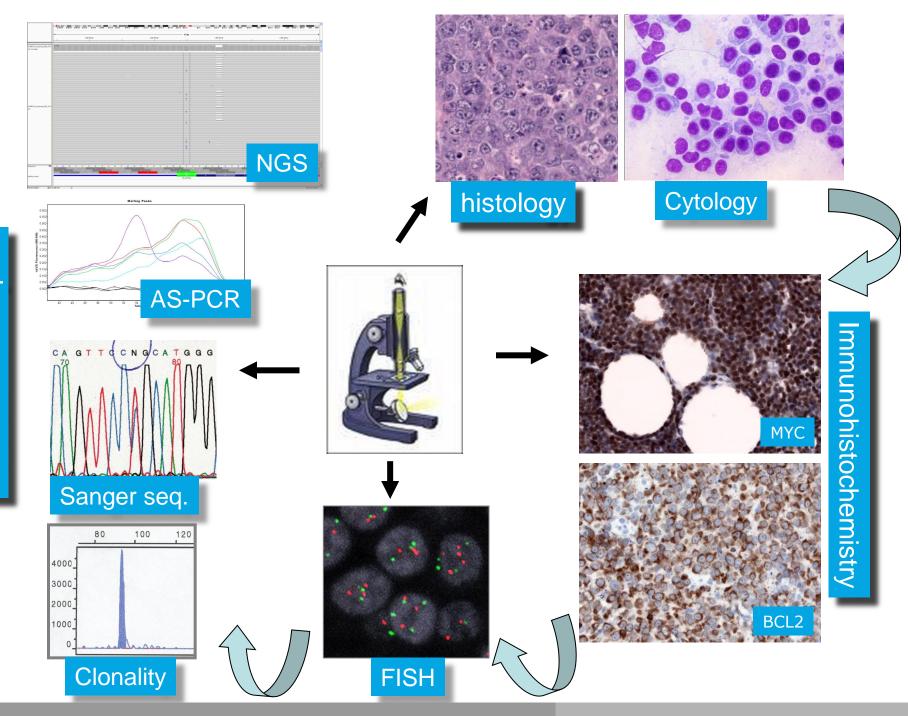


Institut für Pathologie

Methods used to diagnose lymphomas

Prof. Dr.Med. Leticia Quintanilla-Fend



Methods use to diagnose lymphomas

- There is probably no other method that has so revolutionized the field of pathology during the past 50 years as the immunohistochemical technique
- ➤ Immunophenotyping has contributed importantly to the diagnosis and understanding of lymphomas







Immunohistochemical approach.

Immunophenotyping in Lymphomas:

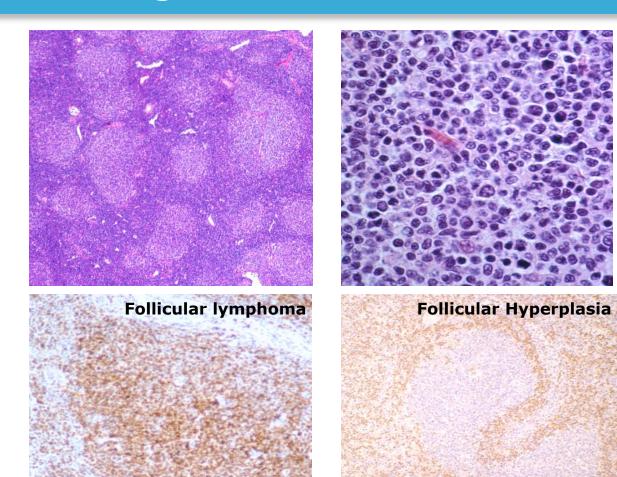
- > As a surrogate marker of molecular changes
- Increases diagnostic accuracy
 - Cell lineage determination
 - ✓ B-cell NHL 73% to 87%
 - ✓ Peripheral T-cell lymphomas from 41% to 86%
- Gives prognostic information

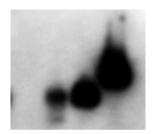




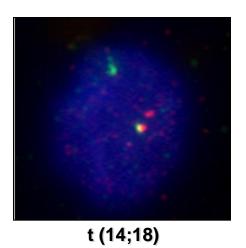


Surrogate marker of molecular changes





Rearrangement of BCL-2





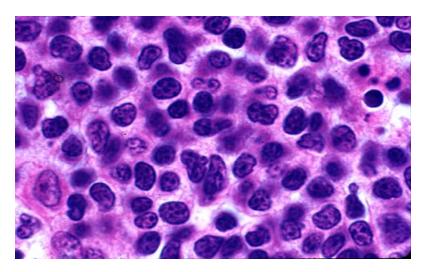


bcl-2

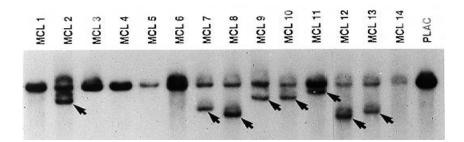




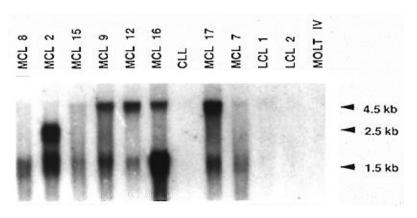
Surrogate marker of molecular changes



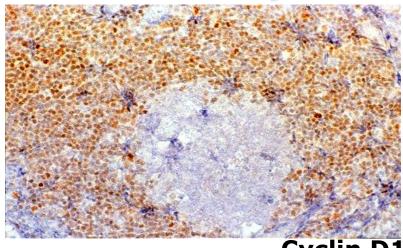
t (11;14)



