AFFYMETRIX®

Data Sheet

GeneChip® Human Mapping 10K Array Xba 142 2.0

The GeneChip® Human Mapping 10K Array Xba 142 2.0 (GeneChip® Mapping 10K 2.0 Array) is a powerful SNP genotyping tool for investigating the genetics of simple and complex human disease. The GeneChip Human Mapping 10K 2.0 Array contains the content of the original Mapping 10K Array, but due to an evolutionary advancement in the original platform, the array is available at a more affordable price, enabling researchers to conduct SNP analysis at a cost comparable to research with microsatellites.

The major benefits of the Mapping 10K 2.0 Array include:

- Requires only 250 ng of genomic DNA per sample
- Easy-to-use, proven assay that has been validated in over 15 publications
- 10,000 SNPs provide higher information content for better results
- Export data in MERLIN- and GeneHunter-compatible formats
- Automated genotype calling with 99.6 percent accuracy on a proven platform
- Extensive SNP annotation in the NetAffx™ Analysis Center
- Cost comparable with microsatellite markers
- Better SNP coverage on chromosomes 19 and X

Introduction

The GeneChip® Mapping 10K 2.0 Array belongs to Affymetrix' suite of robust DNA Analysis products, which offer a rapid, accurate, and cost-effective solution for genetic research from whole-genome scans to focused genotyping and resequencing experiments.

Continual advancements in photolithography manufacturing technology enable Affymetrix to produce higher content on lower cost arrays. The new GeneChip Mapping 10K 2.0 Array contains equivalent content as the previous-generation Mapping 10K Array, but because it is manufactured with a smaller format, approximately 10,204 SNPs fit on the Mapping 10K 2.0 Array, compared to 11,555 on the original Mapping 10K Array. As with the original GeneChip Mapping 10K Array, the GeneChip Mapping 10K 2.0 Array can advance your research for applications including:

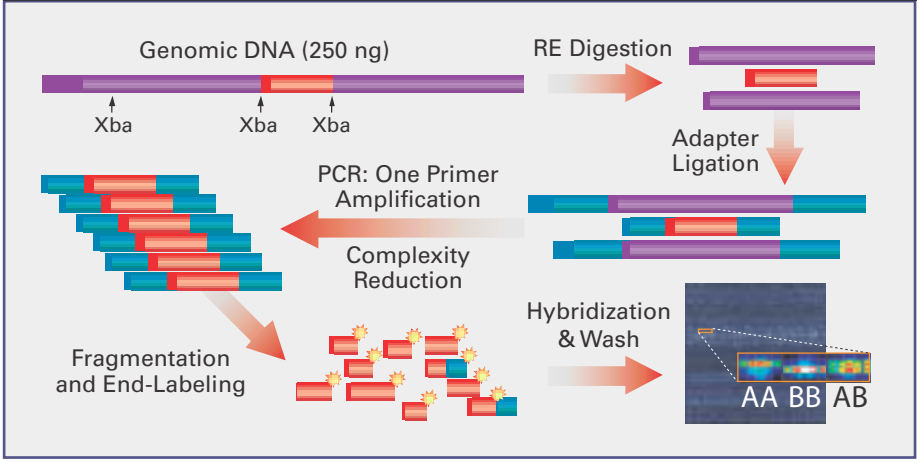
- Linkage analysis
- Cancer genetics
- Population genetics

PROVEN ASSAY ELIMINATES THE NEED FOR LOCUS-SPECIFIC PCR:

The GeneChip Mapping Assay uses a simple approach for reducing complexity of the genome, allowing efficient genotyping of over 10,000 SNPs on a single array. The assay uses basic steps as outlined in Figure 1 and below:

Total genomic DNA (250 ng) is digested with a restriction enzyme (XbaI) and ligated to adapters that recognize the cohesive four basepair (bp) overhangs. All fragments resulting from restriction enzyme digestion, regardless of size, are substrates for adapter ligation. A generic primer that recognizes the adapter sequence is used to amplify adapter ligated DNA fragments.

Figure 1: GeneChip® Mapping Assay Overview.



PCR conditions have been optimized to preferentially amplify fragments in the 250 to 1,000 bp size range. The amplified DNA is then fragmented, labeled, and hybridized to the GeneChip Mapping 10K 2.0 Array.

