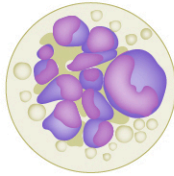


# The applicability of a simple gene expression assay for the classification of peripheral T-cell lymphomas



## Peripheral T-cell lymphomas (PTCLs)

- highly heterogeneous and rare tumors
- ~ 1/3 of PTCLs remain unclassifiable: **PTCL-NOS**



270 lymphoma samples (multicentric T-cell lymphoma consortium (TENOMIC) of the Lymphoma Study Association (LYSA))



Reverse transcriptase-multiplex ligation-dependent probe amplification gene expression profiling (**RT-MLPA**) assay



20 genes

- 17 markers relevant to T-cell immunology and lymphoma biopathology
- 1 EBV-related transcript
- Variants of *RHOA* (G17V) and *IDH2* (R172K/T)



Identification of 33/33 *RHOA*G17V and 9/10 *IDH2* R172K/T mutations

## • Unsupervised hierarchical clustering



- 21/21 ALK/positive anaplastic large cell lymphoma
- 16/16 extranodal NK/T-cell lymphomas
- 6/6 hepatosplenic T-cell lymphomas
- 13/13 adult T-cell leukemia/lymphomas

## • Support vector machine (SVM) predictor model based on RT-MLPA data

Attributed a molecular class to 27/77 not specified T-cell lymphomas:



- 17 T<sub>FH</sub>
- 5 cytotoxic ALK-negative anaplastic
- 5 NK/ T-cell leukemia/lymphomas