Rearrangement of BCL-1



Northern blot cyclin D1



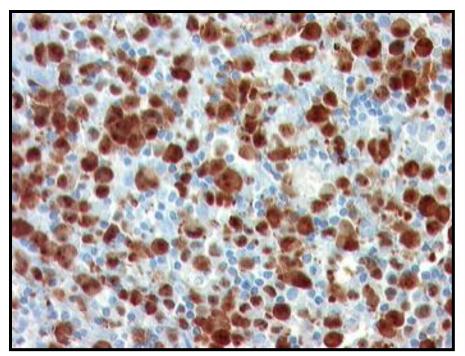


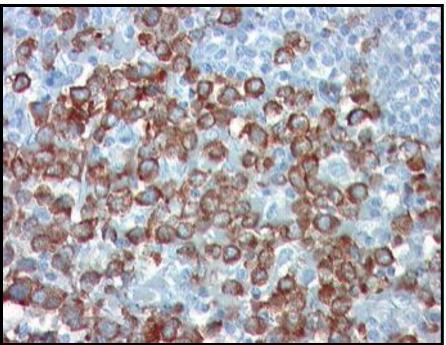






ALK+ Anaplastic large cell lymphoma.





NPM-ALK - t(2;5)

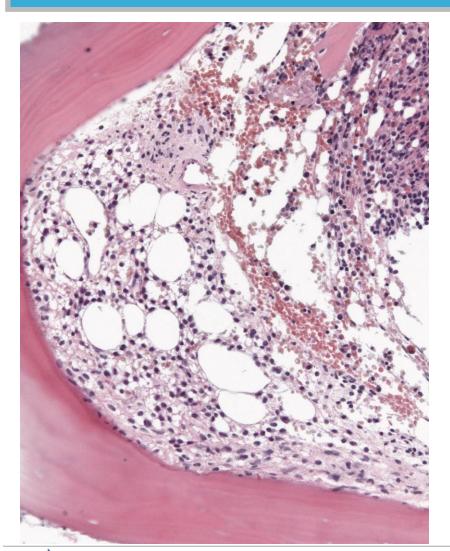
Variant fusion protein

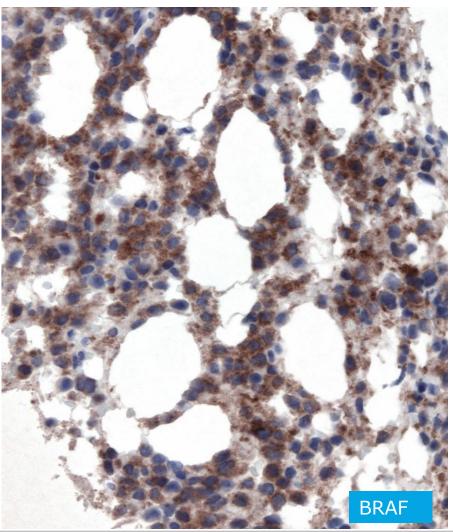






Hairy cell leukemia BRAF antibody











Immunohistochemical approach.

Immunophenotyping in Lymphomas:

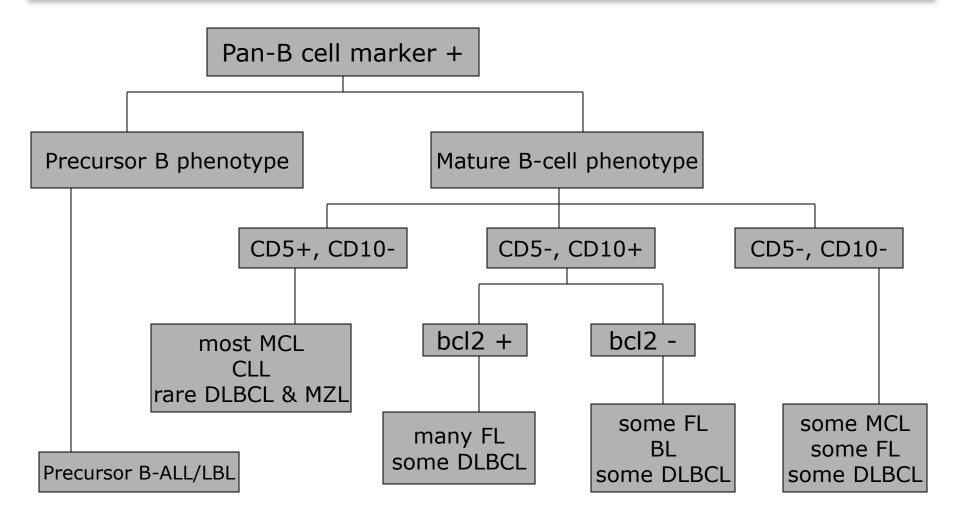
- As a surrogate marker of molecular changes
- Increases diagnostic accuracy

