



Data Sheet

GeneChip® Made-to-Order Array Program

Enhanced Flexibility

Affymetrix is dedicated to providing you with high-quality, gene expression tools. The GeneChip® Made-to-Order Array Program gives you the flexibility to utilize arrays from selected custom designs and previous-generation Affymetrix® arrays no longer available as catalog products. Sequence information and probe set descriptions for Made-to-Order arrays can be accessed on the NetAffx™ Analysis Center at www.affymetrix.com. For previous-generation Affymetrix expression products, protein annotations are also provided. Probe sets from any of the Made-to-Order expression arrays are available for CustomExpress® array designs. Arrays offered through the GeneChip Made-to-Order Array Program are designed using Affymetrix rigorous probe selection and manufacturing standards to ensure optimal sensitivity, specificity, and reproducibility.

Ordering Information

GeneChip Made-to-Order arrays are listed to the right. Previous-generation catalog designs available as Made-to-Order arrays are ordered in whole-lot increments and are typically manufactured and shipped within four weeks. Select CustomExpress designs that are available as Made-to-Order arrays can be ordered in increments of six arrays. These arrays are typically shipped in two to four weeks. Please contact your Affymetrix Account Manager or Affymetrix Customer Service Representative to place your order.

GeneChip® Made-to-Order Arrays

	Select CustomExpress® Arrays	cDNA Synthesis Kit	Labeling Reagents
900515	GeneChip Barley Genome Array Order size: 6 arrays	GeneChip One- or Two-Cycle cDNA Synthesis Kits	3'-Amplification Reagent for IVT Labeling
900513	GeneChip <i>B. subtilis</i> Genome Array (Antisense) Order size: 6 arrays	See Expression Analysis Technical Manual	See Expression Analysis Technical Manual
900514	GeneChip <i>S. aureus</i> Genome Array Order size: 6 arrays	See Expression Analysis Technical Manual	See Expression Analysis Technical Manual
900516	GeneChip Human X3P Array Order size: 6 arrays	Arcturus Paradise™ Reagent System	3'-Amplification Reagent for IVT Labeling
	Previous-Generation Catalog Arrays	cDNA Synthesis Kit	Labeling Reagents
510429	GeneChip Arabidopsis Genome Array Order size: 40+/-5	GeneChip One- or Two-Cycle cDNA Synthesis Kits	3'-Amplification Reagent for IVT Labeling
511026	GeneChip <i>E. coli</i> Genome Array (Sense) Order size: 40+/-5	See Expression Analysis Technical Manual	See Expression Analysis Technical Manual
510559	GeneChip Human Genome U95Av2 Array Order size: 40+/-5	GeneChip One- or Two-Cycle cDNA Synthesis Kits	3'-Amplification Reagent for IVT Labeling
510462	GeneChip Human Genome U95B Array Order size: 40+/-5	GeneChip One- or Two-Cycle cDNA Synthesis Kits	3'-Amplification Reagent for IVT Labeling
510463	GeneChip Human Genome U95C Array Order size: 40+/-5	GeneChip One- or Two-Cycle cDNA Synthesis Kits	3'-Amplification Reagent for IVT Labeling
510464	GeneChip Human Genome U95D Array Order size: 40+/-5	GeneChip One- or Two-Cycle cDNA Synthesis Kits	3'-Amplification Reagent for IVT Labeling
510465	GeneChip Human Genome U95E Array Order size: 40+/-5	GeneChip One- or Two-Cycle cDNA Synthesis Kits	3'-Amplification Reagent for IVT Labeling
510137	GeneChip HuGeneFL Array Order size: 90+/-5	GeneChip One- or Two-Cycle cDNA Synthesis Kits	3'-Amplification Reagent for IVT Labeling
510332	GeneChip Human Cancer Array Order size: 90+/-5	GeneChip One- or Two-Cycle cDNA Synthesis Kits	3'-Amplification Reagent for IVT Labeling
510568	GeneChip Murine Genome U74Av2 Array Order size: 40+/-5	GeneChip One- or Two-Cycle cDNA Synthesis Kits	3'-Amplification Reagent for IVT Labeling

