



Data Sheet

GeneChip® CustomSeq™ Resequencing Arrays

Redefining Large-Scale Comparative Sequencing

CustomSeq™ Resequencing Arrays provide an efficient and cost-effective method for resequencing large amounts of DNA. This array presents the opportunity to sequence 30,000 bases of user-specified sequence. Utilizing Affymetrix' core technology and manufacturing superiority, CustomSeq arrays deliver the highest quality sequencing data to your bench top.

Benefits of CustomSeq™ Arrays Array Profile

MORE INFORMATION PER EXPERIMENT

CustomSeq arrays enable the analysis of up to 30,000 bases of double-stranded sequence (60,000 bases total) on a single array, providing the most efficient and cost-effective method of interrogating large amounts of sequence in a single experiment. The selected sequences may cover a single contiguous sequence, or multiple dispersed fragments, facilitating the analysis of either large chromosomal regions or multiple genes on a single array.

MORE EFFICIENT AND COST-EFFECTIVE SEQUENCE ANALYSIS

CustomSeq arrays provide customers with a faster, more efficient way to perform large-

scale resequencing while reducing the overall cost per base. CustomSeq arrays deliver complete sequence within 48 hours with minimal alignment, curation, or hand editing. A single array experiment delivers the equivalent to sequencing approximately 60,000 bases by traditional methods.

HIGH ACCURACY

CustomSeq arrays provide base calls at >99.99% accuracy when compared to capillary sequencing.

HIGH QUALITY AND REPRODUCIBILITY

Built on Affymetrix' proven photolithographic manufacturing process and strict quality control standards, CustomSeq arrays provide the same high quality that has made GeneChip® arrays the industry standard in

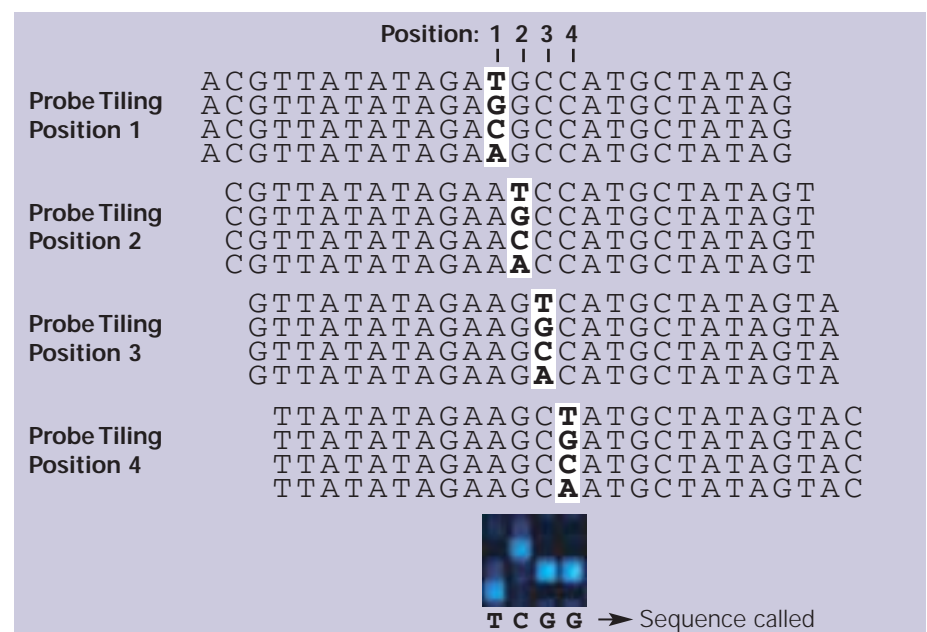


Figure 1: CustomSeq™ arrays tile four probes per strand for each individual base. The central position of each probe varies to incorporate each of the four possible nucleotides—A, C, G, or T.

microarrays—replicate experiments demonstrate >99.99% reproducibility. This reliability enables identification of single nucleotide polymorphisms (SNPs) across various populations and facilitates the comparison of data across multiple experiments.

IDENTIFY AND GENOTYPE SNPS IN A SINGLE EXPERIMENT

CustomSeq arrays tile all four probes for each individual base on both strands. The central position of each probe varies to incorporate each of the four possible nucleotides—A, C, G, or T (Figure 1). This tiling strategy provides, in a single experiment, both complete sequencing of each strand and identification of any known or novel SNPs.

Applications

CustomSeq™ arrays are virtually limitless in their potential to support a variety of resequencing applications.

COMPLETE SEQUENCE ANALYSIS OF LARGE GENOMIC REGIONS

Nucleotide analysis of chromosomal regions was previously considered too onerous by traditional sequencing methods. CustomSeq arrays deliver 30,000 bases of double-stranded sequence in a single hybridization, facilitating large scale resequencing experiments.

CANDIDATE GENE ANALYSIS

Candidate gene studies are often limited to genotyping only a small set of known mutations. Using CustomSeq arrays, scientists are now able to broaden the experimental scope to analyze complete sequence and genotype information in a single experiment.

PHARMACOGENETIC STUDIES

Analysis of genetic variation within clinical trial populations requires high data quality and reproducibility. CustomSeq arrays facilitate the comparison of data across populations and experiments.

