>phe</i> , <i>thr</i> , <i>trp</i>	<i>dap</i> , <i>lys</i> , <i>phe</i> , <i>thr</i> , <i>trp</i>	<i>dap</i> , <i>lys</i> , <i>phe</i> , <i>thr</i> , <i>trp</i>
Library files	HuGene-1_1-st-v1 or newer	MoGene-1_1-st-v1 or newer	RaGene-1_1-st-v1 or newer

## Ordering information

Part number	Description	Details
901626	Affymetrix® Human Gene 1.1 ST Array Strip	Contains 1 four-array strip and necessary hybridization, wash, and scan trays
901628	Affymetrix® Mouse Gene 1.1 ST Array Strip	Contains 1 four-array strip and necessary hybridization, wash, and scan trays
901627	Affymetrix® Rat Gene 1.1 ST Array Strip	Contains 1 four-array strip and necessary hybridization, wash, and scan trays
901525	GeneChip® WT Terminal Labeling and Controls Kit	Sufficient for 10 reactions; contains GeneChip® WT Terminal Labeling Kit, Poly-A Control Kit, and Hybridization Control Kit
901524	GeneChip® WT Terminal Labeling and Controls Kit	Sufficient for 30 reactions; contains GeneChip® WT Terminal Labeling Kit, Poly-A Control Kit, and Hybridization Control Kit
901667	GeneAtlas™ Hybridization, Wash, and Stain Kit for WT Array Strips	Sufficient for 60 reactions
4411973	Ambion® WT Expression Kit*	10 reactions
4411974	Ambion® WT Expression Kit*	30 reactions

\*Must be ordered directly from Ambion, Inc.

## Related products

Part number	Description	Details
900670	GeneChip® WT Terminal Labeling Kit	Sufficient for 10 reactions
900671	GeneChip® WT Terminal Labeling Kit	Sufficient for 30 reactions
900433	GeneChip® Poly-A Control Kit	Sufficient for 100 reactions
900454	GeneChip® Hybridization Control Kit	Sufficient for 30 reactions

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