SNP SELECTION AND GENOME COVERAGE

Content on the Mapping 10K 2.0 Array is almost identical to content on the previous-generation GeneChip Mapping 10K Array. Most of the SNPs on the Mapping 10K 2.0 Array are from The SNP Consortium (TSC) database and lie within one of the 250 to 1,000 base XbaI fragments amplified by the Mapping Assay. Fourteen hundred of the 11,555 SNPs on the original GeneChip Mapping 10K Array were removed because the new array can accommodate approximately 10,200 SNPs. These SNPs were removed based on relatively lower call rates or close proximity to other SNPs. In addition, approximately seventy new SNPs from Perlegen Sciences, Inc. and public databases were added to supply additional genome coverage.

MORE POWER FROM 10,000 GENOTYPES

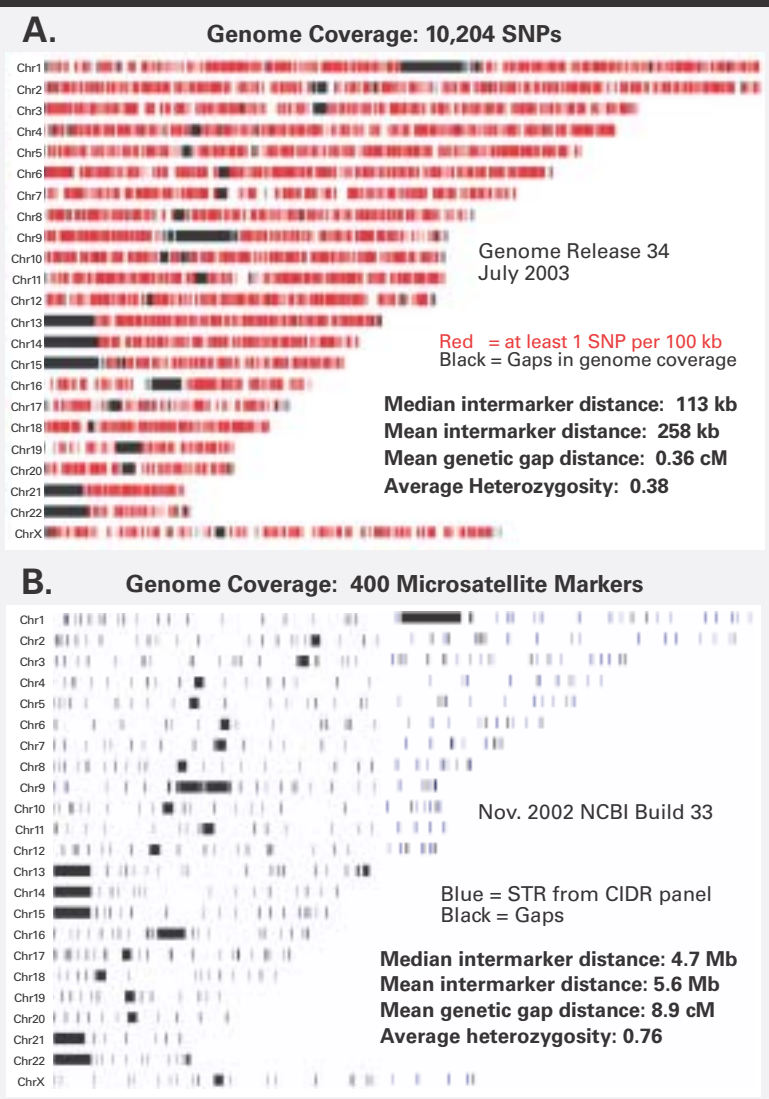
Marker informativeness varies from population to population and family to family. However, the performance of the 10,000 SNPs on the GeneChip Mapping 10K 2.0 Array has been validated across a wide range of populations and ethnicities to ensure sufficient coverage and meaningful data for linkage analysis studies. The Mapping 10K 2.0 Array provides significant genetic power for higher experimental success rates, including the identification of additional loci, and decreased linkage intervals.

Customers can expect call rates greater than or equal to 92 percent. Internal validation studies consistently result in call rates of over 97 percent over more than 150 individuals from Caucasian, African American, and Asian populations.

USE LESS DNA STARTING MATERIAL

The GeneChip Mapping Assay requires only 250 ng genomic DNA as starting material for the entire assay.

Figure 2: A. Genome Coverage of Mapping 10K 2.0 SNPs by chromosome. Black areas represent gaps in the human genome sequence, primarily centromeres and telomeres. **B.** Genome coverage of 400 microsatellite markers from the CIDR panel, by chromosome.