CustomSeq™ Array Design Process

1. Select Sequence

- Download from public or proprietary databases

```
ACGTCGTAGTGCTCGTAACGCTATG
ACGATCGATGCTACGACTACGATCG
TACACGTCGATCGTAGCTACGATCG
TAGTCTCGTAGCTACGTAGCTAGCTA
GTACGATCGATCGATCGACTGACTA
AGCCGATGCTAGCTAGTAGCTGACT
```

2. Select and Test Primers

- LR PCR recommended

```
ACGTCGTAGTGCTCGTAACGCTATG
ACGATCGATGCTACGACTACGATCG
TACACGTCGATCGTAGCTACGATCG
TAGTCTCGTAGCTACGTAGCTAGCTA
GTACGATCGATCGATCGACTGACTA
AGCCGATGCTAGCTAGTAGCTGACT
```



3. Format and Submit sequence

- FASTA format
- Remove ambiguous sequence
- Remove repetitive elements
- Screen for homology

```
>AA618977
gttttgtctttggttaaagtacctt
ttctagttcccgaatggcttatgat
gataagttgttgtgtgagaatcatt
tcgtatagctctgatyaactggttta

>AA618981
agatcttcggactatctgatgaaga
acgacgacagcggaacgtgagatag
tgtgttatgttgccctggatttcga
gttcggcgttgagaagagttatga
```

4. Affymetrix QC Design — Design Confirmed

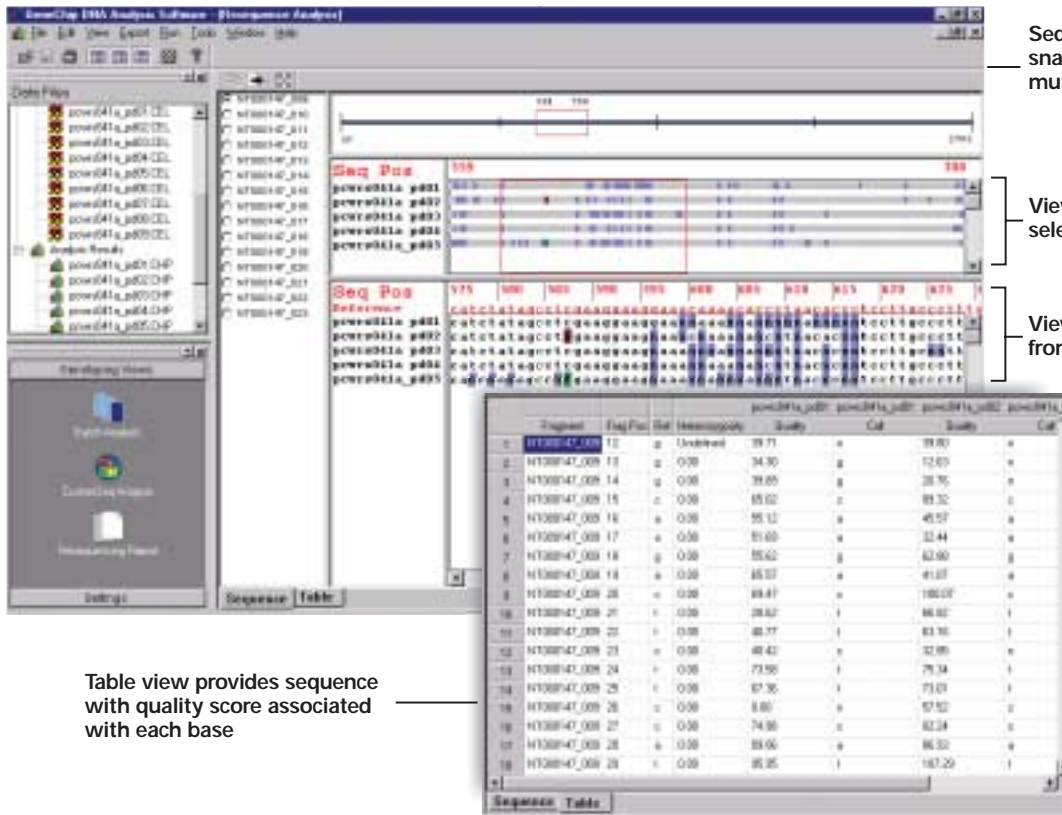
5. Array Manufactured and Shipped (eight weeks)



CustomSeq™ Array Benefits

- High Quality → >99.99% Reproducibility
- High Accuracy → >99.99%
- High Call Rate → >90%*
- Flexible → Contiguous or dispersed fragments
Multiple organisms
- More information in one experiment → ~30 Kb unique sequence, 60 Kb of total information on a single array

*Call rate may vary depending on genomic sequence



Sequence viewer provides a snapshot of sequence across multiple samples

View SNPs from region selected above

View individual base calls from region selected above

Table view provides sequence with quality score associated with each base

PATHOGEN SUBTYPING

Mutation analysis of microorganisms requires technology that genotypes for known mutations and identifies novel SNPs. CustomSeq arrays allow researchers to analyze whole sequence and identify known and new mutants that may contribute to the pathogenicity, or therapeutic resistance, of an organism.

REFERENCES

D.J. Cutler, et al. High-throughput variation detection and genotyping using microarrays. *Genome Res* 11(11): 1913-25 (2001).

J.A. Warrington, et al. New developments in high-throughput resequencing and variation detection using high-density microarrays. *Hum Mutat* 19: 402-9 (2002).

Critical Specifications

Feature size	20 x 25 µm
Array size	Standard
Oligonucleotide probe length	25-mer
Probes per base	8
Controls	Tag IQ Ex Oligo B2

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