Heme/Onc Array
Chromosomal Microarray analysis (CMA) of hematological malignancies is now available through the Medical Genetics Laboratories at Baylor College of Medicine using a custom designed Heme/Onc Oligo array. The Medical Genetic Laboratories were the first to offer chromosomal microarray analysis for clinical application and we remain a leader in the implementation of new technology for whole genome analysis in clinical diagnostics. We offer a Heme/Onc Oligo array which consists of a high density custom DNA microarray specifically targeting 494 genes implicated in Leukemogenesis with 1 oligo per 7.5 kb covering the disease regions and backbone coverage at 78 kb resolution. The Heme/Onc Oligo array utilizes the latest array technology and genome knowledge to produce a diagnostic tool far superior to karyotype and/or FISH and represents a major advance in genomic profiling of hematological malignancies at high resolution. The Heme/Onc Oligo array will detect DNA abnormalities that would otherwise be missed by karyotype analysis or FISH.

**Reason for Referral:**
The Heme/Onc Oligo array may be ordered to identify unbalanced chromosomal rearrangements in patients with:
- Acute leukemias
- CLL
- Multiple myeloma
- Lymphomas
- Myelodysplastic syndrome (MDS)

**Testing Methodology:**
The Heme/Onc Oligo array (44K Oligo array) utilizes array-based comparative genomic hybridization (aCGH) with approximately 44,000 oligos (60mers) covering 494 known genomic locations. The disease gene regions have on average 1 oligo per 7.5 kb whereas the backbone regions have an average resolution of 1 oligo per 78 kb. The backbone region is defined as the region between the disease gene minus the simple repetitive elements and low copy repeats. Genomic DNA from the test sample and a control sample are differentially labeled with fluorescent dyes and hybridized to the oligos. Results are analyzed using quantitative imaging methods and analytical software to assist in identifying each targeted-DNA sequence as loss of copy number (deletion), gain of copy number (duplication) or normal copy number. CMA is limited to detection of gains or losses of genomic material. It will not detect low level mosaicism, balanced translocations, inversions or point mutations that may be responsible for the clinical phenotype.

**Specimen Requirements:**
Blood or Bone Marrow in both EDTA (purple top) and Na Heparin (Green top) tubes: Adult: 2-3 cc per tube

**Turnaround Time:**
7-10 days

**Shipping and Handling:**
- Label all specimen tubes with full name and date of birth of the patient. Provide billing information. If we are billing patient insurance, provide a copy of the front and back of the insurance card.
- For additional information, contact the laboratories at 713-798-6555 or 1-800-411-GENE (4363).

**Sample Shipping Address:**
Baylor College of Medicine
Medical Genetics Laboratories
2450 Holcombe
Grand Blvd. - Receiving Dock
Houston, Texas 77021-2024
Phone: 1-800-411-GENE (4363)
Fax: 713-798-6584
E-mail: genetictest@bcm.edu

**CPT Codes:**
For information on fees or CPT Codes for Heme/Onc CMA, please contact our Billing Office at 713-798-3295
The Heme/Onc Array provides coverage of 494 genes associated with Acute Leukemias, CLL, Multiple Myeloma, Lymphomas, and MDS at 7.5 kb resolution. Array technology also allows for the simultaneous survey of the entire genome at a resolution orders of magnitude better than older chromosomal analysis (78 kb versus 5 – 10 megabases).

**Targeted Regions:**
- 494 Cancer Genes
- 1 Oligo every 7.5 kb
- Backbone Region
- 1 Oligo every 78 kb

**Excluded Regions:**
- Repetitive Elements
- Low Copy Repeats
- Assembly Gaps
- Copy Number Ploymorphism (TCAG V1+UCSC)

**Target Genes Implicated in Leukemias**

**Resolution of the Heme/Onc Array (44k)**

**Figure 1**  Schematic diagram of the design of the Heme/Onc oligo array.

**Figure 2**  A. Whole Genome view from chromosome 1 to Y. aCGH revealed a LOSS in copy number in the long arm of chromosome 13 as indicated by the circle.

B. Zoom in view of the entire chromosome 13 showing the coverage as well as the boundaries of the copy number LOSS segment.

C. The size of the copy number LOSS segment and genes involved.

D. A portion of the segment within the copy number LOSS showing a homozygous LOSS and the genes involved.

E. Confirmation FISH analysis using the CLL FISH panel from Vysis: 63% (313/500) cells had one signal for the D13S319 probe and 27% (146/500) cells had no signals (homozygous loss) for the D13S319 probe localized to chromosome 13q14 consistent with the results from array CGH.
Figure 3  An example of the aCGH analysis in a patient with an indication of Non-Hodgkins B-cell lymphoma. Conventional chromosome analysis showed an apparently balanced translocation between the long arm of one chromosome 2 at band 2q24 and the long arm of one chromosome 6 at band 6q14, and a translocation between the short arm of the same chromosome 2 homolog at band 2p23 and the long arm of one chromosome 8 at band 8q22 (shown on the right). aCGH showed a loss at each of the translocation breakpoints and in addition showed an interstitial loss at 2p34q35. This example shows the strength of aCGH in detecting copy number changes in the cancer genome at a much higher resolution than conventional cytogenetics.
Figure 4. An example of a patient with MDS. Chromosome analysis revealed a 47,XX,inv(3)(q21q26),+mar[11]/46,idem,-7 chromosome pattern. aCGH detected a loss of chromosome 7 except the pericentromeric region of chromosome 7. Subsequent FISH analysis using a centromeric probe for chromosome 7 confirmed the marker chromosome is of chromosome 7 in origin as shown on the left panel. aCGH is limited to detection of gain or loss of genomic material but not balanced rearrangements such as the inversions and translocations such as inversion 3 presented here.
References: