

KaryoNIM[®] Leukemia

For your future



Chronic lymphocytic leukemia (CLL)

Chronic lymphocytic leukemia (CLL) is the most frequent adult leukemia in Western countries.

It accounts for 30% of the leukemias in this population and affects mainly older individuals.⁽¹⁾

- Establishing the prognosis, treatment options, and monitoring of CLL requires the identification of Identification of genetic biomarkers.
- Highly effective treatment options based on monoclonal antibodies or tyrosine kinase inhibitors depend on the presence or absence of deletions 17p and 11q.⁽³⁻⁵⁾

CNVs are the main chromosomal and genetic abnormalities seen in CLL, and are powerful prognosis markers.⁽²⁾

The mutational status determines the prognosis and treatment of CLL

Risk group	Frequency	Mutation	Survival at 5 years	Survival at 10 years
High	27%	del(17p)-TP53 and/or BIRC3	51%	29%
Intermediate	39%	NOTCH1 and/or SF3B1 and/or del(11q23)	66%	37%
Low	17%	Normal karyotype or Trisomy 12	78%	57%
Extremely low	17%	Del(13q14)	87%	69%



KaryoNIM[®]Leukemia improves upon conventional techniques.
Designed by NIMGenetics, it combines **Oligonucleotide Array-Based CGH** and **SNParray** technologies.

aCGH

- More sensitive whole-genome CNV analysis
- More accurate CNV detection

SNPs

Detection of LOH* due to uniparental disomy

Proprietary design

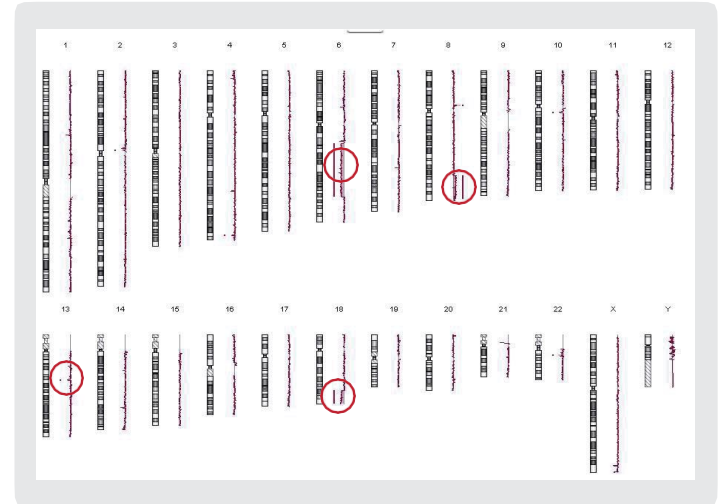
Specifically targets CLL biomarkers

*LOH: *Loss of heterozygosity*

Array CGH: assessing prognosis in CLL

aCGH is the technique of choice for prognostic assessment in CLL:

- ✓ **It offers whole genome information**
- ✓ **It improves performance testing**
70% of cases with CLL showed genetic alterations detected by aCGH compared with 50% of cases diagnosed by FISH.
- ✓ **It simplifies the transport and handling of samples.** The cellular status of the sample is not a limiting factor since the test uses DNA. Cell culturing is not required.



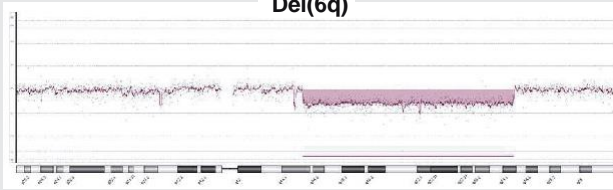
aCGH from a sample of CLL with multiple CNVs.



Array Comparative Genomic Hybridization (aCGH) is the most efficient genetic test to diagnose chromosomal alterations in CLL.⁽⁶⁻⁹⁾

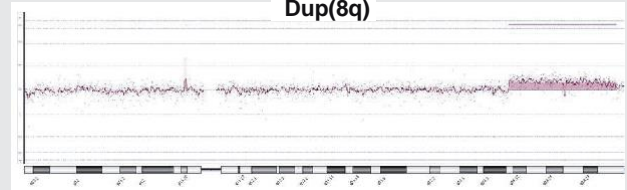
Not detected by FisH

Del(6q)