B-cell NHL 73% to 87%

Peripheral T-cell lymphomas from 41% to 86%

Gives prognostic information

Diagnostic Accuracy in B-cell lymphomas

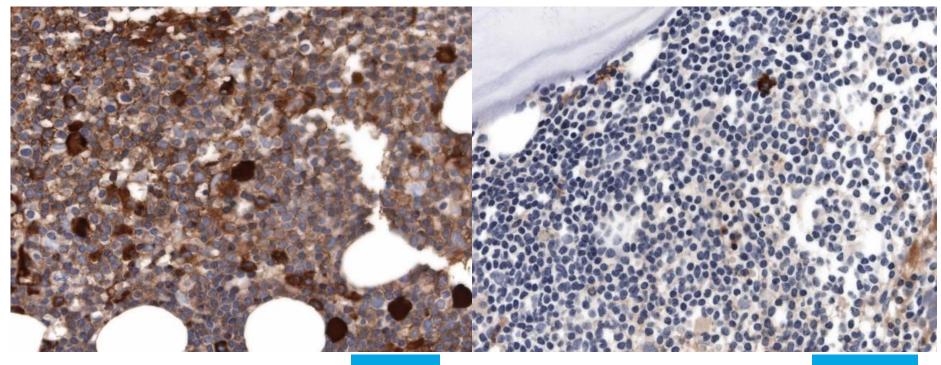








Light chain restriction for clonality



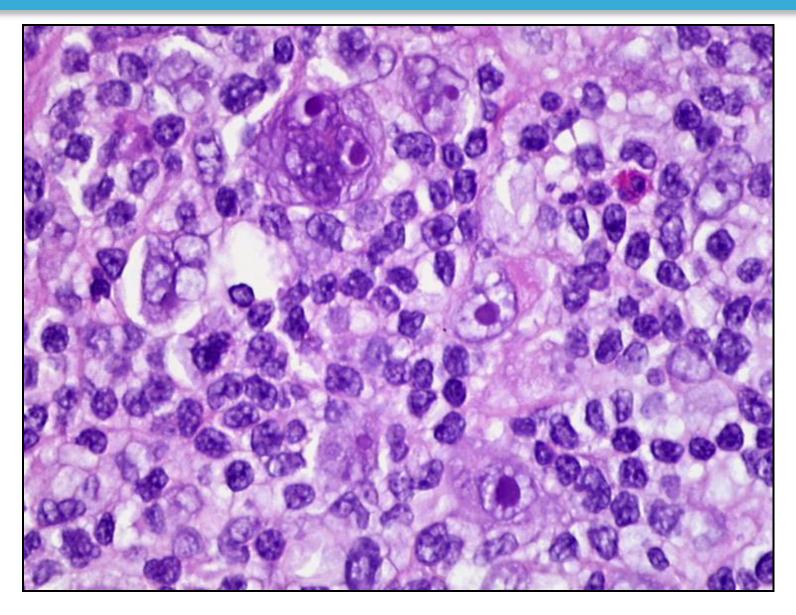
Kappa

Lambda



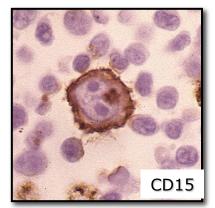


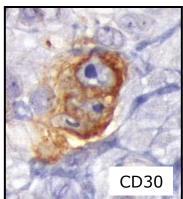
Accuracy in the diagnosis of CHL

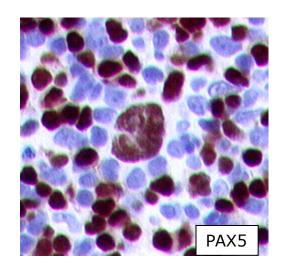


Accuracy in the diagnosis. Hodgkin lymphoma

- Immunophenotype
- CD30 + (100%)
- CD15 + (75-85%)
- CD20 (weak positivity in a minority of tumor cells)
- PAX5 (90%)
- MUM1
- LMP1 +/-
- Oct2 and BOB.1 -