	<u>Previous-Generation Catalog Arrays</u>	<u>cDNA Synthesis Kit</u>	<u>Labeling Reagents</u>
510570	GeneChip Murine Genome U74Bv2 Array Order size: 40+/-5	GeneChip One- or Two-Cycle cDNA Synthesis Kits	3'-Amplification Reagent for IVT Labeling
510571	GeneChip Murine Genome U74Cv2 Array Order size: 40+/-5	GeneChip One- or Two-Cycle cDNA Synthesis Kits	3'-Amplification Reagent for IVT Labeling
510243 510244	GeneChip Murine 11K Array Mu11KsubA Mu11KsubB Order size: 40+/-5	GeneChip One- or Two-Cycle cDNA Synthesis Kits	3'-Amplification Reagent for IVT Labeling
510338	GeneChip Rat Genome U34A Array Order size: 40+/-5	GeneChip One- or Two-Cycle cDNA Synthesis Kits	3'-Amplification Reagent for IVT Labeling
510339	GeneChip Rat Genome U34B Array Order size: 40+/-5	GeneChip One- or Two-Cycle cDNA Synthesis Kits	3'-Amplification Reagent for IVT Labeling
510340	GeneChip Rat Genome U34C Array Order size: 40+/-5	GeneChip One- or Two-Cycle cDNA Synthesis Kits	3'-Amplification Reagent for IVT Labeling
510424	GeneChip Rat Neurobiology U34 Array Order size: 155+/-10 arrays	GeneChip One- or Two-Cycle cDNA Synthesis Kits	3'-Amplification Reagent for IVT Labeling
510330	GeneChip Rat Toxicology U34 Array Order size: 155+/-10 arrays	GeneChip One- or Two-Cycle cDNA Synthesis Kits	3'-Amplification Reagent for IVT Labeling

Select CustomExpress® Arrays

GeneChip® Barley Genome Array

The GeneChip® Barley Genome Array was designed and funded by the USDA-IFAFS Triticeae Improvement Group (R. Wise, T. Close, G. Muehlbauer, R. Wing, and A. Kleinhofs www.reeusda.gov/ifafs) in collaboration with Affymetrix and the international barley community. A community effort resulted in a significant improvement to sequence quality through better clustering and derived annotations.

Sequences used for the Barley Genome Array design were collected from consortia labs submitting EST sequences and by collecting sequences from the NCBI/

GenBank® non-redundant database. Approximately 400,000 raw barley ESTs were submitted from 84 libraries, and about 350,000 survived quality pruning.

Stringent CAP3 clustering (-p95 -d60 -f100 -h50) was performed and resulted in 53,030 “unigenes” (26,634 contigs and 26,396 singletons). 25,500 contigs and singletons had complete 3' ends suitable for array design (see HarvEST Triticeae v0.95 and higher). This included all 1,145 known barley genes (including alleles) from the NCBI non-redundant database. The non-redundant cloned gene set was integrated with the EST clusters to aid in

scaffolding the ESTs and also to retrieve any rare interesting genes (e.g., *Mla*, *Rar1*, *Sgt1*, *Rpg1*) for inclusion on the GeneChip microarray. After pruning against an enhanced Triticeae repeat element database (TREP), the exemplar set of 25,500 contigs and singletons was submitted to Affymetrix for initial computation.

Potential applications for the barley array include analysis of malting properties, pest and disease control, abiotic stress tolerance, nutritional characteristics, and reproductive development. The GeneChip Barley Genome Array was released in June 2003.

SPECIFICATIONS

Feature size:	18 micron
Oligo length:	25-mer
Probe pairs/gene:	11
Control sequences included:	— Hybridization controls: <i>bioB</i> , <i>bioC</i> , <i>bioD</i> from <i>E. coli</i> , and <i>cre</i> from P1 Bacteriophage — Poly-A controls: <i>dap</i> , <i>lys</i> , <i>phe</i> , <i>thr</i> , <i>trp</i> from <i>B. subtilis</i> — Barley maintenance genes: actin, GAPDH, ubiquitin, tubulin alpha subunit, and translation initiation factor 5A
Selected references:	— Matthews DE, Carollo VL, Lazo GR, Anderson OD. GrainGenes, the genome database for small-grain crops. <i>Nucleic Acids Res.</i> PMID: 12519977 <i>PubMed - indexed for MEDLINE</i> 31(1):183-6 (2003 Jan 1). — Ware DH, Jaiswal P, Ni J, Yap IV, Pan X, Clark KY, Teytelman L, Schmidt SC, Zhao W, Chang K, Cartinhour S, Stein LD, McCouch SR. Gramene, a tool for grass genomics. <i>Plant Physiol. Review.</i> PMID: 12481044 <i>PubMed - indexed for MEDLINE</i> 130(4):1606-13 (2002 Dec).

