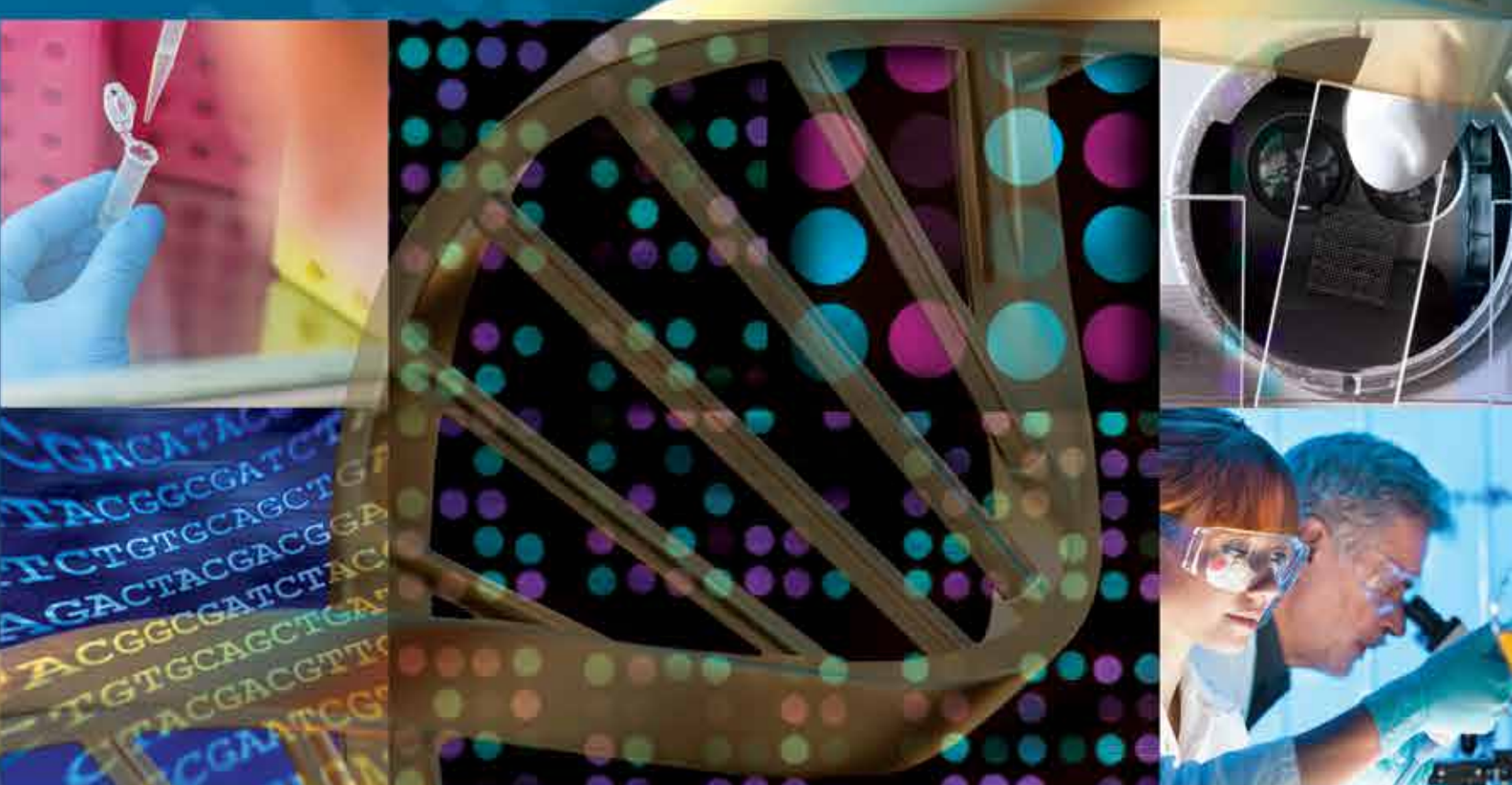
Baylor Miraca
Genetics Laboratories

Chromosomal Microarray Analysis

(Array Comparative Genomic Hybridization)



Baylor Miraca Genetics Laboratories (BMGL) continues to provide high quality state of the art testing to the medical community through Chomosomal Microarray Analysis Products. We were one of the first to offer CMA for clinical applications and we remain a leader in the implementation of new technology for CMA.