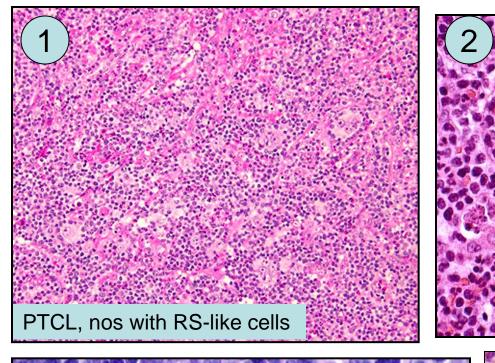


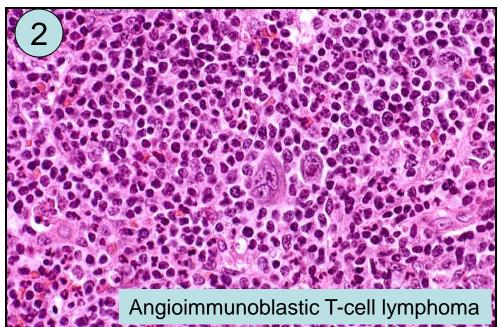


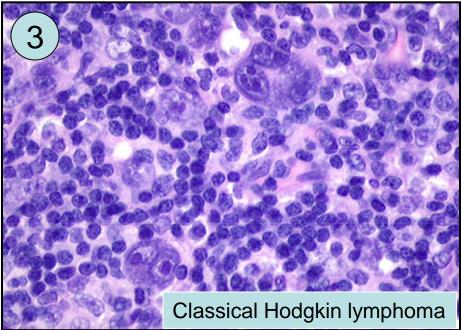


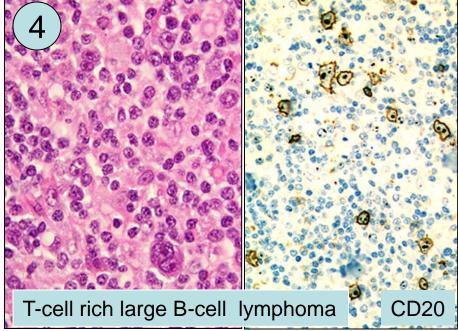




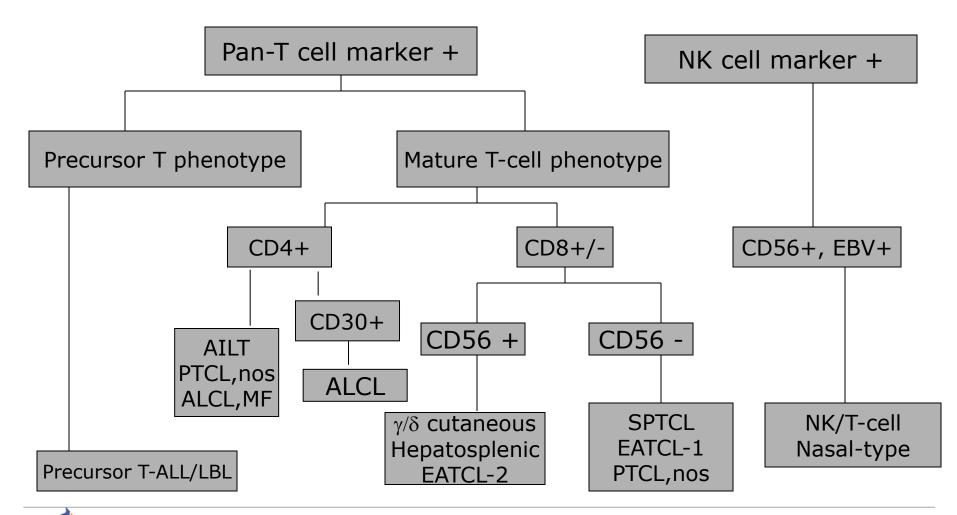








Diagnostic Accuracy in T/NK-cell lymphomas

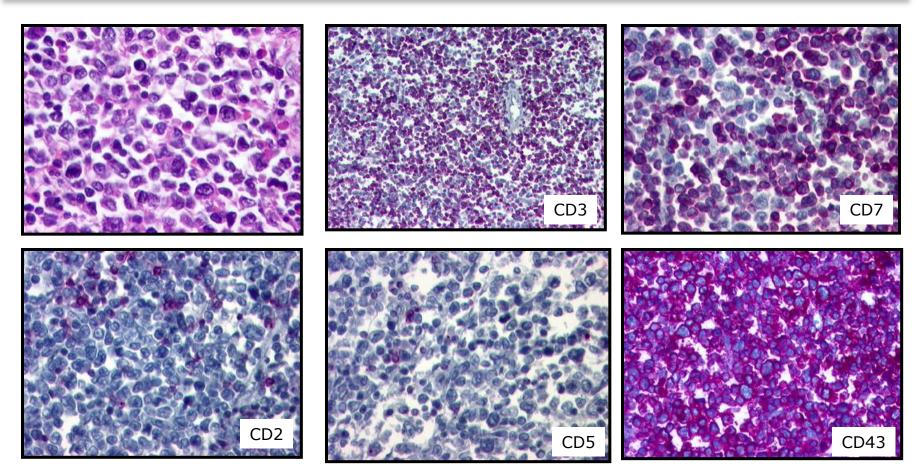








Diagnostic accuracy. T-cell NHL



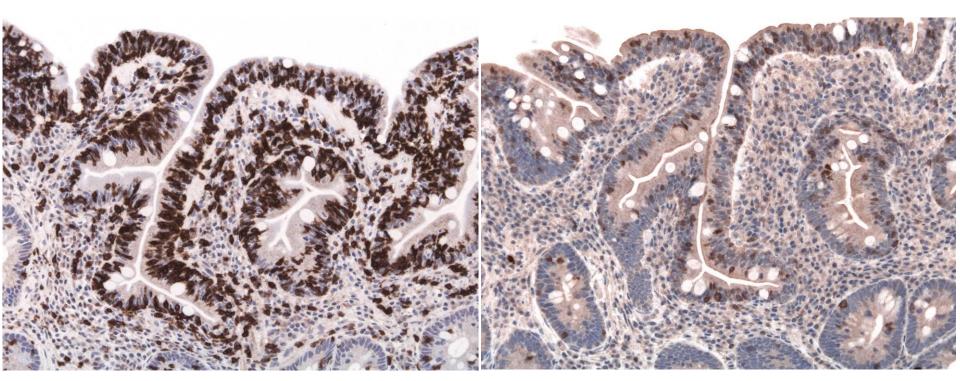
Aberrant phenotype: loss of one or more pan-T-cell markers







Biomarkers of cell lineage/differentiation



 $TCR\alpha\beta$

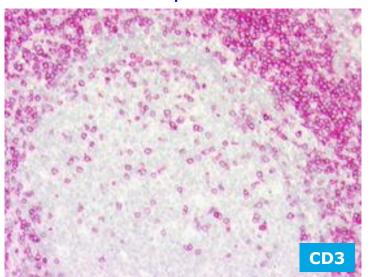


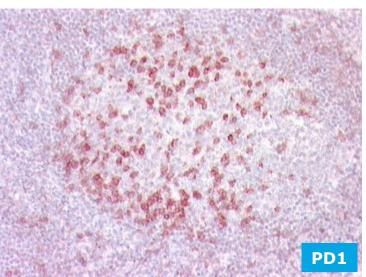




Follicular helper T-cells (Tfh) markers in AlLT

T_{FH} are a minor subset of T-cells normally residing in germinal centers and act as critical regulators of the B-cell immune response





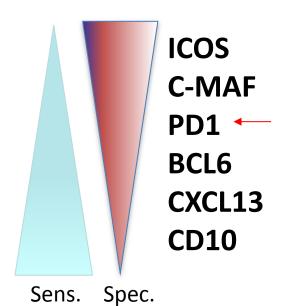
- >Hypergammaglobulinemia and autoimmune manifestations
- ▶T_{FH} express BCL6 and c-MAF