GeneChip *B. subtilis* Genome Array (Antisense)

The Affymetrix GeneChip *B. subtilis* Genome Array is a single array that enables the relative monitoring of mRNA transcripts from approximately 5,000 gene sequences from the bacterium *B. subtilis*. The array contains probe sets to interrogate approximately 4,350 ORFs and 600 intergenic

regions with an additional 45 control probe sets, and contains probes that are complementary to the labeled 1st strand cDNA target that is hybridized to the array. For preparing samples for hybridization it is recommended to use the *E. coli* Antisense protocol, an experimental protocol available through Affymetrix. This design was completed as a custom design for Genencor

International, Inc. in June 1998 and made available broadly in 2002. EST data for the design were from the *Bacillus subtilis* Genome Sequencing Project of the Institut Pasteur, Release 10.1, December 1997. Probe sets have been reannotated to the RefSeq genome sequence, NC_000964.

SPECIFICATIONS

Feature size:	28 micron
Oligo length:	25-mer
Probe pairs/gene:	~20 probe pairs
Control sequences included:	— <i>bioB</i> , <i>bioC</i> , <i>bioD</i> , and <i>cre</i> from P1 Bacteriophage — Poly-A controls: <i>dap</i> , <i>lys</i> , <i>phe</i> , <i>thr</i> , <i>trp</i> from <i>B. subtilis</i>
Selected references:	— Caldwell, R. <i>et al.</i> Correlation between <i>Bacillus subtilis</i> <i>scoC</i> phenotype and gene expression determined using microarrays for transcriptome analysis. <i>Bacteriol</i> 183 : 7371–80 (2001).

GeneChip *S. aureus* Genome Array (Antisense)

For comprehensive monitoring of the relative mRNA abundance of *S. aureus* sequences.

The GeneChip *S. aureus* Genome Array is useful for studying the expression of sequences in the following four strains of *Staphylococcus aureus*: N315 (National Institute of Technology and Evaluation, Japan), Mu50 (National Institute of

Technology and Evaluation, Japan), NCTC 8325 (OU, lab strain), and COL (TIGR). The open reading frames (ORFs) in all four strains were found *de novo* using Glimmer (standard settings) and a proprietary algorithm developed by Dr. Terry Gaasterland, Rockefeller Univ., called splice-ORF which is part of the Magpie sequence annotation system. This array was designed in collaboration with Pfizer

through the GeneChip® CustomExpress® program.

The array contains probe sets to over 3,300 *S. aureus* open reading frames. Additionally, the array also contains probes to study both forward and reverse orientation of over 4,800 intergenic regions throughout the *S. aureus* genome.

SPECIFICATIONS

Feature size:	18 micron
Oligo length:	25-mer
Probe pairs/gene:	20 pp per ORF; additional probe pairs spaced ~26 base pairs through intergenic regions
Control sequences included:	— Hybridization controls: <i>bioB</i> , <i>bioC</i> , <i>bioD</i> , and <i>cre</i> from P1 Bacteriophage — Poly-A controls: <i>dap</i> , <i>lys</i> , <i>phe</i> , <i>thr</i> , <i>trp</i> from <i>B. subtilis</i> — r2: <i>bioB</i> , <i>bioC</i> , <i>bioD</i> , <i>cre</i> , <i>dap</i> , <i>phe</i> and <i>thr</i>

GeneChip Human X3P Array

The GeneChip® X3P Array was designed specifically for whole-genome expression profiling of formalin fixed, paraffin-embedded (FFPE) samples.

Resulting from a collaboration between Affymetrix and Arcturus, this array is optimized as part of a system solution together with the Paradise™ Reagent System from Arcturus for expression analysis of FFPE samples.