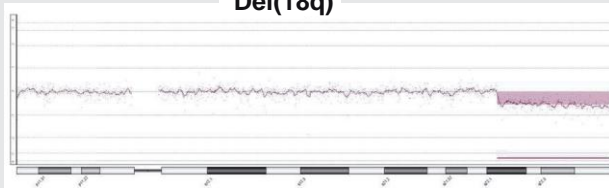
Not detected by FisH

Dup(8q)



Not detected by FisH

Del(18q)

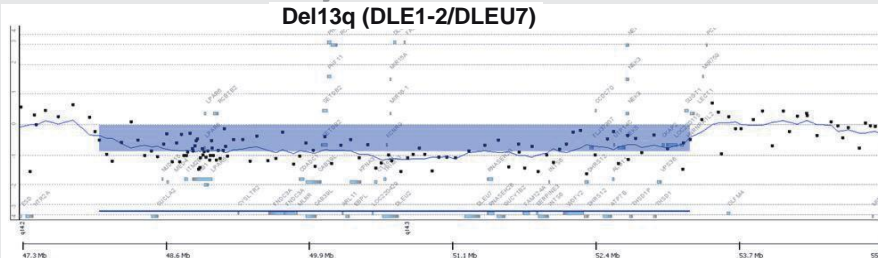


✓ It can change prognosis

FISH technology does not analyze the whole genome, only a defined group of alterations.

Not detected by FisH

Del13q (DLE1-2/DLEU7)



✓ It increases resolution:

- Completely defines CNV
- Identifies the genes involved.

Complete coverage of the classical regions for CLL prognosis	Locus	
	DETECTION CAPACITY	RESOLUTION
Trisomy of chromosome 12		
Deletion 11q23 , including the gene ATM	130 kb	1 probe/25.5 kb
Deletion 13q14 , including the DLEU region		
Deletion 17p13 , including the gene TP53		

OTHER REGIONS/GENES OF INTEREST	DETECTION CAPACITY
Genes of interest in CLL <i>ATM, BIRC2, BIRC3, IKZF1, KLHL6, MYB, MYD88, NOTCH1, POT1, SF3B1, TP53, XPO1</i>	<17 kb
LOH regions	10 Mb
Genes included in Cancer Consensus	Complete coverage

KaryoNIM[®]Leukemia

The best aCGH for the evaluation of CLL

- ✓ **Improves the detection of CNVs in regions of prognostic interest.**
- ✓ **Provides relevant information on:**
 - genes related to CLL
 - clonality and loss of heterozygosity
- ✓ **Increases the diagnostic effectiveness by 20% with respect to those cases detected by FISH.**
- ✓ **Easier handling of the sample as no cell culturing is required.**
- ✓ **More complete prognosis: examines all regions of the genome compared with those by routine FISH.**
- ✓ **Maximum precision in defining the alteration and its boundaries, revealing the genes involved thanks to its superior resolution.⁽⁶⁻⁹⁾**
- ✓ **Provides the medical team with the most current genetic diagnosis of CLL, in accordance with international guidelines and the most advanced laboratories worldwide.⁽¹⁰⁾**

Sample handling and shipping:

- **Type of sample:** 3-5 mL of blood or bone marrow in EDTA. Ship at room temperature within 48 hours of sample collection.
- **DNA sample:** 500 ng of DNA at a concentration greater than 10 ng/μL dissolved in TE *low* buffer or H₂O. Ship at room temperature.
- **Documents to be included with the sample:** Informed consent form
Request form
- **Delivery of results:** 15 working days

Bibliography

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- 10: **schoumans J, suela J et al.** Guidelines for genomic array analysis in acquired haematological neoplastic disorders. Genes Chromosomes Cancer, 2016; 55(5):480-91



Comprehensive approach to the diagnosis of CLL

- **Integrated solutions.** NIMGenetics has an extensive portfolio of molecular genetic tests to meet the needs of the patient. Including:

NIMFISH probes, to monitor CLL. Unique catalog of probes characterized by their high specificity, precision and luminiscence, which are regularly updated.

TP53 sequencing

Our NGS platform for TP53 is certified by ERIC (European Research Initiative on CLL).

- **Opinion leaders in Oncology.** Our team has published more than 200 scientific articles on genetics and oncohematology in international journals.
- Our laboratories follow the quality control standards of **EMQN** (*European Molecular Genetics Quality Network*).
- We are accredited by the Spanish Association of Human Genetics: *Asociación Española de Genética Humana* (**AEGH**).
- The reports by **NIMGenetics** are rated as excellent by opinion leaders in oncology, clinical genetics, and other disciplines.

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La Suma de Todos

Comunidad de Madrid

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