

# In-depth molecular analysis using a multi-gene lymphoma NGS panel in lymphomas with lymphoplasmacytic differentiation may provide more precise diagnosis, differentiation of entities and may optimize rational treatment allocations

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## Introduction:

Lymphoplasmacytic lymphoma (LPL) is a B-cell neoplasia defined by a variable mixture of lymphocytes, lymphocytes with plasmacytic differentiation and plasma cells and is known as Waldenstroems macroglobulinaemia (WM)(1,2). However, (lympho)plasmacytic differentiation can also be found in other low-grade B-cell lymphomas resulting in diagnostic complexities, only partly relieved by the detection of the MYD88 mutation (1,3-5). Clinically the presence or absence of either MYD88 and/or CXCR4 mutations has been shown to influence treatment response (6-8). Similarly, other oncogenic mutations indicate a poor outcome, though its impact on prognosis and treatment remains to be determined (6-8).

We attempted to integrate morphology and molecular pathology for a more precise diagnosis by performing next generation sequencing (NGS) in primary and relapsed LPL/WM.

## Material and Methods

### Next Generation sequencing

- 43 bone marrow trephine biopsies including primary diagnosis and relapses of 24 WM, 6 small B-cell lymphomas with plasmacytic differentiation (SBCL-PC) and 3 (IgM) MM patients.
- Lymphoma Panel (Lymphoma Solution, SophiaGenetics, Geneva, Switzerland) with 54 relevant genes.