FFPE samples introduce unique challenges for microarray analysis, including potential fragmentation and chemical

modification of RNA molecules. In order to overcome these challenges, the Paradise Reagent System was developed to provide RNA isolation and amplification reagents optimized for FFPE samples. In addition, the Human X3P Array is designed to focus on interrogating sequences located closer to the 3' end of the transcripts compared with standard GeneChip brand arrays. Together, the reagents and array accommodate the characteristics of the FFPE RNA samples, enabling genome-wide profiling.

The target sequences on the Human X3P arrays are identical to those used for

designing the Human Genome U133 Plus 2.0 Array, for a total of 47,000 transcripts with 61,000 probe sets, although the probes on the two types of arrays are significantly different.

As a result of the modification to the probe selection criteria, the majority of the probe sets on the Human X3P arrays are selected from the 300 bases at the most 3' end of the transcripts. This is different from the standard Affymetrix design strategy which selects probe sets within the region of 600 bases proximal to the 3' ends.

It was not possible to select optimal

probe sets within the shorter 300 base probe selection region for all 47,000 transcripts we wished to represent on the X3P Array. For 4,000 transcripts, two sets of probes are represented on the arrays to ensure that expression data would not be lost by incomplete representation of the

transcriptome should the less optimal probe set fail. In these cases, 3' probe sets from the shorter 300 base probe selection region and the original probe sets from the standard Human Genome U133 Plus 2.0 Array design are replicated on the X3P arrays.

In addition, 200 transcripts could not be represented with the new extreme 3' probe sets. These 200 transcripts are represented by the original probe sets from the standard Human Genome U133 Plus 2.0 Array.

SPECIFICATIONS

Feature size:	11 micron Instrument and Software Requirements — GeneChip® Scanner 3000, enabled for High-Resolution Scanning — GeneChip® Operating Software (GCOS) including the GeneChip Scanner 3000 High-Resolution Scanning Patch
Oligo length:	25-mer
Probe pairs/gene:	11
Control sequences included:	— Hybridization controls: <i>bioB</i> , <i>bioC</i> , <i>bioD</i> and <i>cre</i> from P1 Bacteriophage — Poly-A controls: <i>dap</i> , <i>lys</i> , <i>phe</i> , <i>thr</i> from <i>B. subtilis</i> — Normalization: 100 probe sets — Housekeeping: GAPDH, beta-Actin, ISGF-3 (STAT-1)

Previous-Generation Catalog Arrays

GeneChip Arabidopsis Genome Array

The Affymetrix GeneChip Arabidopsis Genome Array was the first-generation Arabidopsis array to monitor the relative abundance of mRNA transcripts of approximately 8,300 gene sequences. The sequences used to develop this array were obtained from GenBank in collaboration

with Novartis Agriculture Discovery Institute, Inc. (NADII). Eighty percent of the genes represented on the array are predicted coding sequences from genomic BAC entries. Twenty percent are high-quality cDNA sequences. The array also contains 100 EST clusters, sharing homology with the predicted coding sequences from BAC

clones. Affymetrix offers a second-generation Arabidopsis array, the GeneChip Arabidopsis ATH1 Genome Array, developed in collaboration with TIGR, that can monitor up to 24,000 gene sequences. Please visit www.affymetrix.com for more information.

SPECIFICATIONS

Feature size:	24 micron
Oligo length:	25-mer
Probe pairs/gene:	~16
Control sequences included:	— Hybridization controls: <i>bioB</i> , <i>bioC</i> , <i>bioD</i> from <i>E. coli</i> and <i>cre</i> from P1 Bacteriophage — Poly-A controls: <i>dap</i> , <i>lys</i> , <i>phe</i> , <i>thr</i> , <i>trp</i> from <i>B. subtilis</i> — Arabidopsis maintenance genes: actin, GAPDH, ubiquitin, 25 S rRNA, 5 S rRNA
Selected references:	— Zhu, T., Wang, X. Large-scale profiling of the Arabidopsis transcriptome. <i>Plant Physiol</i> 124 (4): 1472–6 (2000). — Harmer, S.L. Hogenesch, J.B., Straume, M., Chang, H.S., Han, B., Zhu, T., Wang, X., Kreps, J.A., Kay, S.A. Orchestrated transcription of key pathways in Arabidopsis by the circadian clock. <i>Science</i> 290 (5499): 2110–2113 (2000).