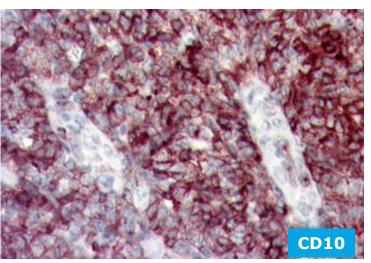


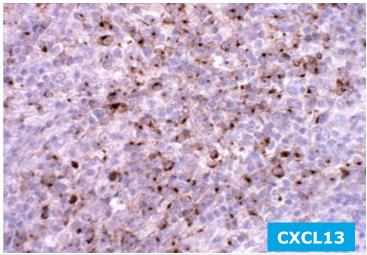


Follicular helper T-cells (Tfh)



Am J Surg Pathol 2006, 30: 490 Modern Pathol 2006, 19: 337 Blood 2005, 106: 1501 Blood 2002, 99: 627



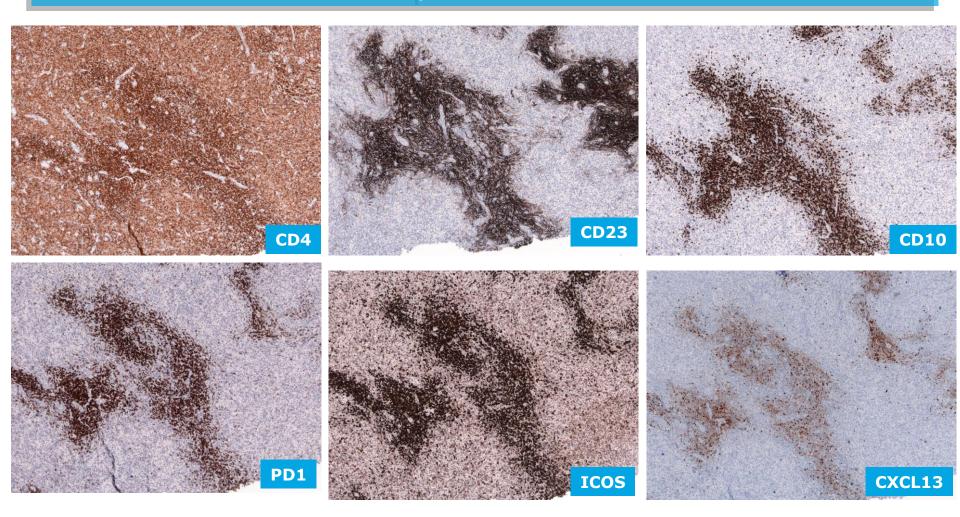








Microenvironmental imprint in AILT









Biological Prognostic markers.

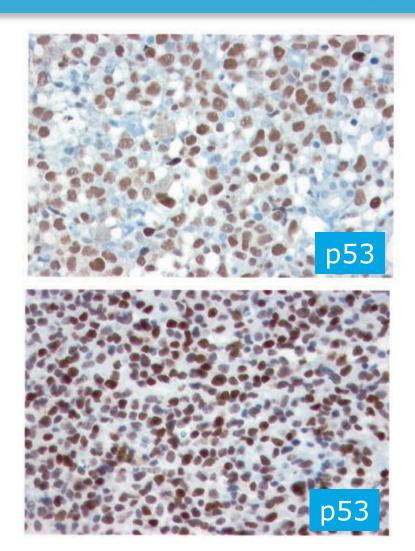
- > Cell cycle
- p53, p27, ki-67, cyclins
- Apoptosis related molecules
- BCL-2, survivin
- > Transcription factors
 - MYC, NOTCH1
- > B-cell differentiation molecules
- BCL-6, CD10, CD5, Zap-70, Foxp-1,
 CD21
- Other molecules
- ICAM, sCD44, PD-L1

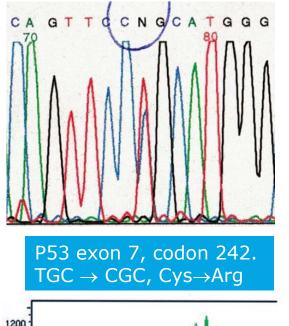




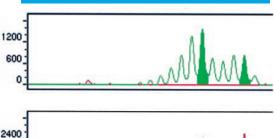


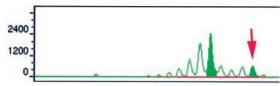
P53 mutational analysis in NK/T-cell lymphoma





20%





Quintanilla-Martinez et al, 2001 Am J Pathol:159;2095



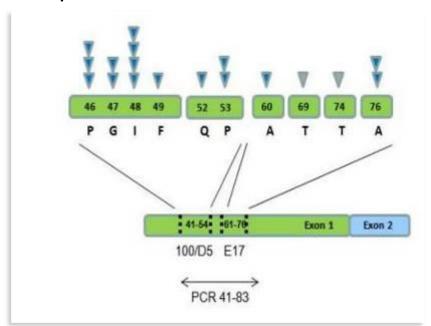


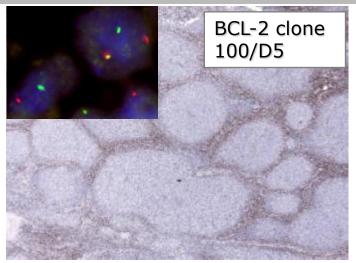


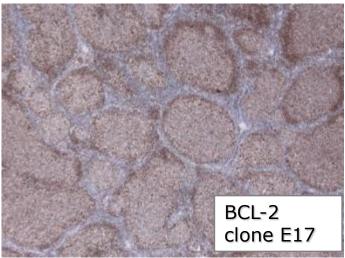
BCL2 mutations in Follicular lymphoma

• t(14;18)+ FL

- show Exon 1 missense mutations leading to conformational change of 100/D5 epitope
- functional BH2 domains are spared







