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| cLINICAL UTILITY OF MOLECULAR TESTING IN  THE INVESTIGATION OF POSSIBLE T-CELL LYMPHOMA  DIAGNOSTIC utility  The differentiation of reactive and malignant T-cell processes can be difficult based on histological features alone.  Historically, T-cell receptor gene rearrangement studies have been performed however these generally lack sufficient sensitivity and specificity to reliably distinguish reactive from clonal (and oligoclonal) T-cell proliferations1-4.  As well as serving as markers of a clonal process within the specimen, the detection of variants in *TET2*, *DNMT3A*, *JAK3*, *STAT3*, *STAT5B*, *FYN*, *RHOA*, *IDH2* (Arg172), *NOTCH1* and *PLCG1* on this panel support a diagnosis of T-cell lymphoma and aid subclassification5.  Whilst the absence of variants detected in the genes listed above in this assay make T-cell lymphoma less likely, investigation of further genomic markers of T-cell lymphoma should be considered including other gene mutations (*e.g.* *DDX3X*, *KMT2D*), copy number changes and structural variants (*e.g.* inv(14)(q11q32) in T-PLL) depending on clinicopathological context.  REFERENCES  **1.** Syrykh C, et al. Molecular Diagnosis of T-cell Lymphoma: A correlative study of PCR-based T-cell clonality assessment and targeted NGS. *Blood Adv* 2021. **2.** Mahe E, et al. T cell clonality assessment: past, present and future. *J Clin Pathol* 2018; **71**(3): 195-200. **3.** Bagg A, et al. Immunoglobulin Heavy Chain Gene Analysis in Lymphomas. *J Mol Diagn* 2002; **4**(2): 81-9. **4.** Cushman-Vokoun AM, et al. Assay design affects the interpretation of T-cell receptor gamma gene rearrangements: comparison of the performance of a one-tube assay with the BIOMED-2-based TCRG gene clonality assay. *J Mol Diagn* 2010; **12**(6): 787-96. **5.** Swerdlow SH CE, Harris NL, Jaffe ES, Pileri SA, Stein H, Thiele J. WHO Classification of Tumours of Haematopoietic and Lymphoid Tissues (revised 4th edition). Lyon: IARC; 2017. |