GeneChip *E. coli* Genome Array (Sense)

The *E. coli* Genome Array (Sense) can be used for examining expression of all known *E. coli* genes and discovering novel uncharacterized intergenic transcripts. The array contains probe sets to detect the sense

strand of more than 4,200 known open reading frames. In addition, over 1,350 intergenic sequences can be interrogated in both directions permitting functional characterization of potentially important shorter expressed sequences. Sequence

information for probes on the array correspond to the M49 version of the *E. coli* Genome Project database at the University of Wisconsin.

SPECIFICATIONS

Feature size:	24 micron
Oligo length:	25-mer
Probe pairs/gene:	~15
Control sequences included:	Poly-A controls: <i>dap</i> , <i>lys</i> , <i>phe</i> , <i>thr</i> , <i>trp</i> from <i>B. subtilis</i>
Selected references:	— Wassarman, K.M. <i>et al.</i> Identification of novel small RNAs using comparative genomics and microarrays. <i>Genes & Development</i> 15 :1637-1651 (2001). — Rosenow, C. Saxena, R.M., Durst, M., Gingeras, T.R. Prokaryotic RNA preparation methods, useful for high density array analysis: comparison of two approaches. <i>Nucleic Acids Research</i> , 29 (22):E112, (2001).

GeneChip Human Genome U95 Set

This set of five GeneChip probe arrays contains almost 63,000 probe sets interrogating approximately 54,000 UniGene

clusters derived from Build 95 of UniGene. Based on this UniGene build and associated annotations, the GeneChip Human Genome U95Av2 Array (HG-U95Av2)

represents approximately 10,000 full-length genes, while arrays B-E represent EST clusters.

SPECIFICATIONS

Number of arrays/set:	5
Feature size:	20 micron
Oligo length:	25-mer
Probe pairs/gene:	~16
Control sequences included:	— Hybridization controls: <i>bioB</i> , <i>bioC</i> , <i>bioD</i> , and <i>cre</i> from P1 Bacteriophage — Poly-A controls: <i>dap</i> , <i>lys</i> , <i>phe</i> , <i>thr</i> , <i>trp</i> from <i>B. subtilis</i> — Human maintenance genes: actin, GAPDH, transferrin receptor and ISGF-3
Selected references:	— Riewald, M. <i>et al.</i> Activation of endothelial cell protease activated receptor 1 by the protein C pathway. <i>Science</i> 296 (5574): 1800–2 (2002). — Cicala, C. <i>et al.</i> HIV envelope induces a cascade of cell signals in non-proliferating target cells that favor virus replication. <i>Proc Natl Acad Sci USA</i> 99 (14): 9380–5 (2002).

GeneChip HuGeneFL Array

The Affymetrix GeneChip HuGeneFL Array is a single array that enables the relative monitoring of mRNA transcripts

of approximately 5,600 full-length human genes. The full-length genes were selected from three databases: exemplars from UniGene Build 18 supplemented with

additional genes from GenBank and TIGR. This array was initially released by Affymetrix in November of 1998.

SPECIFICATIONS

Feature size:	24 micron
Oligo length:	25-mer
Probe pairs/gene:	~20
Control sequences included:	— Hybridization controls: <i>bioB</i> , <i>bioC</i> , <i>bioD</i> , and <i>cre</i> from P1 Bacteriophage — Poly-A controls: <i>dap</i> , <i>lys</i> , <i>phe</i> , <i>thr</i> , <i>trp</i> from <i>B. subtilis</i> — Human maintenance genes: actin, GAPDH, transferrin receptor
Selected references:	— Stamey, T.A., Warrington, J.A., Caldwell, M.C., Chen, Z., Mahadevappa, M., McNeal, J.E., Nolley, R., Zhang, Z. Molecular genetic profiling of Gleason grade 4/5 prostate cancers compared to benign prostatic hyperplasia. <i>Journal of Urology</i> 166 (6): 2171–2177 (2001). — Mutter, G.L., Baak, J.P., Fitzgerald, J.T., Gray, R., Neuberger, D., Kust, G.A., Gentleman, R., Gullans, S.R., Wei, L.J., Wilcox, M. Global expression changes of constitutive and hormonally regulated genes during endometrial neoplastic transformation. <i>Gynecologic Oncology</i> 83 (2): 177–185 (2001).

