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## Virtual Karyotyping of Hematologic Malignancies

### The Benefits of SNP Array Virtual Karyotypes

- Genome-wide high resolution copy number and loss-of-heterozygosity (LOH) status in one assay
- 100-fold higher resolution than conventional cytogenetics
- Analogous to 250,000 FISH probes in one assay
- Less expensive and more informative than FISH panels
- Able to identify clinically relevant genetic lesions not detectable by FISH, conventional cytogenetics, or array comparative genomic hybridization
- Does not require cell culture

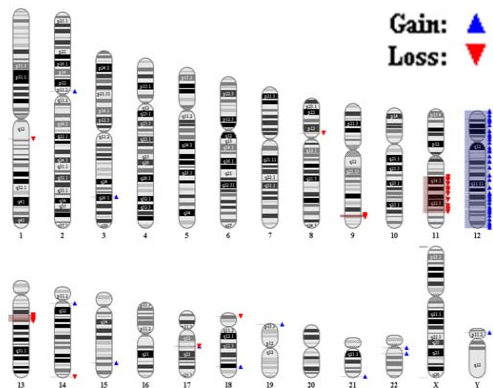
### Clinical Applications

Applicable to hematologic malignancies with copy number changes relevant to diagnosis or patient management, including chronic lymphocytic leukemia, multiple myeloma, and myelodysplastic syndrome.

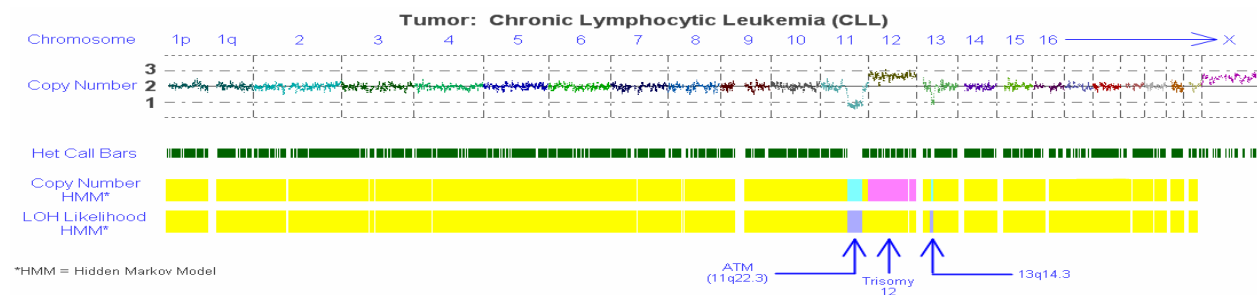
### What is a Virtual Karyotype?

Combining the breadth of conventional cytogenetics with the specificity of FISH, virtual karyotypes

reconstruct the genome *in silico* from disrupted DNA. Array-based karyotyping is used routinely for the identification of genomic copy number variants in patients with constitutional disorders, and it is now available for oncology applications.



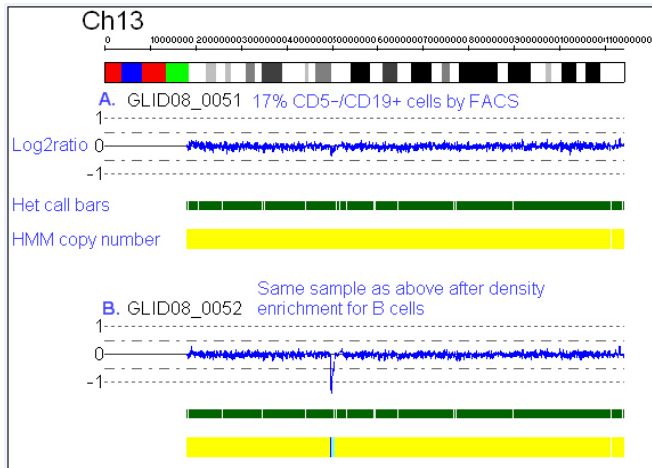
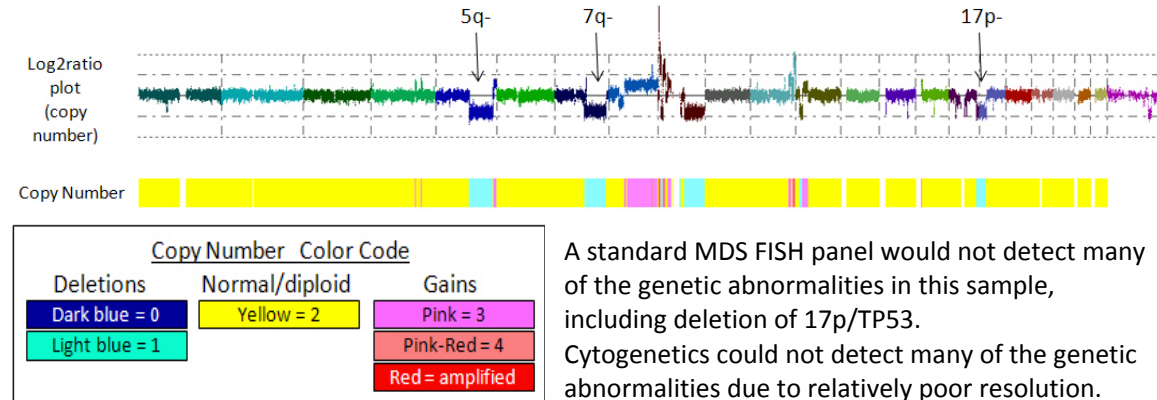
Karyogram view (left) and corresponding log<sub>2</sub>ratio plot (below) for a chronic lymphocytic leukemia (CLL) sample with deletion of 11q22.3 (ATM), trisomy 12, and deletion of 13q14. The 13q14 deletion was not detected by the commercial FISH probe used for this locus.



## Key features of SNP Array Virtual Karyotypes at Creighton Medical Laboratories

- Enrichment prior to DNA extraction provides robust virtual karyotypes of clonal population
- Specimens: 1-5 ml EDTA anti-coagulated peripheral blood or bone marrow aspirate (purple top)
- 7 day turn-around time
- Karyotypes obtained using Affymetrix GeneChip® SNP arrays
- Karyogram, ISCN, and clinic-pathological interpretation are provided with each report

## Myelodysplastic Syndrome



## The Efficacy of Enrichment for Clonal Population

B-cell enrichment reveals a 13q14 deletion in this CLL sample that appears partially heterozygously deleted (light blue) and partially homozygously deleted (dark blue), representing clonal evolution.

For requisition forms, sample reports, and additional information, visit our website at <http://www.cml.md/genomics/>

## Select References

- Hagenkord JM and Chang CC, The rewards and challenges of array-based karyotyping for clinical oncology applications, *Leukemia*, 2009 May 13, in press.
- Gondek LP, et al. Chromosomal lesions and uniparental disomy detected by SNP arrays in MDS, MDS/MPS, and MDS-derived AML. *Blood* Feb 1;111(3):1534-42.
- Pfiefer D, et al. Genome-wide analysis of DNA copy number changes and LOH in CLL using high-density SNP arrays. *Blood* 2007 Feb 1;109(3):1202-10.

Log2ratios generated with CNAGv3.0 copy number analysis software (Yamamoto G, et al. Highly sensitive method for genome-wide detection of allelic composition in non-paired, primary tumor specimens by use of Affymetrix™ single-nucleotide-polymorphism genotyping microarrays. *Am J Hum Genet* 2007 Jul;81(1):114-26.).