BMGL has several arrays designed to provide you with the most up to date technology and sophistication patients demand. **Our arrays are custom designed to provide the highest detection rates possible.** We have incorporated features such as exon coverage, whole genome coverage, SNP analysis for AOH/UPD, mitochondrial genome coverage, microRNAs, and other unique features that collectively yield the most comprehensive array analysis possible. In addition, BMGL custom designed arrays cover all subtelomere regions as well as pericentromic regions.

- **CMA-HR + SNP Screen (Comprehensive)**
  High Resolution Copy Number plus SNP
- **CMA-HR**
  High Resolution Copy Number Analysis Array
- **CMA-SNP**
  For UPD and Copy Number Analysis

Specimen Requirements:

Please refer to web site for specific requirements: *www.BMGL.com*

Turnaround Time:

Turnaround times are available on our web site: *www.BMGL.com*

Shipping Information

Forms: Requisition and signed consent form must accompany specimen. Prior to any genetic testing, we recommend discussion of the risks and benefits of testing with a physician or genetic counselor.

To receive our forms, additional information, or kits, please contact our laboratory: *1-800-411-GENE.*

Baylor Miraca Genetics Laboratories
2450 Holcombe
Grand Blvd. - Receiving Dock
Houston, Texas 77021-2024

CMA-HR

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CMA-HR

- High resolution copy number analysis
- Custom BCM design-180K Agilent

BENEFITS

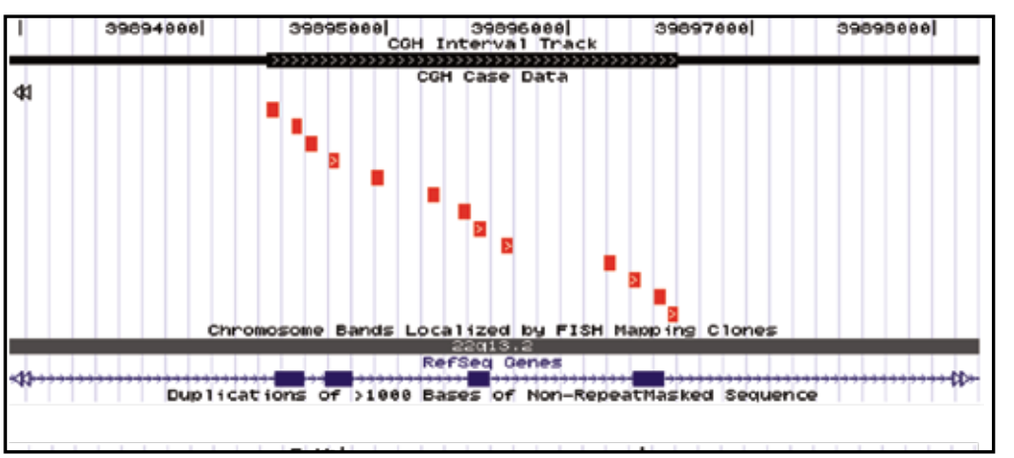
- Maximum sensitivity for detection of gains and losses
- 700 microRNAs
- Exon by exon coverage of over 1700 genes
- Tiling coverage of Mitochondrial Genome
- Whole genome coverage at a 30 kb resolution

Limitations: Does not detect absence of heterozygosity (AOH), uniparental disomy (UPD), or consanguinity.

With this design, we can detect intragenic single exon deletions and duplications that would otherwise be missed. This level of detail is ONLY available on the Baylor CMA-HR, and CMA-HR + SNP.

Exon 24-27 Deletion within EP300

Rubinstein-Taybi syndrome



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CMA-SNP

CMA-SNP

- Excellent SNP coverage
- Affymetrix-CytoScan® HD

BENEFITS

- Detection of absence of heterozygosity (AOH) associated with uniparental disomy (UPD) or consanguinity
- Copy number coverage for classical deletion/duplication syndromes and detection of novel variants over 300 kb

Limitations: Does not detect small copy number changes in regions outside classical deletion/duplication loci.