GeneChip Human Cancer G110 Array

This array enables focused and cost-effective expression studies in cancer biology. A panel

of leading cancer researchers selected the specific set of 1,700 full-length human genes implicated in cancer that comprise

this array. Accession numbers for sequences selected were selected from GenBank flat file release number 110.0.

SPECIFICATIONS

Feature size:	24 micron
Oligo length:	25-mer
Probe pairs/gene:	~16
Control sequences included:	— Hybridization controls: <i>bioB</i> , <i>bioC</i> , <i>bioD</i> from <i>E. coli</i> and <i>cre</i> from P1 Bacteriophage — Poly-A controls: <i>dap</i> , <i>lys</i> , <i>phe</i> , <i>thr</i> , <i>trp</i> from <i>B. subtilis</i> — Human maintenance genes: actin, GAPDH, transferrin receptor, transcription factor ISGF-3, 18 S rRNA, <i>alu</i>
Selected references:	— Paxton, W. <i>et al.</i> Reduced HIV-1 infectability of CD+4 lymphocytes from exposed-uninfected individuals: association with low expression of CCR5 and high expression of beta-chemokines. <i>Virology</i> 244 :66-73 (1998). — Golub, T. <i>et al.</i> Molecular classification of cancer: class discovery and class prediction by gene expression monitoring. <i>Science</i> 286 :531-537 (1999). — Harkin, P. <i>et al.</i> BRCA1 induces GADD45 and triggers JNK/SAPK-dependent apoptosis. <i>Cell</i> 97 :575-586 (1999). — Lee, S.B. <i>et al.</i> The Wilms tumor suppressor WT1 encodes a transcriptional activator of Amphiregulin. <i>Cell</i> 98 :663-673 (1999).

GeneChip Murine Genome U74v2 Set

The GeneChip Murine Genome U74v2 Set, consisting of three GeneChip® probe

arrays, contains probe sets interrogating approximately 36,000 full-length mouse genes and EST clusters from the UniGene

database (Build 74).

SPECIFICATIONS

Number of arrays/set:	3
Feature size:	20 micron
Oligo length:	25-mer
Probe pairs/gene:	~16
Control sequences included:	— Hybridization controls: <i>bioB</i> , <i>bioC</i> , <i>bioD</i> from <i>E. coli</i> and <i>cre</i> from P1 Bacteriophage — Poly-A controls: <i>dap</i> , <i>lys</i> , <i>phe</i> , <i>thr</i> , <i>trp</i> from <i>B. subtilis</i> — Murine maintenance genes: actin, GAPDH, hexkinase
Selected references:	— Molecular diversity of astrocytes with implications for neurological disorders. Bachoo, R. M. <i>et al. Proceedings of the National Academy of Sciences</i> 101 (22): 8384-9 (2004). — Efficient isolation and gene expression profiling of small numbers of neural crest stem cells and developing Schwann cells. Buchstaller, J. <i>et al. Journal of Neuroscience</i> 24 (10): 2357-65 (2004).

GeneChip Murine 11K Set

The Murine 11K Set represents over 11,000 full-length genes and EST clusters on two, high-density oligonucleotide arrays. The primary sequence source for this two-array set is UniGene database (Build 4).

SPECIFICATIONS

# of arrays/set:	2
Feature size:	24 micron
Oligo length:	25-mer
Probe pairs/gene:	~20
Control sequences included:	— Hybridization controls: <i>bioB</i> , <i>bioC</i> , <i>bioD</i> from <i>E. coli</i> and <i>cre</i> from P1 Bacteriophage — Poly-A controls: <i>dap</i> , <i>lys</i> , <i>phe</i> , <i>thr</i> , <i>trp</i> from <i>B. subtilis</i> — Murine maintenance genes: actin, GAPDH, hexokinase
Selected references:	— Voehringer, D.W. <i>et al.</i> Gene microarray identification of redox and mitochondrial elements that control resistance or sensitivity to apoptosis. <i>PNAS</i> 97 :2680-2685 (2000). — Simbulan-Rosenthal, C.M. <i>et al.</i> Misregulation of gene expression in primary fibroblasts lacking poly (ADP-ribose) polymerase. <i>PNAS</i> 97 :11274-11279 (2000). — Reilly, T.P. <i>et al.</i> Expression profiling of acetaminophen liver toxicity in mice using microarray technology. <i>Biochem Biophys Res Commun</i> 282 :321-328 (2001).