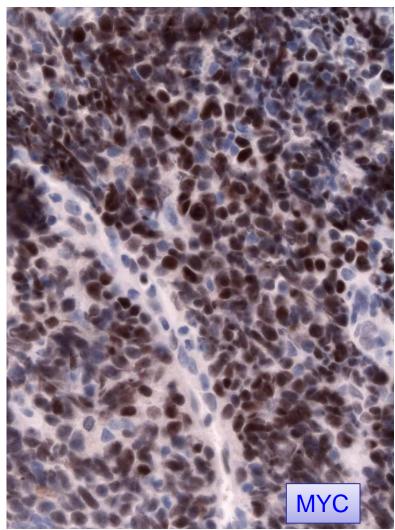
Adam et al, Hum Pathol 2013



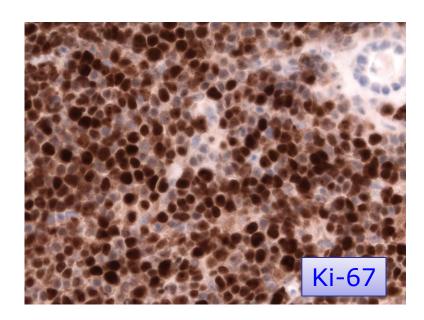


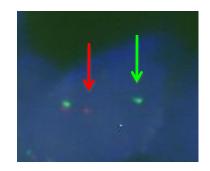


DLBCL with MYC translocation



Monoclonal rabbit antibody





MYC break-apart

Ruzinova et al, AJSP 2010;34:882

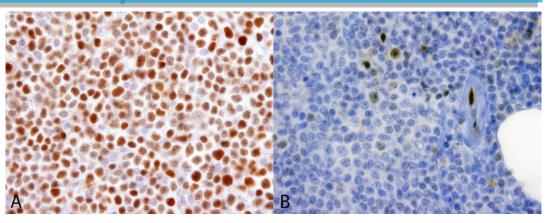




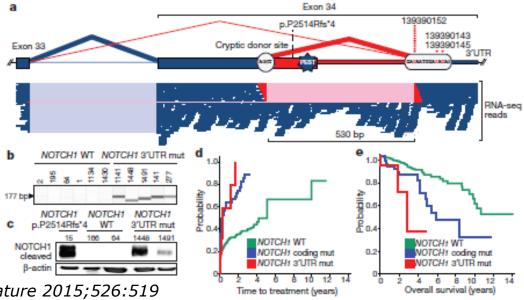


NOTCH1 expression

- 50-60% of T-ALL have activating mutations
- 20% CLL
- 29% DLBCL
- 23% FL
- 5% MCL



Ho C and Rodig SJ, Sem Diag Pathol 2015;32:381











Techniques in molecular diagnosis

- Diagnostic ancillary methods
 - > FISH (fluorescence in situly hybridization)
 - PCR based techniques
 - Quantitative (Real-time PCR)
 - Allele specific PCR (mutation detection)
 - Qualitative (clonality analysis)
 - Sequence analysis
 - Next generation sequencing



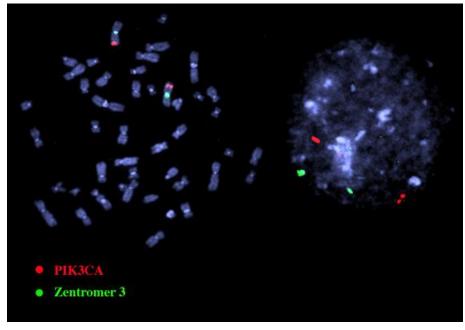




Fluorescence in situ hybridization (FISH)

- Examine individual cells
- Detect heterogeneity within tumor cells
- Interphase FISH can be apply to paraffin-tissue
- Best method to detect
 - translocations
 - amplifications
 - polisomy

PIK3CA /Centromere 3



Metaphase

Interphase

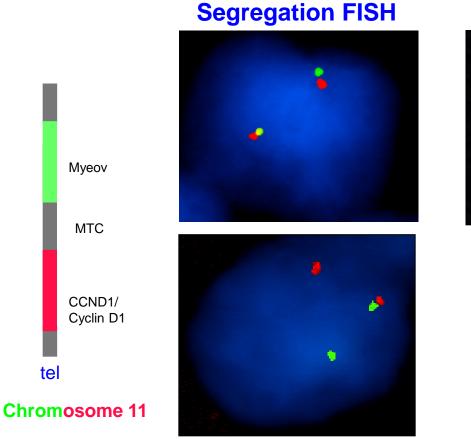
Haralambieva et al, J Pathol 2002, 198:163







Fluorescence in situ hybridization (FISH)



Break in chromosome 11

Eα2 Enhancer $\gamma 4$ γ 2 CCND1/ Cyclin D1 **Eµ** Enhancer tel t(11;14) **Chromosome 14**

Colocalization FISH

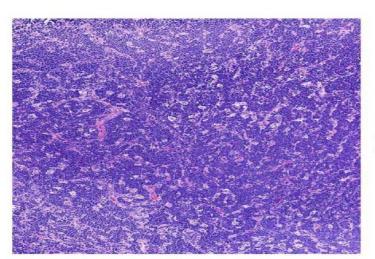


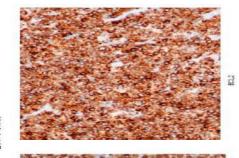


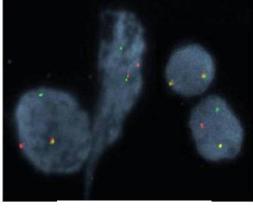


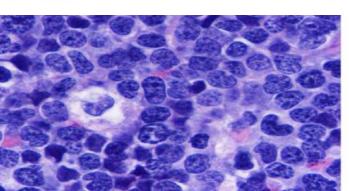
Chromosome 11 Chromosome 14

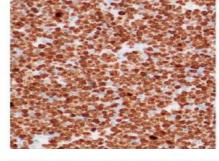
Transformed follicular lymphoma "double hit"