HIGHLY ACCURATE AND REPRODUCIBLE

Results on the GeneChip Mapping 10K 2.0 Array are 99.9 percent concordant with the previous-generation Mapping 10K Array, which showed >99.6 percent concordance across >21,000 reference genotypes generated by single-base extension and capillary sequencing.

Six samples from three different ethnic groups were run in triplicate on three different wafer lots for a total of nine arrays for each sample. Reproducibility was calculated for each triplicate on each wafer lot, averaged among lots, and found to be 99.99 percent.

AUTOMATED GENOTYPE CALLS IN SOFTWARE

The GeneChip Mapping 10K 2.0 Array is compatible with the GeneChip® DNA Analysis Software 2.0 (GDAS 2.0) or greater. GDAS 2.0 uses an automated genotype calling algorithm that provides a quality score for each individual genotype. This algorithm was developed and validated as part of the entire Mapping 10K System.

GDAS 3.0 SUPPORTS FAMILY-BASED STUDIES

GDAS 3.0 incorporates advanced functionality that supports family-based studies. Researchers can batch import pedigree and other sample information, check for Mendelian errors, and export the data into MERLIN- or GeneHunter-compatible formats.

SNP ANNOTATION AVAILABLE THROUGH THE NETAFFX™ ANALYSIS CENTER

Extensive annotation for each SNP is provided within both GDAS 2.0/3.0 and in the NetAffx™ Analysis Center, which is freely available. The NetAffx Analysis Center combines data from multiple sources within the public domain and consolidates it into a single database, providing a level of standardization that facilitates collaboration and sharing of data.

SNP annotation includes TSC ID, dbSNP ID, nearest microsatellite markers, nearest gene, physical map location, cytoband, genetic map location, and allele frequencies in multiple populations.

ARRAY SPECIFICATIONS

Each array includes more than 420,000 features, each consisting of more than one million copies of a 25 bp oligonucleotide probe of a defined sequence, synthesized in parallel by proven photolithographic manufacturing. Each SNP is interrogated by five probe quartets. Each quartet is comprised of four pairs of Perfect Match and Mismatch probes for a total of 40 different 25 bp oligonucleotides for each SNP. Each of the 40 probes has a slight variation in perfect matches, mismatches, and flanking sequence around the SNP.

NEW APPLICATIONS BUILT FOR THE GENECHIP® 2.0 PLATFORM

The GeneChip Mapping 10K 2.0 Array runs on the GeneChip 2.0 Platform. Therefore, it is compatible with the GeneChip® Fluidics Station 450, the GeneChip Scanner 3000 with the complimentary High-Resolution Update, and the GeneChip AutoLoader. The Mapping 10K 2.0 Array is also compatible with the previous-generation GeneChip Fluidics Station 400.

Critical Specifications	
DNA Required	250 ng per sample
Number of SNPs on Array	10,204
Call Rate	≥92%
Reproducibility	≥99.96%
Concordance with Reference Genotypes	≥99.6%
Genotype Calling	Automated with confidence score
SNP Annotation	NetAffx™ Analysis Center
PCR Primers	1 per sample
PCR Reactions	4 per sample
Capital Equipment	GeneChip® 2.0 Platform

REAGENT KIT VALIDATED AS PART OF THE MAPPING 10K SYSTEM

The GeneChip Mapping 10K 2.0 Array uses the same Reagent Kit as the previous-generation GeneChip Mapping 10K Array. The GeneChip Mapping Assay Kit contains validated and qualified reagents for the most critical steps in the GeneChip Mapping Assay. The kit was developed and validated during the process of developing the Mapping 10K System.

REFERENCE GENOMIC DNA SERVES AS A PROCESS CONTROL

Each GeneChip Mapping 10K Xba Assay Kit contains a sample of human genomic DNA to serve as a control for the entire process from DNA to data, as well as for troubleshooting. Customers can expect a call rate of greater than or equal to 92 percent when using this DNA in their lab. In addition, Affymetrix provides the consensus genotypes for this sample from five independent replicates.

REAGENT KIT PACKAGING DESIGNED TO MINIMIZE DNA CROSS CONTAMINATION

As with all genotyping applications, DNA cross contamination is a concern, as it can lead to genotyping errors and, therefore, a reduction in genetic power. The GeneChip Mapping 10K Xba Assay Kit is subdivided into three boxes to support a recommended workflow designed to minimize the possibility of DNA contamination. Additionally, the GDAS 2.0 or greater software provides a report to help identify samples that may have otherwise undetected DNA cross contamination.