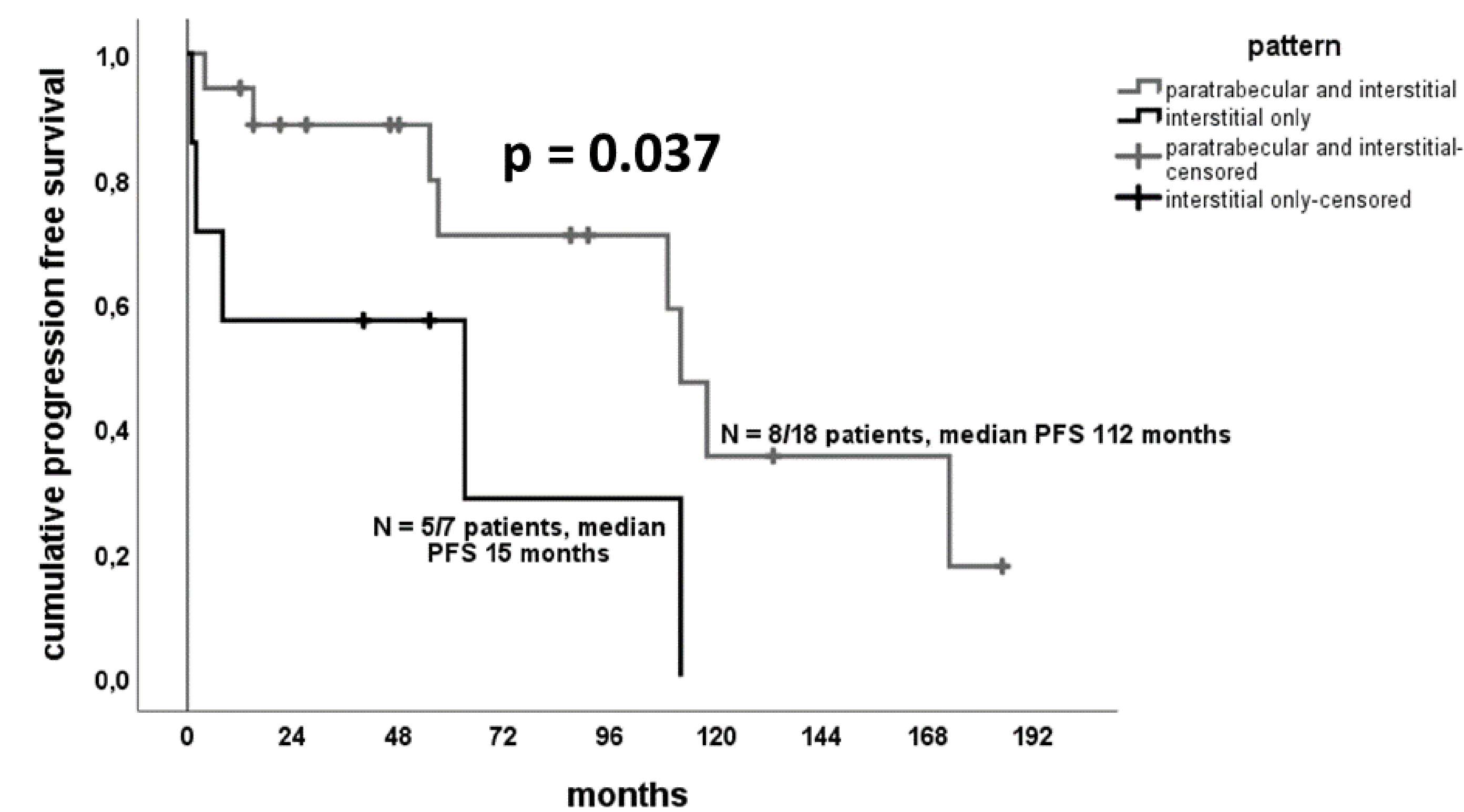
## Results

- MYD88 mutation in 95% and CXCR4 mutation in 25% of WM
- MYD88 mutation in 50% of SBCL-PC, but not in MM
- Novel BIRC 3 mutation described in a patient with progressive WM.

Type of Mutation	Missense mutation (%)	Nonsense mutation (%)	Frameshift mutation (%)	Splice-site mutation (%)
<b>MYD88</b>	37 (86.04%)	-	-	-
<b>CXCR4</b>	-	2 (4.6%)	10 (23.2%)	-
<b>ARIDA1</b>	1 (2.3%)	1 (2.3%)	6 (13.9%)	1 (2.3%)
<b>KMT2D</b>	5 (11.6%)	-	1 (2.3%)	-
<b>TP53</b>	4 (9.3%)	-	-	4 (9.3%)
<b>POT1</b>	2 (4.6%)	-	1 (2.3%)	-
<b>TNFAIP3</b>	3 (6.9%)	-	-	-