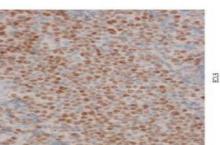




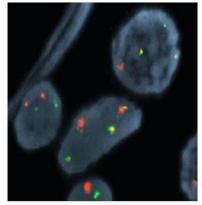








MYC break apart



IGH-BCL2







Techniques in molecular diagnosis

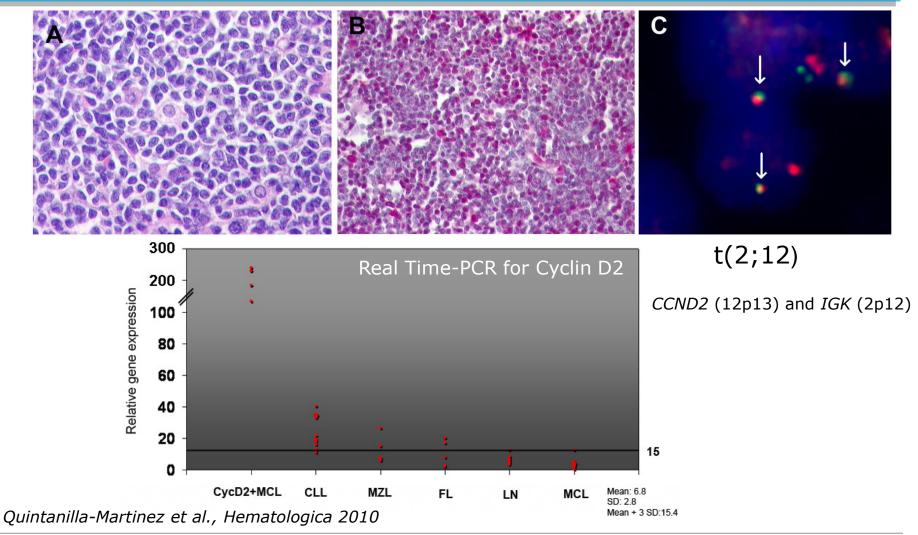
- Diagnostic ancillary methods
 - FISH (fluorescence in situly hybridization)
 - PCR based techniques
 - Quantitative (Real-time PCR)
 - Allele specific PCR (mutation detection)
 - Qualitative (clonality analysis)
 - Sequence analysis
 - Next generation sequencing
 - Targeted amplification
 - clonality







Cyclin D2+ Mantle cell lymphomas





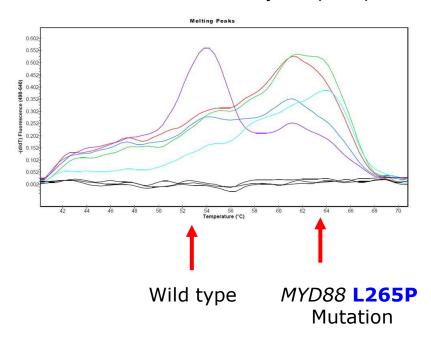




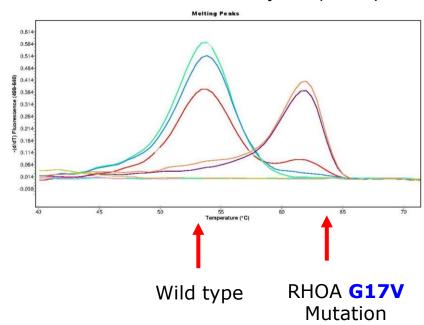
Allelic specific PCR (mutation detection)

AS-PCR with melting curve for mutations with hot spots.

MYD88 mutation analysis (LPL)



RHOA mutation analysis (AITL)



Schmidt J et al, BJH 2015, 169:795-803 Bonzheim I et al Blood 2015

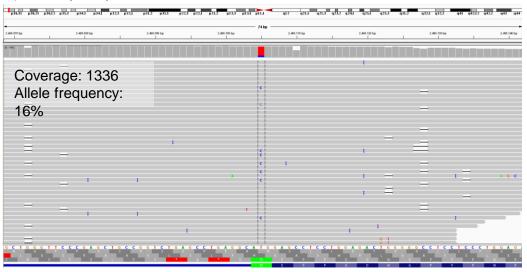






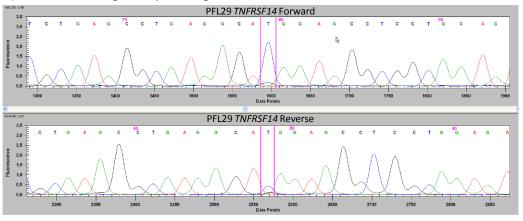
TNFRSF14 mutations in PFL

A) Ion AmpliSeq Custom Panel



PFL29 TNFRSF14
p.Met1_Gln97del

B) Validation Sanger sequencing









Clonality as marker of lymphoid neoplasia

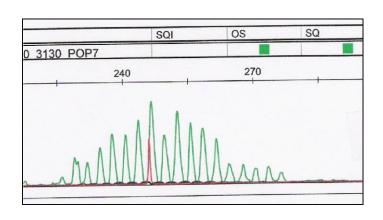
- Immunoglobulin gene or T-cell receptor gene rearrangements
 - Malignant vs. bening
 - Cell lineage B vs T
- Diagnosis of residual disease
 - For MRD specialized approaches (e.g. patient specific probes) required
- In disease
 - Unique molecular fingerprint
 - Determination of clonal relationship
 - Transformation vs. second malignancy