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CMA-HR + SNP SCREEN (COMPREHENSIVE)

- High resolution copy number analysis + SNPs (for detection of AOH & UPD)
- Custom BCM design - 400K Agilent

BENEFITS

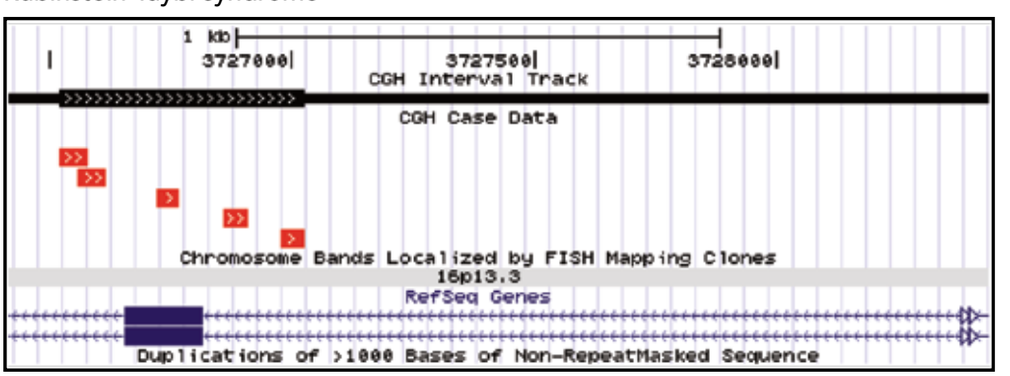
- Maximum sensitivity for detection of gains and losses
- 700 microRNAs
- Exon by exon coverage of over 4,200 genes
- Tiling coverage of Mitochondrial Genome
- Whole genome coverage at a 30 kb resolution
- Detection of absence of heterozygosity (AOH) associated with uniparental disomy (UPD) or consanguinity
- 38 non-coding regulatory regions

Limitations: AOH less than 5Mb in size will not be reported. The detection rate of heterodisomies is currently not known for this assay.

With this design, we can detect intragenic single exon deletions and duplications that would otherwise be missed. This level of detail is ONLY available on the Baylor CMA-HR, and CMA-HR + SNP.

Exon 27 Deletion within CREBBP

Rubinstein-Taybi syndrome



CMA–HR + SNP SCREEN (COMPREHENSIVE)

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CMA–HR + SNP SCREEN (COMPREHENSIVE)

For the first time ever, high resolution exon by exon copy number and SNP analysis is available from one array. The CMA-HR + SNP (Comprehensive) offers exon level deletion/duplication analysis for over 4,200 genes, and includes 57,000 probes used for SNP analysis. The SNP data will detect absence of heterozygosity (AOH) that is seen with consanguinity or uniparental disomy (UPD). Each patient will now benefit from both technologies, removing the obstacle of choosing one over the other. This combination of exon copy number and SNP data represents the most significant advance in array technology since the introduction of oligonucleotides.

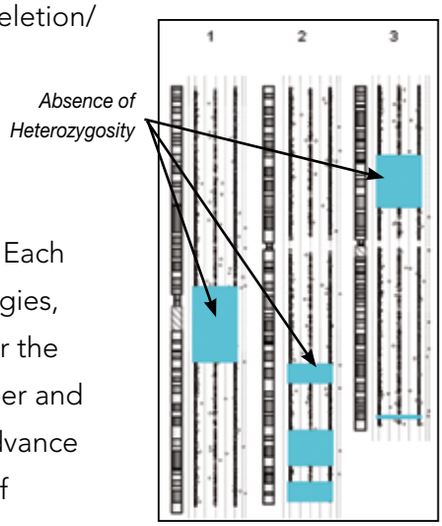
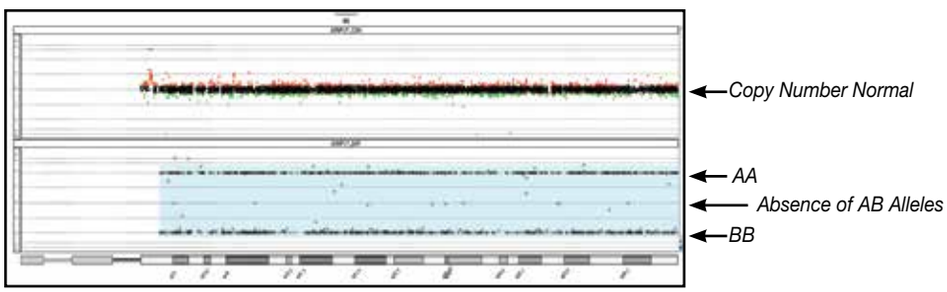


Figure 1: Chromosomes 1-3 for a first cousin offspring.

Figure 2: UPD 15.