**Table 1:** Most frequently found mutations in the 43 trephine biopsies

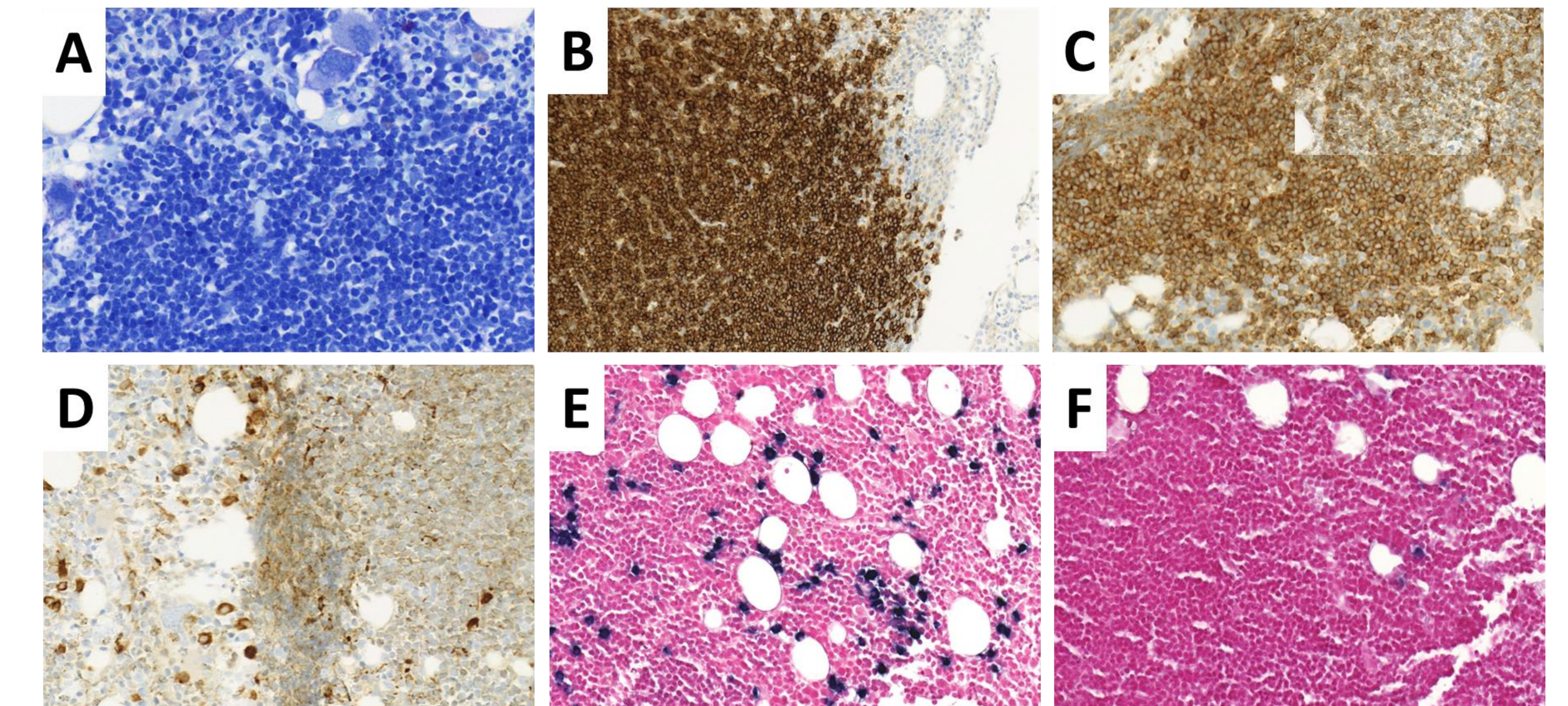
- Oncogenic mutations are associated with progressive disease ( $p = 0.015$ ) and transformation ( $p = 0.01$ ); a low mast cell count is associated with progression ( $p = 0.022$ )
- a diffuse infiltration pattern predicts a worse PFS (see fig. 1).



**Figure 1:** Kaplan-Meier survival analysis for progression free survival A significantly longer PFS was seen in patients with a paratrabeular and interstitial infiltration pattern compared to those with a purely interstitial pattern (N= number of events/number of patients)

## Literature

1. Wang W, Lin P. Pathology. 2020;52(1):6-14.
2. Owen RG, Treon SP, Al-Katib A et al. Semin Oncol. 2003;30(2):110-5.
3. Gertz MA. Am J Hematol. 2023;98(2):348-58.



**Figure 2:** SBCL-PC finally diagnosed as CLL with a predominant lymphocytic infiltrate A) positive for CD20 (B), CD5 (C) and CD23 (C-inlet), but admixed clonal plasmacells (D – Vs38c; E and F: kappa and lambda in situ hybridisation) and MYD88L265P mutation

## Discussion

- Assessment of classical morphological features is a prerequisite in the diagnosis of WM
- Careful morphological evaluation, immune phenotyping and molecular analysis in debatable cases best way to achieve a proper diagnosis
- Overlapping features exist in the SBCL-PC group including shared mutations with CLL such as POT1, FBXW7, XPO1.

**Patients with LPL/WM might benefit from thorough pathological work-up and detailed molecular analysis in terms of a precise diagnosis and targeted treatment allocation.**

4. Naderi N, Yang DT. Arch Pathol Lab Med. 2013;137(4):580-5.
5. W6. Treon SP, Tripsas CK, Meid K, et al. N Engl J Med. 2015;372(15):1430-40.
6. Willenbacher W, Willenbacher E, Brunner A, et al. Br J Haematol. 2013;161(6):902-4.
7. Treon SP, Hunter ZR, Branagan AR et al. Castillo JJ. Hemasphere. 2019;3(Suppl).
8. Varettoni M, Zibellini S, Defrancesco I, et al. Haematologica. 2017;102(12):2077-85