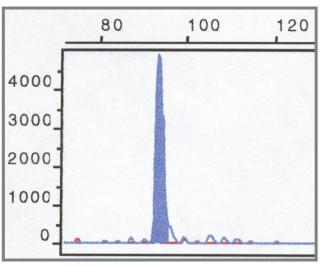




IgH heavy chain clonality analysis



Polyclonal pattern FR2
3-bp spacing
Gaussian distribution



Automated fragment length analysis

Monoclonal peak FR3
Faint polyclonal background

GeneScan

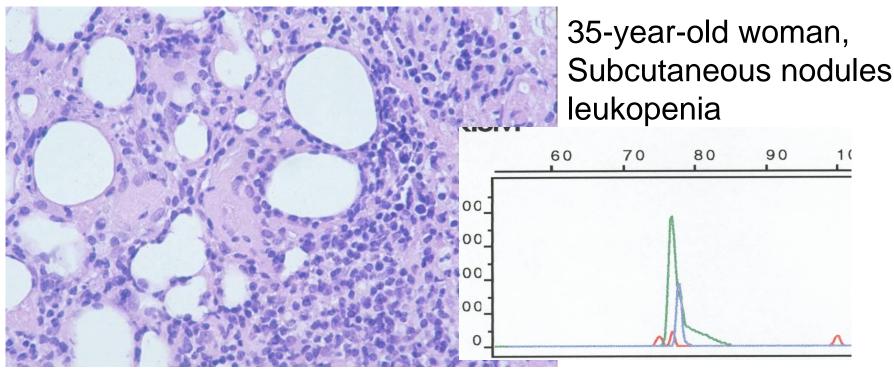






Benign vs. Malignant

- Polymorphous infiltrates in subcutaneous tissue
- Predominance of T-cells, rimming of fat cells





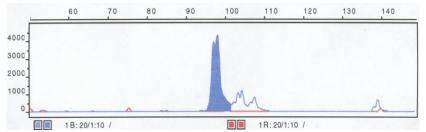






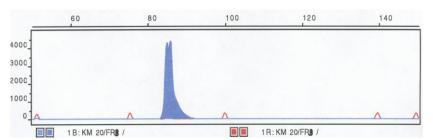
Discordant lymphomas





97 bp

In 30% of the cases a second neoplasia is found!



85 bp

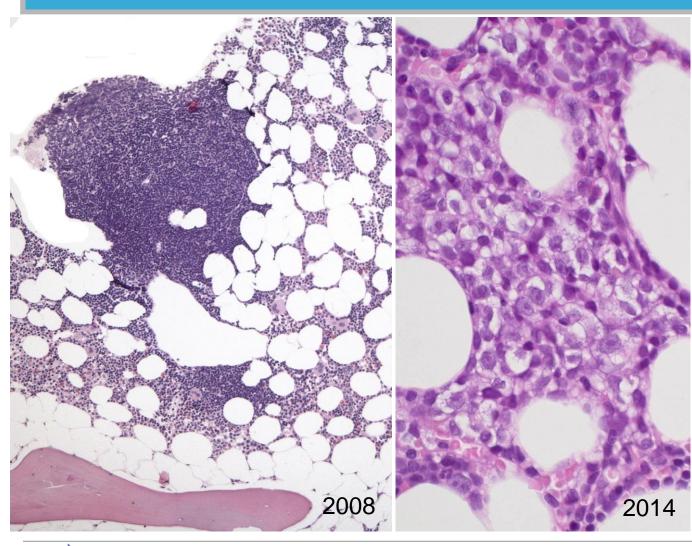
Kremer et al, Lab Invest 2003







Lymphoma transformation



60-year-old male, with history of CLL now with retroperitoneal lymphadenopathy, B-symptoms, lymphocytosis of PB







Richter's transformation

Transformation or secondary neoplasia? 78% related

22% unrelated





Mao, Quintanilla-Martinez et al, AJSP 2007

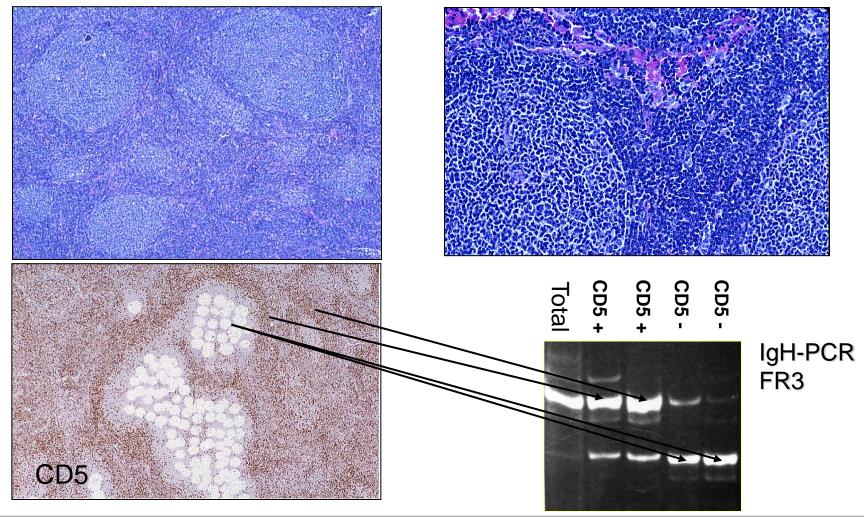
FR3 IgH-PCR







Composite lymphoma Follicular lymphoma and CLL









Molecular diagnosis in Hematopathology