SUPERIOR COPY NUMBER DATA

- 280,000 oligos chosen for optimum data quality
- Exon by exon coverage for over 4,200 genes associated with MR, developmental delay, heart defects, etc.
- 38 non-coding regulatory regions

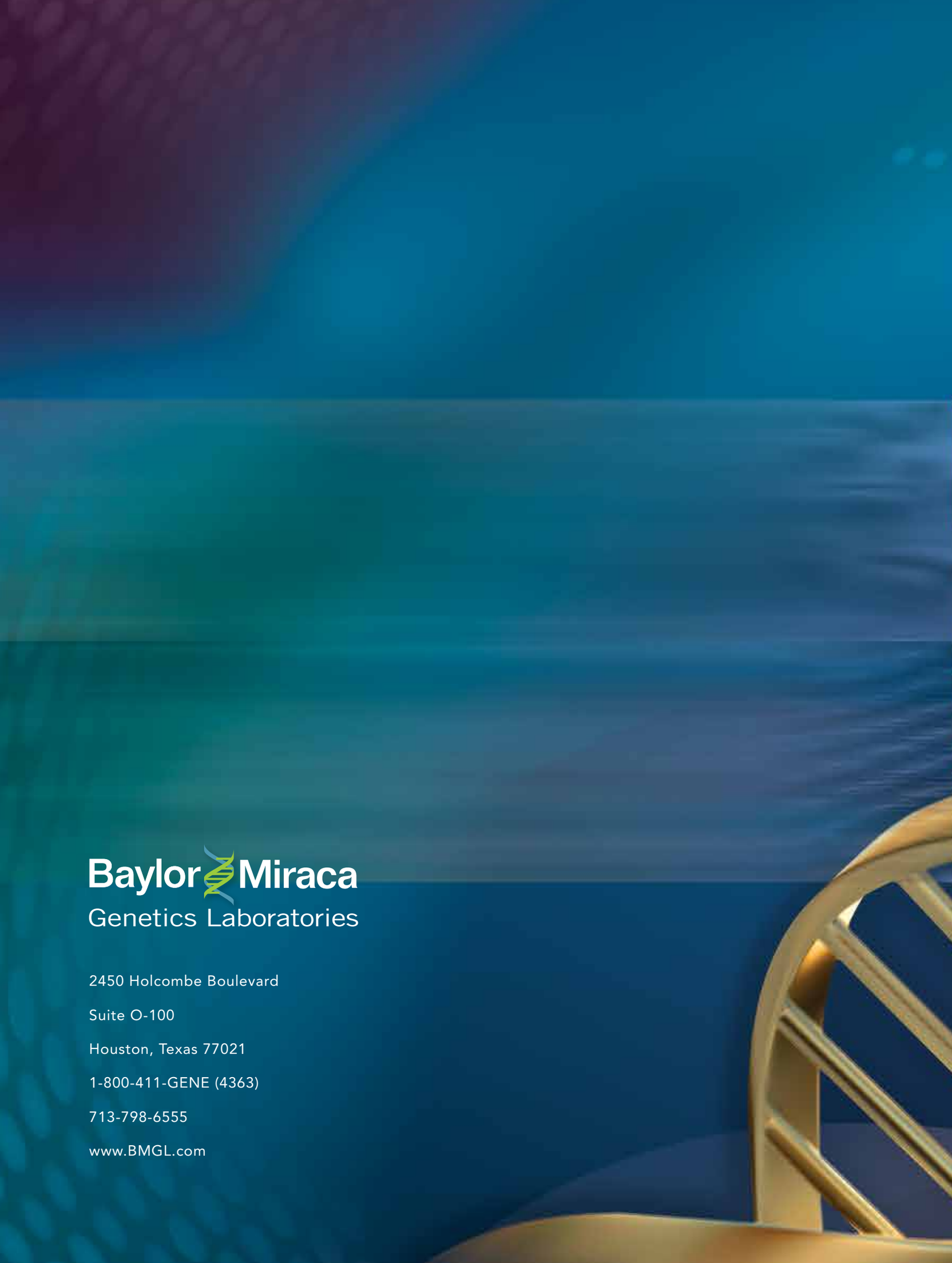
HIGH RESOLUTION WHOLE GENOME COVERAGE

- 30 kb resolution between known genes
- MicroRNAs
- Mitochondrial (for detection of deletions present in blood)

SNP COVERAGE FOR:

- 57,000 oligos used for SNP analysis
- Uniparental disomy (UPD)
- Detection of consanguinity
- Identification of regions of absence of heterozygosity (AOH)

For more information, or to request shipping kit, requisition forms, etc., please visit our website at www.BMGL.com.



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