GeneChip Rat Genome U34 Set

The GeneChip Rat Genome U34 Set, consisting of three GeneChip arrays, contains probe sets interrogating more than 24,000 mRNA transcripts and EST clusters from the UniGene database (Build 34). Array A of the set analyzes approximately 7,000 full-length sequences and approximately 1,000 EST clusters. Arrays B and C each analyze approximately 8,000 EST clusters. All of the sequences analyzed by the Rat Toxicology U34 Array and the Rat Neurobiology U34 Array are also analyzed by Array A of this set.

SPECIFICATIONS

Number of arrays/set:	3
Feature size:	24 micron
Oligo length:	25-mer
Probe pairs/gene:	~16
Control sequences included:	— Hybridization controls: <i>bioB</i> , <i>bioC</i> , <i>bioD</i> from <i>E. coli</i> and <i>cre</i> from P1 Bacteriophage — Poly-A controls: <i>dap</i> , <i>lys</i> , <i>phe</i> , <i>thr</i> , <i>trp</i> from <i>B. subtilis</i> — Murine maintenance genes: actin, GAPDH, hexkinase
Selected references:	— Gene expression analysis points to hemostasis in livers of rats cotreated with lipopolysaccharide and ranitidine. Luyendyk, J. P. <i>et al. Toxicological Sciences</i> 80 : 203-13 (2004). — Patterns of gene expression reveal a temporally orchestrated wound healing response in the injured spinal cord. Velardo, M. J. <i>et al. Journal of Neuroscience</i> 24 (39): 8562-76 (2004).

GeneChip Rat Neurobiology U34 Array

The GeneChip Rat Neurobiology U34 Array contains over 1,200 sequences relevant to the study of neurobiology (including genes for kinases, cell surface

receptors, cytokines, growth factors, and oncogenes). The sequences were selected from the UniGene database (Build 34) in collaboration with academic and industrial

neuroscientists. All of the sequences represented on the Rat Neurobiology U34 Array are also represented on Array A of the Rat Genome U34 Set.

SPECIFICATIONS

# of arrays/set:	1
Feature size:	24 micron
Oligo length:	25-mer
Probe pairs/gene:	~16
Control sequences included:	— Hybridization controls: <i>bioB</i> , <i>bioC</i> , <i>bioD</i> from <i>E. coli</i> and <i>cre</i> from P1 Bacteriophage — Poly-A controls: <i>dap</i> , <i>lys</i> , <i>phe</i> , <i>thr</i> , <i>trp</i> from <i>B. subtilis</i> — Murine maintenance genes: actin, GAPDH, hexokinase
Selected references:	— Microarray analysis of acute and delayed gene expression profile in rats after focal ischemic brain injury and reperfusion. Lu, X. C. <i>et al. Journal of Neuroscience Research</i> 77(6): 843-57 (2004)

GeneChip Rat Toxicology U34 Array

The GeneChip Rat Toxicology U34 Array interrogates more than 850 mRNA transcripts and EST clusters from the

UniGene database (Build 34). Represented sequences were collaboratively selected with pharmaceutical toxicologists and from published scientific literature. All of the

sequences represented on the Rat Toxicology U34 Array are also represented on the Rat Genome U34A Array.

SPECIFICATIONS

Number of arrays/set:	1
Feature size:	24 micron
Oligo length:	25-mer
Probe pairs/gene:	~16
Control sequences included:	— Hybridization controls: <i>bioB</i> , <i>bioC</i> , <i>bioD</i> from <i>E. coli</i> and <i>cre</i> from P1 Bacteriophage — Poly-A controls: <i>dap</i> , <i>lys</i> , <i>phe</i> , <i>thr</i> , <i>trp</i> from <i>B. subtilis</i> — Murine maintenance genes: actin, GAPDH, hexkinase

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