SAMPLE THROUGHPUT

With the standard instrument configuration of one scanner and two fluidics stations, one person can typically process 96 samples per week from DNA to data. The modular GeneChip System can be easily expanded to accommodate high-throughput needs enabling tens of thousands of samples per year.

GeneChip® Mapping 10K Xba Assay Kit Components
Adapter, Xba
PCR Primer 001
Reference Genomic DNA, 103
GeneChip® Fragmentation Reagent
10X Fragmentation Buffer
GeneChip® DNA Labeling Reagent fragmented PCR amplicons
Terminal Deoxynucleotidyl Transferase
5X Terminal Deoxynucleotidyl Transferase Buffer
Oligonucleotide Control Reagent

Proof is in the Publication

The GeneChip® Mapping 10K 2.0 Array provides better results with less work. In less than a year since its launch, the Mapping 10K Array and Assay have been featured in over 15 published studies.

• Mapping 10K Array uses a proven assay to process > 96 samples a week	Large-Scale Genotyping of Complex DNA. G.C. Kennedy, *et al.*, *Nature Biotechnology* **21**: 1233–1237 (2003).
• Requires only 250 ng DNA **• Automated genotype calls provide >99.5% accuracy**	Parallel Genotyping of over 10,000 SNPs using a One-Primer Assay on a High-Density Oligonucleotide Array. H. Matsuzaki, *et al.*, Genome Research **3**: 414-25 (2004).
• Mapping 10K Array finds new loci missed by previous microsatellite scans	A Novel Gene for Neonatal Diabetes Maps to Chromosome 10p12.1p13. G.S. Sellick, *et al.*, *Diabetes* **52**: 2636-38 (2003).
• Validates previous microsatellite linkage data with decreased linkage intervals	Genome Wide Linkage Analysis of Bipolar Disorder Using High Density Single Nucleotide Polymorphisms (SNP) Genotyping Arrays: A Comparison with Microsatellite Markers and the Finding of a Significant Linkage to Chromosome 6q22. F.A. Middleton, *et al.*, *American Journal of Human Genetics* **5**: 886-97 (2004).
• Requires less fine mapping	Whole Genome Scan in a Complex Disease Using 11,245 SNPs: Comparison to Microsatellites. Shepard, J.S., *et al.*, *American Journal of Human Genetics* **75**: 54-64 (2004).
• The Mapping 10K Array enables you to quickly clone genes following linkage studies	A HOX Gene Mutation in a Family with Isolated Congenital Vertical Talus and Charcot-Marie-Tooth Disease. A.E. Shrimpton, *et al.*, *American Journal of Human Genetics* **75**: 92-96 (2004). Mapping of Sudden Infant death with Dysgenesis of the Testes Syndrome (SIDDT) by a high-density SNP genome scan and identification of TSPYL loss-of-function. E. Puffenberger, *et al.*, *PNAS* 2004: in press. Missense Mutations of ACTA 1 Cause Dominant Congenital Myopathy with Cores A. M. Kaindl, *et al.*, *Journal of Medical Genetics* 2004: in press. Mutations in VPS33B, Encoding a Regulator of SNARE-Dependent Membrane Fusion, Cause Arthrogryposis-Renal Dysfunction-Cholestasis (ARC) Syndrome. G. P, Johnson *et al.*, *Nature Genetics* **36**(4):400-4, 2004 Epub 2004 Mar 28.
• Detect regions of chromosomal deletion, amplification, and loss of heterozygosity during cancer progression	An integrated view of copy number and allelic alterations in the cancer genome using single nucleotide polymorphism arrays. Zhao X, *et al.*, *Cancer Research* **64**(9): 3060-71 (2004).

Ordering Information

GeneChip® Human Mapping 10K Array and Assay Kit

GeneChip® Human Mapping 10K Array Xba 142 2.0

900540 *Contains 30 GeneChip® Mapping 10K 2.0 Arrays*

GeneChip® Mapping 10K Xba Assay Kit

900441 *Sufficient for 30 reactions*

Supporting Products

GeneChip® Operating Software (GCOS)

690031 *GCOS is the core operating software for the GeneChip system providing instrument control, image analysis, work-flow/ sample management, and expression analysis*

GeneChip® DNA Analysis Software (GDAS)

690030 *GDAS provides data analysis for Affymetrix GeneChip DNA arrays, including automated SNP and sequence analysis with quality scores*

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